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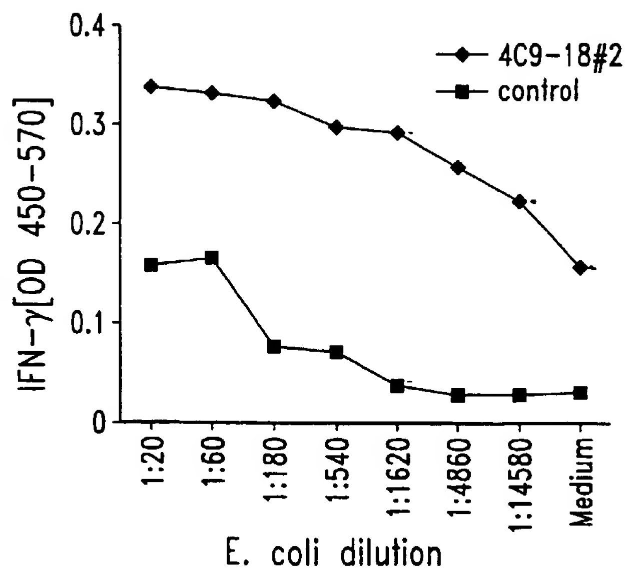
(54) Title: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION



(57) Abstract: Compounds and methods for the diagnosis and treatment of Chlamydial infection are disclosed. The compounds provided include polypeptides that contain at least one antigenic portion of a *Chlamydia* antigen and DNA sequences encoding such polypeptides. Pharmaceutical compositions and vaccines comprising such polypeptides or DNA sequences are also provided, together with antibodies directed against such polypeptides. Diagnostic kits containing such polypeptides or DNA sequences and a suitable detection reagent may be used for the detection of Chlamydial infection in patients and in biological samples.

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COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

TECHNICAL FIELD

The present invention relates generally to the detection and treatment of Chlamydial infection. In particular, the invention is related to polypeptides comprising a *Chlamydia* antigen and the use of such polypeptides for the serodiagnosis and treatment of Chlamydial infection.

BACKGROUND OF THE INVENTION

Chlamydiae are intracellular bacterial pathogens that are responsible for a wide variety of important human and animal infections. *Chlamydia trachomatis* is one of the most common causes of sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. *Chlamydia trachomatis* may also play a role in male infertility. In 1990, the cost of treating PID in the US was estimated to be $4 billion. Trachoma, due to ocular infection with *Chlamydia trachomatis*, is the leading cause of preventable blindness worldwide. *Chlamydia pneumonia* is a major cause of acute respiratory tract infections in humans and is also believed to play a role in the pathogenesis of atherosclerosis and, in particular, coronary heart disease. Individuals with a high titer of antibodies to *Chlamydia pneumonia* have been shown to be at least twice as likely to suffer from coronary heart disease as seronegative individuals. Chlamydial infections thus constitute a significant health problem both in the US and worldwide.

Chlamydial infection is often asymptomatic. For example, by the time a woman seeks medical attention for PID, irreversible damage may have already occurred resulting in infertility. There thus remains a need in the art for improved vaccines and pharmaceutical compositions for the prevention and treatment of *Chlamydia* infections. The present invention fulfills this need and further provides other related advantages.

SUMMARY OF THE INVENTION

The present invention provides compositions and methods for the diagnosis and therapy of *Chlamydia* infection. In one aspect, the present invention

provides polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, or a variant of such an antigen. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments,, the polypeptide comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of (a) a sequence of SEQ ID NO: 358-361, 366-385, 406-430, 455-489, 516-517, 523-559, and 582-596; (b) the complements of said sequences; and (c) sequences that hybridize to a sequence of (a) or (b) under moderate to highly stringent conditions. In specific embodiments, the polypeptides of the present invention comprise at least a portion of a *Chlamydial* protein that includes an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO:362-365, 386-405, 431-454, 490-515, 518-522, 560-581, and 597-599 and variants thereof.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a *Chlamydial* protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

In a related aspect, polynucleotide sequences encoding the above polypeptides, recombinant expression vectors comprising one or more of these polynucleotide sequences and host cells transformed or transfected with such expression vectors are also provided.

In another aspect, the present invention provides fusion proteins comprising an inventive polypeptide, or, alternatively, an inventive polypeptide and a known *Chlamydia* antigen, as well as polynucleotides encoding such fusion proteins, in combination with a physiologically acceptable carrier or immunostimulant for use as pharmaceutical compositions and vaccines thereof.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody, both polyclonal and monoclonal, or antigen-binding fragment thereof that specifically binds to a *Chlamydial* protein; and (b) a physiologically acceptable carrier. Within other aspects, the present invention provides pharmaceutical compositions that comprise one or more *Chlamydia* polypeptides disclosed herein, e.g., a polypeptide according to SEQ ID NO:362-365, 386-405, 431-454, 490-515, 518-522, 560-581, and 597-599, or a polynucleotide molecule encoding

such a polypeptide, such as a polynucleotide according to SEQ ID NO:358-361, 366-385, 406-430, 455-489, 516-517, 523-559, and 582-596, and a physiologically acceptable carrier. The invention also provides vaccines for prophylactic and therapeutic purposes comprising one or more of the disclosed polypeptides and an immunostimulant, as defined herein, together with vaccines comprising one or more polynucleotide sequences encoding such polypeptides and an immunostimulant.

In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above pharmaceutical compositions or vaccines.

In yet a further aspect, methods for the treatment of *Chlamydia* infection in a patient are provided, the methods comprising obtaining peripheral blood mononuclear cells (PBMC) from the patient, incubating the PBMC with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated T cells and administering the incubated T cells to the patient. The present invention additionally provides methods for the treatment of *Chlamydia* infection that comprise incubating antigen presenting cells with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated antigen presenting cells and administering the incubated antigen presenting cells to the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient. In certain embodiments, the antigen presenting cells are selected from the group consisting of dendritic cells, macrophages, monocytes, B-cells, and fibroblasts. Compositions for the treatment of *Chlamydia* infection comprising T cells or antigen presenting cells that have been incubated with a polypeptide or polynucleotide of the present invention are also provided. Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, within other aspects, methods for removing *Chlamydial*-infected cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a *Chlamydial* protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of *Chlamydial* infection in a patient, comprising administering to a patient a biological sample treated as described above. In further aspects of the subject invention, methods and diagnostic kits are provided for detecting *Chlamydia* infection in a patient. In one embodiment, the method comprises: (a) contacting a biological sample with at least one of the polypeptides or fusion proteins disclosed herein; and (b) detecting in the sample the presence of binding agents that bind to the polypeptide or fusion protein, thereby detecting *Chlamydia* infection in the biological sample. Suitable biological samples include whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine. In one embodiment, the diagnostic kits comprise one or more of the polypeptides or fusion proteins disclosed herein in combination with a detection reagent. In yet another embodiment, the diagnostic kits comprise either a monoclonal antibody or a polyclonal antibody that binds with a polypeptide of the present invention.

The present invention also provides methods for detecting *Chlamydia* infection comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers. In one embodiment, the oligonucleotide primer comprises at least about 10 contiguous nucleotides of a polynucleotide sequence peptide disclosed herein, or of a sequence that hybridizes thereto.

In a further aspect, the present invention provides a method for detecting *Chlamydia* infection in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe. In one embodiment, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence disclosed herein, or a sequence that hybridizes thereto.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are

hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined DNA sequence for the *C. trachomatis* clone 1-B1-66.

SEQ ID NO: 2 is the determined DNA sequence for the *C. trachomatis* clone 4-D7-28.

SEQ ID NO: 3 is the determined DNA sequence for the *C. trachomatis* clone 3-G3-10.

SEQ ID NO: 4 is the determined DNA sequence for the *C. trachomatis* clone 10-C10-31.

SEQ ID NO: 5 is the predicted amino acid sequence for 1-B1-66.

SEQ ID NO: 6 is the predicted amino acid sequence for 4-D7-28.

SEQ ID NO: 7 is a first predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 8 is a second predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 9 is a third predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 10 is a fourth predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 11 is a fifth predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 12 is the predicted amino acid sequence for 10-C10-31.

SEQ ID NO: 13 is the amino acid sequence of the synthetic peptide 1-B1-66/48-67.

SEQ ID NO: 14 is the amino acid sequence of the synthetic peptide 1-B1-66/58-77.

SEQ ID NO: 15 is the determined DNA sequence for the *C. trachomatis* serovar LGV II clone 2C7-8

SEQ ID NO: 16 is a DNA sequence of a putative open reading frame from a region of the*C. trachomatis* serovar D genome to which 2C7-8 maps

SEQ ID NO: 17 is the predicted amino acid sequence encoded by the DNA sequence of SEQ ID NO: 16

SEQ ID NO: 18 is the amino acid sequence of the synthetic peptide CtC7.8-12

SEQ ID NO: 19 is the amino acid sequence of the synthetic peptide CtC7.8-13

SEQ ID NO: 20 is the predicted amino acid sequence encoded by a second putative open reading from *C. trachomatis* serovar D

SEQ ID NO: 21 is the determined DNA sequence for clone 4C9-18 from *C. trachomatis* LGV II

SEQ ID NO: 22 is the determined DNA sequence homologous to Lipoamide Dehydrogenase from *C. trachomatis* LGV II

SEQ ID NO: 23 is the determined DNA sequence homologous to Hypothetical protein from *C. trachomatis* LGV II

SEQ ID NO: 24 is the determined DNA sequence homologous to Ubiquinone Mehtyltransferase from *C. trachomatis* LGV II

SEQ ID NO: 25 is the determined DNA sequence for clone 4C9-18#2 BL21 pLysS from *C. trachomatis* LGV II

SEQ ID NO: 26 is the predicted amino acid sequence for 4C9-18#2 from *C. trachomatis* LGV II

SEQ ID NO: 27 is the determined DNA sequence for Cp-SWIB from *C. pneumonia* strain TWAR

SEQ ID NO: 28 is the predicted amino acid sequence for Cp-SWIB from *C. pneumonia* strain TWAR

SEQ ID NO: 29 is the determined DNA sequence for Cp-S13 (CT509) from *C. pneumonia* strain TWAR

SEQ ID NO: 30 is the predicted amino acid sequence for Cp-S13 from *C. pneumonia* strain TWAR

SEQ ID NO: 31 is the amino acid sequence for a 10mer consensus peptide from CtC7.8-12 and CtC7.8-13

SEQ ID NO: 32 is the predicted amino acid sequence for clone 2C7-8 from *C. trachomatis* LGV II

SEQ ID NO: 33 is the DNA sequence corresponding to nucleotides 597304-597145 of the *C. trachomatis* serovar D genome (NCBI, BLASTN search), which shows homology to clone 2C7-8

SEQ ID NO: 34 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 33

SEQ ID NO: 35 is the DNA sequence for C.p. SWIB Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 36 is the DNA sequence for C.p. SWIB EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO : 37 is the DNA sequence for C.p. S13 Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 38 is the DNA sequence for C.p. S13 EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO: 39 is the amino acid sequence for CtSwib 52-67 peptide from *C. trachomatis* LGV II

SEQ ID NO: 40 is the amino acid sequence for CpSwib 53-68 peptide from *C. pneumonia*

SEQ ID NO: 41 is the amino acid sequence for HuSwib 288-302 peptide from Human SWI domain

SEQ ID NO: 42 is the amino acid sequence for CtSWI-T 822-837 peptide from the topoisomerase-SWIB fusion of *C. trachomatis*

SEQ ID NO: 43 is the amino acid sequence for CpSWI-T 828-842 peptide from the topoisomerase-SWIB fusion of *C. pneumonia*

SEQ ID NO: 44 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19783.3,jen.seq(1>509)CTL2#11-3', representing the 3' end.

SEQ ID NO: 45 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19783.4,jen.seq(1>481)CTL2#11-5', representing the 5' end.

SEQ ID NO: 46 is the determined DNA sequence for the *C. trachomatis* LGV II clone19784CTL2_12consensus.seq(1>427)CTL2#12.

SEQ ID NO: 47 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19785.4,jen.seq(1>600)CTL2#16-5', representing the 5' end.

SEQ ID NO: 48 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19786.3,jen.seq(1>600)CTL2#18-3', representing the 3' end.

SEQ ID NO: 49 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19786.4,jen.seq(1>600)CTL2#18-5', representing the 5' end.

SEQ ID NO: 50 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19788CTL2_21consensus.seq(1>406)CTL2#21.

SEQ ID NO: 51 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19790CTL2_23consensus.seq(1>602)CTL2#23.

SEQ ID NO: 52 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19791CTL2_24consensus.seq(1>145)CTL2#24.

SEQ ID NO: 53 is the determined DNA sequence for the *C. trachomatis* LGV II clone CTL2#4.

SEQ ID NO: 54 is the determined DNA sequence for the *C. trachomatis* LGV II clone CTL2#8b.

SEQ ID NO: 55 is the determined DNA sequence for the *C. trachomatis* LGV II clone15-G1-89, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 56 is the determined DNA sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 57 is the determined DNA sequence for the *C. trachomatis* LGV II clone 12-G3-83, sharing homology to the hypothetical protein CT622.

SEQ ID NO: 58 is the determined DNA sequence for the *C. trachomatis* LGV II clone 12-B3-95, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 59 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-H4-28, sharing homology to the dnaK gene CT396.

SEQ ID NO: 60 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-H3-68, sharing partial homology to the PGP6-D virulence protein and L1 ribosomal gene CT318.

SEQ ID NO: 61 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-G1-34, sharing partial homology to the malate dehydrogenase gene CT376 and to the glycogen hydrolase gene CT042.

SEQ ID NO: 62 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-G10-46, sharing homology to the hypothetical protein CT610.

SEQ ID NO: 63 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-C12-91, sharing homology to the OMP2 gene CT443.

SEQ ID NO: 64 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-A3-93, sharing homology to the HAD superfamily gene CT103.

SEQ ID NO: 65 is the determined amino acid sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 66 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#9.

SEQ ID NO: 67 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#7.

SEQ ID NO: 68 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#6.

SEQ ID NO: 69 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#5.

SEQ ID NO: 70 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#2.

SEQ ID NO: 71 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#1.

SEQ ID NO: 72 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 23509.2CtL2#3-5', representing the 5' end.

SEQ ID NO: 73 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 23509.1CtL2#3-3', representing the 3' end.

SEQ ID NO: 74 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 22121.2CtL2#10-5', representing the 5' end.

SEQ ID NO: 75 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 22121.1CtL2#10-3', representing the 3' end.

SEQ ID NO: 76 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19787.6CtL2#19-5', representing the 5' end.

SEQ ID NO: 77 is the determined DNA sequence for the *C. pneumoniae* LGV II clone CpS13-His.

SEQ ID NO: 78 is the determined DNA sequence for the *C. pneumoniae* LGV II clone Cp_SWIB-His.

SEQ ID NO: 79 is the determined DNA sequence for the *C. trachomatis* LGV II clone 23-G7-68, sharing partial homology to the L11, L10 and L1 ribosomal protein.

SEQ ID NO: 80 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-F8-91, sharing homology to the pmpC gene.

SEQ ID NO: 81 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-E8-95, sharing homology to the CT610-CT613 genes.

SEQ ID NO: 82 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-57, sharing homology to the CT858 and recA genes.

SEQ ID NO: 83 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-53, sharing homology to the CT445 gene encoding glutamyl tRNA synthetase.

SEQ ID NO: 84 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-A5-54, sharing homology to the cryptic plasmid gene.

SEQ ID NO: 85 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E11-72, sharing partial homology to the OppC_2 and pmpD genes.

SEQ ID NO: 86 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C1-77, sharing partial homology to the CT857 and CT858 open reading frames.

SEQ ID NO: 87 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-H2-76, sharing partial homology to the pmpD and SycE genes, and to the CT089 ORF.

SEQ ID NO: 88 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-A3-26, sharing homology to the CT858 ORF.

SEQ ID NO: 89 is the determined amino acid sequence for the *C. pnuemoniae* clone Cp_SWIB-His.

SEQ ID NO: 90 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_LPDA_FL.

SEQ ID NO: 91 is the determined amino acid sequence for the *C. pnuemoniae* clone CpS13-His.

SEQ ID NO: 92 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_TSA_FL.

SEQ ID NO: 93 is the amino acid sequence for Ct-Swib 43-61 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 94 is the amino acid sequence for Ct-Swib 48-67 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 95 is the amino acid sequence for Ct-Swib 52-71 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 96 is the amino acid sequence for Ct-Swib 58-77 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 97 is the amino acid sequence for Ct-Swib 63-82 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 98 is the amino acid sequence for Ct-Swib 51-66 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 99 is the amino acid sequence for Cp-Swib 52-67 peptide from *C. pneumonia*.

SEQ ID NO: 100 is the amino acid sequence for Cp-Swib 37-51 peptide from *C. pneumonia*.

SEQ ID NO: 101 is the amino acid sequence for Cp-Swib 32-51 peptide from *C. pneumonia*.

SEQ ID NO: 102 is the amino acid sequence for Cp-Swib 37-56 peptide from *C. pneumonia*.

SEQ ID NO: 103 is the amino acid sequence for Ct-Swib 36-50 peptide from *C. trachomatis*.

SEQ ID NO: 104 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 105 is the amino acid sequence for Ct-S13 60-80 peptide from *C. trachomatis*.

SEQ ID NO: 106 is the amino acid sequence for Ct-S13 1-20 peptide from *C. trachomatis*.

SEQ ID NO: 107 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 108 is the amino acid sequence for Ct-S13 56-75 peptide from *C. trachomatis*.

SEQ ID NO: 109 is the amino acid sequence for Cp-S13 56-75 peptide from *C. pneumoniae.*

SEQ ID NO: 110 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-G12-60, containing partial open reading frames for hypothetical proteins CT875, CT229 and CT228.

SEQ ID NO: 111 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-B3-53, sharing homology to the CT110 ORF of GroEL.

SEQ ID NO: 112 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-A1-49, sharing partial homology to the CT660 and CT659 ORFs.

SEQ ID NO: 113 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E2-9, sharing partial homology to the CT611 and CT 610 ORFs.

SEQ ID NO: 114 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C10-31, sharing partial homology to the CT858 ORF.

SEQ ID NO: 115 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-C7-8, sharing homology to the dnaK-like gene.

SEQ ID NO: 116 is the determined DNA sequence for the *C. trachomatis* LGV II clone 20-G3-45, containing part of the pmpB gene CT413.

SEQ ID NO: 117 is the determined DNA sequence for the *C. trachomatis* LGV II clone 18-C5-2, sharing homology to the S1 ribosomal protein ORF.

SEQ ID NO: 118 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C5-19, containing part of the ORFs for CT431 and CT430.

SEQ ID NO: 119 is the determined DNA sequence for the *C. trachomatis* LGV II clone 16-D4-22, contains partial sequences of ORF3 and ORF4 of the plasmid for growth within mammalian cells.

SEQ ID NO: 120 is the determined full-length DNA sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 121 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 122 is the determined full-length DNA sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 123 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 124 is the determined full-length DNA sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 125 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 126 is the determined full-length DNA sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 127 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 128 is the determined full-length DNA sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 129 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 130 is the determined full-length DNA sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

SEQ ID NO: 131 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

SEQ ID NO: 132 is the determined full-length DNA sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.

SEQ ID NO: 133 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.

SEQ ID NO: 134 is the determined full-length DNA sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.

SEQ ID NO: 135 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.

SEQ ID NO: 136 is the determined full-length DNA sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.

SEQ ID NO: 137 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.

SEQ ID NO: 138 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #124-139 of *C. trachomatis* serovar L2.

SEQ ID NO: 139 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #132-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 140 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-155 of *C. trachomatis* serovar L2.

SEQ ID NO: 141 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #146-163 of *C. trachomatis* serovar L2.

SEQ ID NO: 142 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #154-171 of *C. trachomatis* serovar L2.

SEQ ID NO: 143 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #162-178 of *C. trachomatis* serovar L2.

SEQ ID NO: 144 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 145 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #139-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 146 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #140-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 147 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-146 of *C. trachomatis* serovar L2.

SEQ ID NO: 148 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-145 of *C. trachomatis* serovar L2.

SEQ ID NO: 149 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # F140->I of *C. trachomatis* serovar L2.

SEQ ID NO: 150 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # #S139>Ga of *C. trachomatis* serovar L2.

SEQ ID NO: 151 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # #S139>Gb of *C. trachomatis* serovar L2.

SEQ ID NO: 152 is the determined amino acid sequence for the peptide # 2 C7.8-6 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 153 is the determined amino acid sequence for the peptide # 2 C7.8-7 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 154 is the determined amino acid sequence for the peptide # 2 C7.8-8 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 155 is the determined amino acid sequence for the peptide # 2 C7.8-9 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 156 is the determined amino acid sequence for the peptide # 2 C7.8-10 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 157 is the determined amino acid sequence for the 53 amino acid residue peptide of the 216aa ORF within clone 2C7.8 of *C. trachomatis* serovar L2.

SEQ ID NO: 158 is the determined amino acid sequence for the 52 amino acid residue peptide of the CT529 ORF within clone 2C7.8 of *C. trachomatis* serovar L2.

SEQ ID NO: 159 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 160 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 161 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 for serovars other than L2 and MOPN.

SEQ ID NO: 162 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovars other than L2 and MOPN.

SEQ ID NO: 163 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 164 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 165 is the determined DNA sequence for the 5' (forward) primer for pBIB-KS.

SEQ ID NO: 166 is the determined DNA sequence for the 5' (reverse) primer for pBIB-KS.

SEQ ID NO: 167 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar L2.

SEQ ID NO: 168 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar D.

SEQ ID NO: 169 is the determined full-length DNA sequence for the *C. trachomatis* pmpI (CT874) gene.

SEQ ID NO: 170 is the determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 171 is the determined full-length DNA sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 172 is the determined full-length DNA sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 173 is the determined full-length DNA sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 174 is the determined full-length DNA sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 175 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 176 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 177 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 178 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 179 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 180 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 181 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 182 is a subsequently determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 183 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 184 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 185 is a second determined DNA sequence representing the amino terminus minus the signal sequnce for the *C. trachomatis* pmpD gene.

SEQ ID NO: 186 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 187 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 188 is the determined DNA sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 189 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 190 is subsequently predicted amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 191 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 192 is a first predicted amino acid sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 193 is a second predicted amino acid sequence representing the Amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 194 is a first predicted amino acid sequence representing the Carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 195 is a second predicted amino acid sequence representing the Amino terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 196 is the predicted amino acid sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 197 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 198 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 199 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 200 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 201 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 202 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 203 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 204 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 205 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 206 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 207 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 208 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 209 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 210 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 211 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 212 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 213 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 214 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 215 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 216 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 217 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 218 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 219 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 220 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 221 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 222 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 223 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 224 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 1-20.

SEQ ID NO: 225 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 6-25.

SEQ ID NO: 226 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 12-31.

SEQ ID NO: 227 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 17-36.

SEQ ID NO: 228 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 22-41.

SEQ ID NO: 229 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 27-46.

SEQ ID NO: 230 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 42-61.

SEQ ID NO: 231 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 46-65.

SEQ ID NO: 232 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 51-70.

SEQ ID NO: 233 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 56-75.

SEQ ID NO: 234 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 61-80.

SEQ ID NO: 235 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 66-87.

SEQ ID NO: 236 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 103-122.

SEQ ID NO: 237 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 108-127.

SEQ ID NO: 238 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 113-132.

SEQ ID NO: 239 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 118-137.

SEQ ID NO: 240 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 123-143.

SEQ ID NO: 241 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 128-147.

SEQ ID NO: 242 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 133-152.

SEQ ID NO: 243 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 137-156.

SEQ ID NO: 244 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 142-161.

SEQ ID NO: 245 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 147-166.

SEQ ID NO: 246 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 152-171.

SEQ ID NO: 247 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 157-176.

SEQ ID NO: 248 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 162-181.

SEQ ID NO: 249 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 167-186.

SEQ ID NO: 250 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-190.

SEQ ID NO: 251 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.

SEQ ID NO: 253 is the determined amino acid sequence for the *C. pneumoniae* OMCB peptide 185-198.

SEQ ID NO: 254 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 96-115.

SEQ ID NO: 255 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 101-120.

SEQ ID NO: 256 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 106-125.

SEQ ID NO: 257 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 111-130.

SEQ ID NO: 258 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 116-135.

SEQ ID NO: 259 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 121-140.

SEQ ID NO: 260 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 126-145.

SEQ ID NO: 261 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 131-150.

SEQ ID NO: 262 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 136-155.

SEQ ID NO: 263 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 264 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 265 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 266 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 267 is the determined DNA sequence for the *C. trachomatis* clone 17-G4-36 sharing homology to part of the ORF of DNA-dirrected RNA polymerase beta subunit- CT315 in serD.

SEQ ID NO: 268 is the determined DNA sequence for the partial sequence of the *C. trachomatis* CT016 gene in clone 2E10.

SEQ ID NO: 269 is the determined DNA sequence for the partial sequence of the *C. trachomatis* tRNA syntase gene in clone 2E10.

SEQ ID NO: 270 is the determined DNA sequence for the partial sequence for the *C. trachomatis* clpX gene in clone 2E10.

SEQ ID NO: 271 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-30 representing the 5'end.

SEQ ID NO: 272 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-30 representing the 3'end.

SEQ ID NO: 273 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-28.

SEQ ID NO: 274 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-27.

SEQ ID NO: 275 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-26.

SEQ ID NO: 276 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-24.

SEQ ID NO: 277 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-23.

SEQ ID NO: 278 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-21.

SEQ ID NO: 279 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-18.

SEQ ID NO: 280 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-17.

SEQ ID NO: 281 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 5' end.

SEQ ID NO: 282 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 3' end.

SEQ ID NO: 283 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-13.

SEQ ID NO: 284 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-10.

SEQ ID NO: 285 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-8.

SEQ ID NO: 286 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 5' end.

SEQ ID NO: 287 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 3' end.

SEQ ID NO: 288 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-5.

SEQ ID NO: 289 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-2.

SEQ ID NO: 290 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-1.

SEQ ID NO: 291 is the determined full-length DNA sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 292 is the predicted full-length amino acid sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 293 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 294 is the amino acid sequence of an open reading frame of clone CT603.

SEQ ID NO: 295 is the amino acid sequence of a first open reading frame of clone CT875.

SEQ ID NO: 296 is the amino acid sequence of a second open reading frame of clone CT875.

SEQ ID NO: 297 is the amino acid sequence of a first open reading frame of clone CT858.

SEQ ID NO: 298 is the amino acid sequence of a second open reading frame of clone CT858.

SEQ ID NO: 299 is the amino acid sequence of an open reading frame of clone CT622.

SEQ ID NO: 300 is the amino acid sequence of an open reading frame of clone CT610.

SEQ ID NO: 301 is the amino acid sequence of an open reading frame of clone CT396.

SEQ ID NO: 302 is the amino acid sequence of an open reading frame of clone CT318.

SEQ ID NO: 304 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125 having a modified N-terminal sequence (6-His tag).

SEQ ID NO: 305 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125.

SEQ ID NO: 306 is the sense primer used in the synthesis of the PmpA(N-term) fusion protein.

SEQ ID NO: 307 is the antisense primer used in the synthesis of the PmpA(N-term) fusion protein.

SEQ ID NO: 308 is the DNA sequence encoding the PmpA(N-term) fusion protein.

SEQ ID NO: 309 is the amino acid sequence of the PmpA(N-term) fusion protein.

SEQ ID NO: 310 is the sense primer used in the synthesis of the PmpA(C-term) fusion protein.

SEQ ID NO: 311 is the antisense primer used in the synthesis of the PmpA(C-term) fusion protein.

SEQ ID NO: 312 is the DNA sequence encoding the PmpA(C-term) fusion protein.

SEQ ID NO: 313 is the amino acid sequence of the PmpA(C-term) fusion protein.

SEQ ID NO: 314 is the sense primer used in the synthesis of the PmpF(N-term) fusion protein.

SEQ ID NO: 315 is the antisense primer used in the synthesis of the PmpF(N-term) fusion protein.

SEQ ID NO: 316 is the DNA sequence encoding the PmpF(N-term) fusion protein.

SEQ ID NO: 317 is the amino acid sequence of the PmpF(N-term) fusion protein.

SEQ ID NO: 318 is the sense primer used in the synthesis of the PmpF(C-term) fusion protein.

SEQ ID NO: 319 is the antisense primer used in the synthesis of the PmpF(C-term) fusion protein.

SEQ ID NO: 320 is the DNA sequence encoding the PmpF(C-term) fusion protein.

SEQ ID NO: 321 is the amino acid sequence of the PmpF(C-term) fusion protein.

SEQ ID NO: 322 is the sense primer used in the synthesis of the PmpH (CT412) (N-term) fusion protein.

SEQ ID NO: 323 is the antisense primer used in the synthesis of the PmpH(N-term) fusion protein.

SEQ ID NO: 324 is the DNA sequence encoding the PmpH(N-term) fusion protein.

SEQ ID NO: 325 is the amino acid sequence of the PmpH(N-term) fusion protein.

SEQ ID NO: 326 is the sense primer used in the synthesis of the PmpH(C-term) fusion protein.

SEQ ID NO: 327 is the antisense primer used in the synthesis of the PmpH(C-term) fusion protein.

SEQ ID NO: 328 is the DNA sequence encoding the PmpH(C-term) fusion protein.

SEQ ID NO: 329 is the amino acid sequence of the PmpH(C-term) fusion protein.

SEQ ID NO: 330 is the sense primer used in the synthesis of the PmpB(1) fusion protein.

SEQ ID NO: 331 is the antisense primer used in the synthesis of the PmpB(1) fusion protein.

SEQ ID NO: 332 is the DNA sequence encoding the PmpB(1) fusion protein.

SEQ ID NO: 333 is the amino acid sequence of the PmpB(1) fusion protein.

SEQ ID NO: 334 is the sense primer used in the synthesis of the PmpB(2) fusion protein.

SEQ ID NO: 335 is the antisense primer used in the synthesis of the PmpB(2) fusion protein.

SEQ ID NO: 336 is the DNA sequence encoding the PmpB(2) fusion protein.

SEQ ID NO: 337 is the amino acid sequence of the PmpB(2) fusion protein.

SEQ ID NO: 338 is the sense primer used in the synthesis of the PmpB(3) fusion protein.

SEQ ID NO: 339 is the antisense primer used in the synthesis of the PmpB(3) fusion protein.

SEQ ID NO: 340 is the DNA sequence encoding the PmpB(3) fusion protein.

SEQ ID NO: 341 is the amino acid sequence of the PmpB(3) fusion protein.

SEQ ID NO: 342 is the sense primer used in the synthesis of the PmpB(4) fusion protein.

SEQ ID NO: 343 is the antisense primer used in the synthesis of the PmpB(4) fusion protein.

SEQ ID NO: 344 is the DNA sequence encoding the PmpB(4) fusion protein.

SEQ ID NO: 345 is the amino acid sequence of the PmpB(4) fusion protein.

SEQ ID NO: 346 is the sense primer used in the synthesis of the PmpC(1) fusion protein.

SEQ ID NO: 347 is the antisense primer used in the synthesis of the PmpC(1) fusion protein.

SEQ ID NO: 348 is the DNA sequence encoding the PmpC(1) fusion protein.

SEQ ID NO: 349 is the amino acid sequence of the PmpC(1) fusion protein.

SEQ ID NO: 350 is the sense primer used in the synthesis of the PmpC(2) fusion protein.

SEQ ID NO: 351 is the antisense primer used in the synthesis of the PmpC(2) fusion protein.

SEQ ID NO: 352 is the DNA sequence encoding the PmpC(2) fusion protein.

SEQ ID NO: 353 is the amino acid sequence of the PmpC(2) fusion protein.

SEQ ID NO: 354 is the sense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 355 is the antisense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 356 is the DNA sequence encoding the PmpC(3) fusion protein.

SEQ ID NO: 357 is the amino acid sequence of the PmpC(3) fusion protein.

SEQ ID NO: 358 is the DNA sequence of the oppA1 protein, devoid of the first trans-membrane domain.

SEQ ID NO: 359 is the full length DNA sequence of CT139.

SEQ ID NO: 360 is the full length DNA sequence of ORF-3.

SEQ ID NO: 361 is the full length DNA sequence of CT611.

SEQ ID NO: 362 is the amino acid sequence of oppA1 starting from amino acid 22.

SEQ ID NO: 363 is the amino acid sequence of CT139.

SEQ ID NO: 364 is the amino acid sequence of ORF-3.

SEQ ID NO: 365 is the amino acid sequence of CT611.

SEQ ID NO: 366 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0275, of the Chlamydia trachomatis gene CT190.

SEQ ID NO: 367 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0407, of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 368 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0720, of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 369 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0716, of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 370 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0519, of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 371 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0520, of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 372 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0078, of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 373 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0628, of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 374 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0540, of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 375 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, pmp20, of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 376 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0081, of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 377 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0761, of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 378 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0557, of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 379 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0833, of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 380 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0134, of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 381 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0388, of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 382 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn1028, of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 383 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0875, of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 384 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0908, of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 385 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0728, of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 386 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0275, of the Chlamydia trachomatis gene CT190.

SEQ ID NO: 387 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0407, of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 388 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0720, of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 389 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0716, of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 390 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0519, of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 391 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0520, of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 392 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0078, of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 393 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0628, of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 394 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0540, of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 395 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, pmp20, of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 396 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0081, of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 397 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0761, of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 398 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0557, of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 399 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0833, of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 400 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0134, of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 401 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0388, of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 402 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn1028, of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 403 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0875, of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 404 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0908, of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 405 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0728, of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 406 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT287.

SEQ ID NO: 407 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT858.

SEQ ID NO: 408 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 409 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 410 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 411 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 412 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 413 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 414 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 415 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 416 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 417 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 418 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 419 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 420 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 421 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 422 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT396.

SEQ ID NO: 423 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 424 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 425 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 426 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT104.

SEQ ID NO: 427 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 428 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 429 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 430 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 431 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT858.

SEQ ID NO: 432 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 433 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 434 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 435 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 436 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 437 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 438 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 439 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 440 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 441 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 442 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 443 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 444 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 445 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 446 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT396.

SEQ ID NO: 447 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 448 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 449 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 450 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT104.

SEQ ID NO: 451 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 452 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 453 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 454 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 455 corresponds to the DNA sequence of CPn0894, which is the CP homologue of CT751 (amn), which was identified in clones CTL2-1, and CTL2-5.

SEQ ID NO: 456 corresponds to the DNA sequence of CPn0074, which is the CP homologue of CT322 (tuf), which was identified in clone CTL2-2.

SEQ ID NO: 457 corresponds to the DNA sequence of CPn0122, which is the CP homologue of CT032 (metG), which was identified in clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 458 corresponds to the DNA sequence of CPn0121, which is the CP homologue of CT031, which was identified in clone CTL2-3(5')(3').

SEQ ID NO: 459 corresponds to the DNA sequence of CPn0120, which is the CP homologue of CT030 (gmK), which was identified in clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 460 corresponds to the DNA sequence of CPn0359, which is the CP homologue of CT064 (lepA), which was identified in clone CTL2gam5.

SEQ ID NO: 461 corresponds to the DNA sequence of CPn0414, which is the CP homologue of CT265 (accA), which was identified in clone CTL2-6.

SEQ ID NO: 462 corresponds to the DNA sequence of CPn0413, which is the CP homologue of CT264 (msbA), which was identified in clone CTL2-6.

SEQ ID NO: 463 corresponds to the DNA sequence of CPn0394, which is the CP homologue of CT256 which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 464 corresponds to the DNA sequence of CPn0395, which is the CP homologue of CT257 which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 465 corresponds to the DNA sequence of CPn0487, which is the CP homologue of CT384 which was identified in clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 466 corresponds to the DNA sequence of CPn0592, which is the CP homologue of CT473, which was identified in clone CTL2-8b.

SEQ ID NO: 467 corresponds to the DNA sequence of CPn0593, which is the CP homologue of CT474, which was identified in clone CTL2-8b.

SEQ ID NO: 468 corresponds to the DNA sequence of CPn0197, which is the CP homologue of CT139 (oppA1), which was identified in clone CTL2-8b.

SEQ ID NO: 469 corresponds to the DNA sequence of CPn0363, which is the CP homologue of CT060 (flhA), which was identified in clone CTL2-8b.

SEQ ID NO: 470 corresponds to the DNA sequence of CPn0301, which is the CP homologue of CT242, which was identified in clone CTL2gam8.

SEQ ID NO: 471 corresponds to the DNA sequence of CPn0302, which is the CP homologue of CT243 (lpxD), which was identified in clone CTL2gam8.

SEQ ID NO: 472 corresponds to the DNA sequence of CPn0324, which is the CP homologue of CT089 (lcrE), which was identified in clones CTL2-9, CTL2gam1, CTL2gam17 and CTL2-19(5').

SEQ ID NO: 473 corresponds to the DNA sequence of CPn0761, which is the CP homologue of CT610, which was identified in clone CTL2-10(5')(3').

SEQ ID NO: 474 corresponds to the DNA sequence of CPn0760, which is the CP homologue of CT611, which was identified in clone CTL2-10(5').

SEQ ID NO: 475 corresponds to the DNA sequence of CPn0329, which is the CP homologue of CT154, which was identified in clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 476 corresponds to the DNA sequence of CPn0990, which is the CP homologue of CT833 (infC), which was identified in clone CTL2-12.

SEQ ID NO: 477 corresponds to the DNA sequence of CPn0984, which is the CP homologue of CT827 (nrdA), which was identified in clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 478 corresponds to the DNA sequence of CPn0985 which is the CP homologue of CT828 (nrdB) which was identified in clones CTL2-16(3') CTL2gam15(3').

SEQ ID NO: 479 corresponds to the DNA sequence of CPn0349, which is the CP homologue of CT067 (ytgA), which was identified in clone CTL2gam18.

SEQ ID NO: 480 corresponds to the DNA sequence of CPn0325, which is the CP homologue of CT088 (sycE), which was identified in clone CTL2-19(5').

SEQ ID NO: 481 corresponds to the DNA sequence of CPn0326, which is the CP homologue of CT087 (malQ), which was identified in clone CTL2-19(5').

SEQ ID NO: 482 corresponds to the DNA sequence of CPn0793, which is the CP homologue of CT588 (rbsu), which was identified in clone CTL2gam23.

SEQ ID NO: 483 corresponds to the DNA sequence of CPn0199, which is the CP homologue of CT199 (oppB1), which was identified in clone CTL2gam24.

SEQ ID NO: 484 corresponds to the DNA sequence of CPn0666, which is the CP homologue of CT545 (dnaE), which was identified in clone CTL2-24.

SEQ ID NO: 485 corresponds to the DNA sequence of CPn0065, which is the CP homologue of CT288, which was identified in clone CTL2gam27.

SEQ ID NO: 486 corresponds to the DNA sequence of CPn0444, which is the CP homologue of CT413 (pmpB), which was identified in clone CTL2gam30(5')(3').

SEQ ID NO: 487 corresponds to the DNA sequence of CPn-ORF5, which is the CP homologue of CT-ORF3, which was identified in clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5'), and CTL2-23.

SEQ ID NO: 488 corresponds to the DNA sequence of CPn-ORF6, which is the CP homologue of CT-ORF4, which was identified in clone CTL2-18(3').

SEQ ID NO: 489 corresponds to the DNA sequence of CP-ORF7, which is the CP homologue of CT-ORF5, which was identified in clone CTL2-18(3').

SEQ ID NO: 490 corresponds to the amino acid sequence of CPn0894, which is the CP homologue of CT751 (amn), which was identified in clones CTL2-1 and CTL2-5.

SEQ ID NO: 491 corresponds to the amino acid sequence of CPn0074, which is the CP homologue of CT332 (tuf), which was identified in clone CTL2-2.

SEQ ID NO: 492 corresponds to the amino acid sequence of CPn0122, which is the CP homologue of CT032 (metG), which was identified in clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 493 corresponds to the amino acid sequence of CPn0121, which is the CP homologue of CT031, which was identified in clone CTL2-3(5')(3').

SEQ ID NO: 494 corresponds to the amino acid sequence of CPn0120 which is the CP homologue of CT030 (gmK) which was identified in clones CTL2-3 (3') and CTL2-21.

SEQ ID NO: 495 corresponds to the amino acid sequence of CPn0359, which is the CP homologue of CT064 (lepA), which was identified in clone CTL2gam5.

SEQ ID NO: 496 corresponds to the amino acid sequence of CPn0414, which is the CP homologue of CT265 (accA), which was identified in clone CTL2-6.

SEQ ID NO: 497 corresponds to the amino acid sequence of CPn0413, which is the CP homologue of CT264 (msbA), which was identified in clone CTL2-6.

SEQ ID NO: 498 corresponds to the amino acid sequence of CPn0394, which is the CP homologue of CT256, which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 499 corresponds to the amino acid sequence of CPn0395, which is the CP homologue of CT257, which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 500 corresponds to the amino acid sequence of CPn0487, which is the CP homologue of CT384, which was identified in clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 501 corresponds to the amino acid sequence of CPn0592, which is the CP homologue of CT473, which was identified in clone CTL2-8b.

SEQ ID NO: 502 corresponds to the amino acid sequence of CPn0593, which is the CP homologue of CT474, which was identified in clone CTL2-8b.

SEQ ID NO: 503 corresponds to the amino acid sequence of CPn0197, which is the CP homologue of CT139 (oppA1), which was identified in clone CTL2-8b.

SEQ ID NO: 504 corresponds to the amino acid sequence of CPn0363, which is the CP homologue of CT060 (flhA), which was identified in clone CTL2-8b.

SEQ ID NO: 505 corresponds to the amino acid sequence of CPn0301, which is the CP homologue of CT242, which was identified in clone CTL2gam8.

SEQ ID NO: 506 corresponds to the amino acid sequence of CPn0302, which is the CP homologue of CT243 (lpxD), which was identified in clone CTL2gam8.

SEQ ID NO: 507 corresponds to the amino acid sequence of CPn0324, which is the CP homologue of CT089 (lcrE), which was identified in clones CTL2-9, CTL2gam1, CTL2gam17 and CTL2-19(5').

SEQ ID NO: 508 corresponds to the amino acid sequence of CPn0761, which is the CP homologue of CT610, which was identified in clone CTL2-10(5')(3').

SEQ ID NO: 509 corresponds to the amino acid sequence of CPn0760, which is the CP homologue of CT611, which was identified in clone CTL2-10(5').

SEQ ID NO: 510 corresponds to the amino acid sequence of CPn0329, which is the CP homologue of CT154, which was identified in clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 511 corresponds to the amino acid sequence of CPn0990, which is the CP homologue of CT833 (infC), which was identified in clone CTL2-12.

SEQ ID NO: 512 corresponds to the amino acid sequence of CPn-ORF5, which is the CP homologue of CT ORF3, which was identified in clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5'), and CTL2-23.

SEQ ID NO: 513 corresponds to the amino acid sequence of CPn0984, which is the CP homologue of CT827 (nrdA) which was identified in clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 514 corresponds to the amino acid sequence of CPn0985, which is the CP homologue of CT828 (nrdB) which was identified in clones CTL2-16(3') CTL2gam15(3').

SEQ ID NO: 515 corresponds to the amino acid sequence of CPn0349, which is the CP homologue of CT067 (ytgA), which was identified in clone CTL2gam18.

SEQ ID NO: 516 corresponds to the DNA sequence of CPn-ORF6, which is the CP homologue of CT-ORF4, which was identified in clone CTL2-18(3').

SEQ ID NO: 517 corresponds to the DNA sequence of CP-ORF7, which is the CP homologue of CT-ORF5, which was identified in clone CTL2-18(3').

SEQ ID NO: 518 corresponds to the amino acid sequence of CPn0326, which is the CP homologue of CT087 (malQ), which was identified in clone CTL2-19(5').

SEQ ID NO: 519 corresponds to the amino acid sequence of CPn0325, which is the CP homologue of CT088 (sycE), which was identified in clone CTL2-19(5').

SEQ ID NO: 520 corresponds to the amino acid sequence of CPn0793, which is the CP homologue of CT588 (rbsu), which was identified in clone CTL2gam23.

SEQ ID NO: 521 corresponds to the amino acid sequence of CPn0199, which is the CP homologue of CT199 (oppB1), which was identified in clone CTL2gam24.

SEQ ID NO: 522 corresponds to the amino acid sequence of CPn0666, which is the CP homologue of CT545 (dnaE), which was identified in clone CTL2-24.

SEQ ID NO: 523 corresponds to the DNA sequence of CPn0065, which is the CP homologue of CT288, which was identified in clone CTL2gam27.

SEQ ID NO: 524 corresponds to the DNA sequence of CPn0444, which is the CP homologue of CT413 (pmpB), which was identified in clone CTL2gam30(5')(3').

SEQ ID NO: 525 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT751 (amn) identified from the clones CTL2-1 and CTL2-5.

SEQ ID NO: 526 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT322 (tuff) identified from the clone CTL2-2.

SEQ ID NO: 527 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT032 (metG) identified from the clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 528 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT031 identified from the clone CTL2-3(5')(3').

SEQ ID NO: 529 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT030 (gmK) identified from the clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 530 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT064 (lepA) identified from the clone CTL2gam5.

SEQ ID NO: 531 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT265 (accA) identified from the clone CTL2-6.

SEQ ID NO: 532 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT624 (msbA) identified from the clones CTL2-6.

SEQ ID NO: 533 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT256 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 534 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT257 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 535 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT384 identified from the clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 536 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT473 identified from the clone CTL2-8b.

SEQ ID NO: 537 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT474 identified from the clones CTL2-8b.

SEQ ID NO: 538 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT139 (oppA1) identified from the clones CTL2-8b.

SEQ ID NO: 539 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT060 (flhA) identified from the clone CTL2-8b.

SEQ ID NO: 540 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT242 identified from the clone CTL2gam8.

SEQ ID NO: 541 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT243 (lpxD) identified from the clone CTL2gam8.

SEQ ID NO: 542 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT089 identified from the clones CTL2-9, CTL2gam1, CTL2gam17, and CTL2-19(5').

SEQ ID NO: 543 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT610 identified from the clone CTL2-10 (5')(3').

SEQ ID NO: 544 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT611 identified from the clone CTL2-10(5').

SEQ ID NO: 545 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT154 identified from the clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 546 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT833 (infC) identified from the clone CTL2-12.

SEQ ID NO: 547 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT827 (nrdA) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 548 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT828 (nrdB) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 549 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT067 (ytgA) identified from the clone CTL2gam18.

SEQ ID NO: 550 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT088 (sycE) identified from the clones CTL2-19(5').

SEQ ID NO: 551 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT087 identified from the clone CTL2-19(5').

SEQ ID NO: 552 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT588 (rsbu) identified from the clone CTL2gam23.

SEQ ID NO: 553 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT199 (oppB1) identified from the clone CTL2gam24.

SEQ ID NO: 554 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT545 (dnaE) identified from the clone CTL2-4.

SEQ ID NO: 555 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT288 identified from the clones CTL2gam27.

SEQ ID NO: 556 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT413 (pmpB) identified from the clone CTL2gam30(5')(3').

SEQ ID NO: 557 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF3 identified from the clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5') and CTL2-23.

SEQ ID NO: 558 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for pCT-ORF4 identified from the clone CTL2-18(3').

SEQ ID NO: 559 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF5 identified from the clones CTL2-18(3').

SEQ ID NO: 560 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT751 (amn) identified from the clones CTL2-1 and CTL2-5.

SEQ ID NO: 561 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT322 (tuff) identified from the clone CTL2-2.

SEQ ID NO: 562 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT032 (metG) identified from the clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 563 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT031 identified from the clone CTL2-3(5')(3').

SEQ ID NO: 564 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT030 (gmK) identified from the clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 565 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT064 (lepA) identified from the clone CTL2gam5.

SEQ ID NO: 566 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT265 (accA) identified from the clone CTL2-6.

SEQ ID NO: 567 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT624 (msbA) identified from the clones CTL2-6.

SEQ ID NO: 568 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT256 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 569 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT257 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 570 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT384 identified from the clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 571 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT473 identified from the clone CTL2-8b.

SEQ ID NO: 572 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT474 identified from the clones CTL2-8b.

SEQ ID NO: 573 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT139 (oppA1) identified from the clones CTL2-8b.

SEQ ID NO: 574 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT060 (flhA) identified from the clone CTL2-8b.

SEQ ID NO: 575 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT242 identified from the clone CTL2gam8.

SEQ ID NO: 576 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT243 (lpxD) identified from the clone CTL2gam8.

SEQ ID NO: 577 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT089 identified from the clones CTL2-9, CTL2gam1, CTL2gam17, and CTL2-19(5').

SEQ ID NO: 578 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT610 identified from the clone CTL2-10 (5')(3').

SEQ ID NO: 579 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT611 identified from the clone CTL2-10(5').

SEQ ID NO: 580 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT154 identified from the clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 581 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT833 (infC) identified from the clone CTL2-12.

SEQ ID NO: 582 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF3 identified from the clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5') and CTL2-23.

SEQ ID NO: 583 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT827 (nrdA) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 584 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT828 (nrdB) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 585 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT067 (ytgA) identified from the clone CTL2gam18.

SEQ ID NO: 586 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for pCT-ORF4 identified from the clone CTL2-18(3')

SEQ ID NO: 587 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF5 identified from the clones CTL2-18(3').

SEQ ID NO: 588 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT087 identified from the clone CTL2-19(5').

SEQ ID NO: 589 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT088 (sycE) identified from the clones CTL2-19(5').

SEQ ID NO: 590 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT588 (rsbu) identified from the clone CTL2gam23.

SEQ ID NO: 591 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT199 (oppB1) identified from the clone CTL2gam24.

SEQ ID NO: 592 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT545 (dnaE) identified from the clone CTL2-4.

SEQ ID NO: 593 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT288 identified from the clones CTL2gam27.

SEQ ID NO: 594 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT413 (pmpB) identified from the clone CTL2gam30(5')(3').

SEQ ID NO: 595 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0406, of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 596 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0315, of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 597 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0406, of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 598 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0315, of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 599 sets forth the amino acid sequence for Chlamydia trachomatis serovar D CT287 protein.

DESCRIPTION OF THE FIGURES

Fig. 1 illustrates induction of INF-γ from a *Chlamydia*-specific T cell line activated by target cells expressing clone 4C9-18#2.

Fig. 2 illustrates retroviral vectors pBIB-KS1,2,3 modified to contain a Kosak translation initiation site and stop codons.

Fig. 3 shows specific lysis in a chromium release assay of P815 cells pulsed with *Chlamydia* peptides CtC7.8-12 (SEQ ID NO: 18) and CtC7.8-13 (SEQ ID NO: 19).

Fig. 4 shows antibody isotype titers in C57Bl/6 mice immunized with *C. trachomatis* SWIB protein.

Fig. 5 shows *Chlamydia*-specific T-cell proliferative responses in splenocytes from C3H mice immunized with *C. trachomatis* SWIB protein.

Fig. 6 illustrates the 5' and 3' primer sequences designed from *C. pneumoniae* which were used to isolate the SWIB and S13 genes from *C. pneumoniae.*

Figs. 7A and 7B show induction of IFN-γ from a human anti-*chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* upon activation by monocyte-derived dendritic cells expressing chlamydial proteins.

Fig. 8 shows the identification of T cell epitopes in Chlamydial ribosomal S13 protein with T-cell line TCL 8 EB/DC.

Fig. 9A and B illustrate the proliferative response of CP-21 T-cells generated against *C. pnuemoniae*-infected dendritic cells to recombinant *C. pneumonia*-SWIB protein, but not *C. trachomatis* SWIB protein.

Fig. 10 shows the *C. trachomatis*-specific SWIB proliferative responses of a primary T-cell line (TCT-10 EB) from an asymptomatic donor.

Fig. 11 illustrates the identification of T-cell epitope in *C. trachomatis* SWIB with an antigen specific T-cell line (TCL-10 EB).

Fig. 12 shows the *C. trachomatis*-specific proliferative responses of primary T cell lines generated from two patients against the CT specific antigens CT622, CT875 and CT EB.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis and treatment of Chlamydial infection. In one aspect, the compositions of the subject invention include polypeptides that comprise at least one immunogenic portion of a *Chlamydia* antigen, or a variant thereof.

In specific embodiments, the subject invention discloses polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, wherein the *Chlamydia* antigen comprises an amino acid sequence encoded by a polynucleotide molecule disclosed herein, the complements of said nucleotide sequences, and variants of such sequences.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the inventive antigens may consist entirely of the immunogenic portion, or may contain additional sequences. The additional sequences

may be derived from the native *Chlamydia* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments.

An "immunogenic portion" of an antigen is a portion that is capable of reacting with sera obtained from a *Chlamydia*-infected individual (*i.e.*, generates an absorbance reading with sera from infected individuals that is at least three standard deviations above the absorbance obtained with sera from uninfected individuals, in a representative ELISA assay described herein). Such immunogenic portions generally comprise at least about 5 amino acid residues, more preferably at least about 10, and most preferably at least about 20 amino acid residues. Methods for preparing and identifying immunogenic portions of antigens of known sequence are well known in the art and include those summarized in Paul, *Fundamental Immunology*, 3rd ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native *Chlamydia* protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is

similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I-labeled Protein A.

Examples of immunogenic portions of antigens contemplated by the present invention include, for example, the T cell stimulating epitopes provided in SEQ ID NO: 9, 10, 18, 19, 31, 39, 93-96, 98, 100-102, 106, 108, 138-140, 158, 167, 168, 246, 247 and 254-256. Polypeptides comprising at least an immunogenic portion of one or more *Chlamydia* antigens as described herein may generally be used, alone or in combination, to detect Chlamydial infection in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotide molecules. Such variants include, but are not limited to, naturally occurring allelic variants of the inventive sequences. In particular, variants include other *Chlamydiae* serovars, such as serovars D, E and F, as well as the several LGV serovars which share homology to the inventive polypeptide and polynucleotide molecules described herein. Preferably, the serovar homologues show 95-99% homology to the corresponding polypeptide sequence(s) described herein.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above

polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.,* 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide. Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to

enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A polynucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions such that the immunogenicity of the encoded polypeptide is not diminished, relative to the native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA, 2*:183, 1983). Nucleotide variants may be naturally occurring allelic variants as discussed below, or non-naturally occurring variants. The polypeptides provided by the present invention include variants that are encoded by polynucleotide sequences which are substantially homologous to one or more of the polynucleotide sequences specifically recited herein. "Substantial homology," as used herein, refers to polynucleotide sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing polynucleotide sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode a polypeptide that is the same as a polypeptide of the present invention.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Resarch Foundaiton, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity methods of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. (U.S.A.) 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One illustrative example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul et al. (1990) J. Mol. Biol. 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for

Biotechnology Information (http://www.ncbi.nlm.nih.gov/) In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or amino acid sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention provides polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% or more sequence identity, preferably at least 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (e.g., BLAST analyisis using standard parameters, as described below). One skilled in this art will recognize that these values can be

appropriately adjusted to determine corresponding identity of proteins encoded by two polynucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated polynucleotides or polypeptides comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides and polypeptides encompassed by this invention may comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the disclosed sequences, as well as all intermediate lengths therebetween. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through the 200-500; 500-1,000, and the like.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

Also included in the scope of the present invention are alleles of the genes encoding the nucleotide sequences recited in herein. As used herein, an “allele” or “allellic sequence” is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of

nucleotides. Each of these types of changes may occur alone or in combination with the others, one or more times in a given sequence.

In specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *Chlamydia* antigen (or a variant of such an antigen), that comprises one or more of the amino acid sequences encoded by (a) a polynucleotide sequence selected from the group consisting of SEQ ID NO: 358-361, 407-430, 525-559, 582-598; (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b). As discussed in the Examples below, several of the *Chlamydia* antigens disclosed herein recognize a T cell line that recognizes both *Chlamydia trachomatis* and *Chlamydia pneumoniae* infected monocyte-derived dendritic cells, indicating that they may represent an immunoreactive epitope shared by *Chlamydia trachomatis* and *Chlamydia pneumoniae.* The antigens may thus be employed in a vaccine for both *C. trachomatis* genital tract infections and for *C. pneumonia* infections. Further characterization of these *Chlamydia* antigens from *Chlamydia trachomatis* and *Chlamydia pneumonia* to determine the extent of cross-reactivity is provided in Example 6. Additionally, Example 4 describes cDNA fragments (SEQ ID NO: 15, 16 and 33) isolated from *C. trachomatis* which encode proteins (SEQ ID NO: 17-19 and 32) capable of stimulating a *Chlamydia*-specific murine CD8+ T cell line.

In general, *Chlamydia* antigens, and polynucleotide sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, polynucleotide molecules encoding *Chlamydia* antigens may be isolated from a *Chlamydia* genomic or cDNA expression library by screening with a *Chlamydia*-specific T cell line as described below, and sequenced using techniques well known to those of skill in the art. Additionally, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for *Chlamydia*-associated expression (*i.e.,* expression that is at least two fold greater in *Chlamydia*-infected cells than in controls, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA

prepared from cells expressing the proteins described herein.. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

Antigens may be produced recombinantly, as described below, by inserting a polynucleotide sequence that encodes the antigen into an expression vector and expressing the antigen in an appropriate host. Antigens may be evaluated for a desired property, such as the ability to react with sera obtained from a *Chlamydia*-infected individual as described herein, and may be sequenced using, for example, traditional Edman chemistry. *See* Edman and Berg, *Eur. J. Biochem.* *80*:116-132, 1967.

Polynucleotide sequences encoding antigens may also be obtained by screening an appropriate *Chlamydia* cDNA or genomic DNA library for polynucleotide sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated antigens. Degenerate oligonucleotide sequences for use in such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (and references cited therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a cDNA or genomic library. The library screen may then be performed using the isolated probe.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.,* a *Chlamydia* cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.,* by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see*

Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using techniques well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol. 51*:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989), and software well known in the art may also be employed. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res. 16*:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods*

Applic. 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Transcription-Mediated Amplification, or TMA is another method that may be utilized for the amplification of DNA, rRNA, or mRNA, as described in Patent No. PCT/US91/03184. This autocatalytic and isothermic non-PCR based method utilizes two primers and two enzymes: RNA polymerase and reverse transcriptase. One primer contains a promoter sequence for RNA polymerase. In the first amplification, the promoter-primer hybridizes to the target rRNA at a defined site. Reverse transcriptase creates a DNA copy of the target rRNA by extension from the 3'end of the promoter-primer. The RNA in the resulting complex is degraded and a second primer binds to the DNA copy. A new strand of DNA is synthesized from the end of the primer by reverse transcriptase creating double stranded DNA. RNA polymerase recognizes the promoter sequence in the DNA template and initiates transcription. Each of the newly synthesized RNA amplicons re-enters the TMA process and serves as a template for a new round of replication leading to the expotential expansion of the RNA amplicon. Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length cDNA sequences may also be obtained by analysis of genomic fragments.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA 2*:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a *Chlamydial* protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded

polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a *Chlamydial* polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a *Chlamydial* protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of

particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc. 85*:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

As noted above, immunogenic portions of *Chlamydia* antigens may be prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen for immunogenic properties. The representative ELISAs described herein may generally be employed in these screens. An immunogenic portion of a polypeptide is a portion that, within such representative assays, generates a signal in such assays that is substantially similar to that generated by the full length antigen. In other words, an immunogenic portion of a *Chlamydia* antigen generates at least about 20%, and preferably about 100%, of the signal induced by the full length antigen in a model ELISA as described herein.

Portions and other variants of *Chlamydia* antigens may be generated by synthetic or recombinant means. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the polynucleotide sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a polynucleotide sequence encoding the

polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides as described herein. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known *Chlamydial* protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein. A DNA sequence encoding a fusion protein of the present invention may be constructed using known recombinant

DNA techniques to assemble separate DNA sequences encoding, for example, the first and second polypeptides, into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene 40*:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA 83*:8258-8562, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. As an alternative to the use of a peptide linker sequence (when desired), one can utilize non-essential N-terminal amino acid regions (when present) on the first and second polypeptides to separate the functional domains and prevent steric hindrance.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the

immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, *336*:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium Haemophilus influenza B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemaglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene 43*:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10*:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In another embodiment, a Mycobacterium tuberculosis-derived Ra12 polynucleotide is linked to at least an immunogenic portion of a polynucleotide of this invention. Ra12 compositions and methods for their use inenhancing expression of heterologous polynucleotide sequences is described in U.S. Patent Application

60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (U.S. Patent Application 60/158,585; see also, Skeiky *et al.*, *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference. In one embodiment, the Ra12 polypeptide used in the production of fusion polypeptides comprises a C-terminal fragment of the MTB32A coding sequence that is effective for enhancing the expression and/or immunogenicity of heterologous Chlamydial antigenic polypeptides with which it is fused. In another embodiment, the Ra12 polypeptide corresponds to an approximately 14 kD C-terminal fragment of MTB32A comprising some or all of amino acid residues 192 to 323 of MTB32A.

Recombinant nucleic acids, which encode a fusion polypeptide comprising a Ra12 polypeptide and a heterologous Chlamydia polypeptide of interest, can be readily constructed by conventional genetic engineering techniques. Recombinant nucleic acids are constructed so that, preferably, a Ra12 polynucleotide sequence is located 5' to a selected heterologous Chlamydia polynucleotide sequence. It may also be appropriate to place a Ra12 polynucleotide sequence 3' to a selected heterologous polynucleotide sequence or to insert a heterologous polynucleotide sequence into a site within a Ra12 polynucleotide sequence.

In addition, any suitable polynucleotide that encodes a Ra12 or a portion or other variant thereof can be used in constructing recombinant fusion polynucleotides comprising Ra12 and one or more Chlamydia polynucleotides disclosed herein. Preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.

Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one

or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or polynucleotides encoding such polypeptides or fusion proteins) to induce protective immunity against Chlamydial infection in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be induced to prevent or treat Chlamydial infection.

In this aspect, the polypeptide, fusion protein or polynucleotide molecule is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and an immunostimulant, such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical compositions and vaccines may also contain other *Chlamydia* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

Alternatively, a vaccine may contain polynucleotides encoding one or more polypeptides or fusion proteins as described above, such that the polypeptide is generated *in situ*. In such vaccines, the polynucleotides may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary polynucleotide sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a

preferred embodiment, the polynucleotides may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective) virus. Techniques for incorporating polynucleotides into such expression systems are well known to those of ordinary skill in the art. The polynucleotides may also be administered as "naked" plasmid vectors as described, for example, in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993.Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.,* an artificial membrane vesicle). The uptake of naked polynucleotides may be increased by incorporating the polynucleotides into and/or onto biodegradable beads, which are efficiently transported into the cells. The preparation and use of such systems is well known in the art.

In a related aspect, a polynucleotide vaccine as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known *Chlamydia* antigen. For example, administration of polynucleotides encoding a polypeptide of the present invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the vaccine.

Polypeptides and polynucleotides disclosed herein may also be employed in adoptive immunotherapy for the treatment of *Chlamydial* infection. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous

host immune system with the administration of immune response-modifying agents (for example, vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate anti-*Chlamydia* effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper), killer cells (such as Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast, or B-cells, may be pulsed with immunoreactive polypeptides, or polynucleotide sequence(s) may be introduced into antigen presenting cells, using a variety of standard techniques well known in the art. For example, antigen presenting cells may be transfected or transduced with a polynucleotide sequence, wherein said sequence contains a promoter region appropriate for increasing expression, and can be expressed as part of a recombinant virus or other expression system. Several viral vectors may be used to transduce an antigen presenting cell, including pox virus, vaccinia virus, and adenovirus; also, antigen presenting cells may be transfected with polynucleotide sequences disclosed herein by a variety of means, including gene-gun technology, lipid-mediated delivery, electroporation, osmotic shock, and particlate delivery mechanisms, resulting in efficient and acceptable expression levels as determined by one of ordinary skill in the art. For cultured T-cells to be effective in

therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever, M., *et al*, "Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews, 157*:177, 1997).

The polypeptides disclosed herein may also be employed to generate and/or isolate chlamydial-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed polypeptides. The resulting antigen specific CD8+ or CD4+ T-cell clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate *Chlamydia* reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells which may be subsequently transferred to the patient as described, for example, by Chang *et al, (Crit. Rev. Oncol. Hematol., 22*(3), 213, 1996). Cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as Isolex™ System, available from Nexell Therapeutics, Inc. Irvine, CA. The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

In other embodiments, T-cell and/or antibody receptors specific for the polypeptides disclosed herein can be cloned, expanded, and transferred into other vectors or effector cells for use in adoptive immunotherapy. In particular, T cells may be transfected with the appropriate genes to express the variable domains from chlamydia specific monoclonal antibodies as the extracellular recognition elements and joined to the T cell receptor signaling chains, resulting in T cell activation, specific lysis, and cytokine release. This enables the T cell to redirect its specificity in an MHC-independent manner. See for example, Eshhar, Z., *Cancer Immunol Immunother*, 45(3-

4):131-6, 1997 and Hwu, P., et al, *Cancer Res*, 55(15):3369-73, 1995. Another embodiment may include the transfection of chlamydia antigen specific alpha and beta T cell receptor chains into alternate T cells, as in Cole, DJ, et al, *Cancer Res*, 55(4):748-52, 1995.

In a further embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generate antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate disease in a murine model has been demonstrated by Cheever et al, *Immunological Reviews, 157*:177, 1997). Additionally, vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.,* vaccines). Alternatively, a pharmaceutical composition may comprise an antigen-presenting cell (*e.g.* a dendritic cell) transfected with a *Chlamydial* polynucleotide such that the antigen presenting cell expresses a *Chlamydial* polypeptide. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.,* polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.,* Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other *Chlamydial* antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems 15*:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, adenovirus, baculovirus, togavirus, bacteriophage, and the like), which often involves the use of a non-pathogenic (defective), replication competent virus.

For example, many viral expression vectors are derived from viruses of the retroviridae family. This family includes the murine leukemia viruses, the mouse mammary tumor viruses, the human foamy viruses, Rous sarcoma virus, and the immunodeficiency viruses, including human, simian, and feline. Considerations when designing retroviral expression vectors are discussed in Comstock *et al.* (1997).

Excellent murine leukemia virus (MLV)-based viral expression vectors have been developed by Kim *et al.* (1998). In creating the MLV vectors, Kim *et al.* found that the entire *gag* sequence, together with the immediate upstream region, could be deleted without significantly affecting viral packaging or gene expression. Further, it was found that nearly the entire U3 region could be replaced with the immediately-early promoter of human cytomegalovirus without deleterious effects. Additionally, MCR and internal ribosome entry sites (IRES) could be added without adverse effects. Based on their observations, Kim *et al.* have designed a series of MLV-based expression vectors comprising one or more of the features described above.

As more has been learned about human foamy virus (HFV), characteristics of HFV that are favorable for its use as an expression vector have been

discovered. These characteristics include the expression of pol by splicing and start of translation at a defined initiation codon. Other aspects of HFV viral expression vectors are reviewed in Bodem *et al.* (1997).

Murakami *et al.* (1997) describe a Rous sarcoma virus (RSV)-based replication-competent avian retrovirus vectors, IR1 and IR2 to express a heterologous gene at a high level. In these vectors, the IRES derived from encephalomyocarditis virus (EMCV) was inserted between the *env* gene and the heterologous gene. The IR1 vector retains the splice-acceptor site that is present downstream of the *env* gene while the IR2 vector lacks it. Murakami *et al.* have shown high level expression of several different heterologous genes by these vectors.

Recently, a number of lentivirus-based retroviral expression vectors have been developed. Kafri *et al.* (1997) have shown sustained expression of genes delivered directly into liver and muscle by a human immunodeficiency virus (HIV)-based expression vector. One benefit of the system is the inherent ability of HIV to transduce non-dividing cells. Because the viruses of Kafri *et al.* are pseudotyped with vesicular stomatitis virus G glycoprotein (VSVG), they can transduce a broad range of tissues and cell types.

A large number of adenovirus-based expression vectors have been developed, primarily due to the advantages offered by these vectors in gene therapy applications. Adenovirus expression vectors and methods of using such vectors are the subject of a number of United States patents, including United States Patent No. 5,698,202, United States Patent No. 5,616,326, United States Patent No. 5,585,362, and United States Patent No. 5,518,913, all incorporated herein by reference.

Additional adenoviral constructs are described in Khatri *et al.* (1997) and Tomanin *et al.* (1997). Khatri *et al.* describe novel ovine adenovirus expression vectors and their ability to infect bovine nasal turbinate and rabbit kidney cells as well as a range of human cell type, including lung and foreskin fibroblasts as well as liver, prostate, breast, colon and retinal lines. Tomanin *et al.* describe adenoviral expression vectors containing the T7 RNA polymerase gene. When introduced into cells containing a heterologous gene operably linked to a T7 promoter, the vectors were able to drive gene expression from the T7 promoter. The authors suggest that this system may be useful for the cloning and expression of genes encoding cytotoxic proteins.

Poxviruses are widely used for the expression of heterologous genes in mammalian cells. Over the years, the vectors have been improved to allow high expression of the heterologous gene and simplify the integration of multiple heterologous genes into a single molecule. In an effort to diminish cytopathic effects and to increase safety, vaccinia virus mutant and other poxviruses that undergo abortive infection in mammalian cells are receiving special attention (Oertli *et al.,* 1997). The use of poxviruses as expression vectors is reviewed in Carroll and Moss (1997).

Togaviral expression vectors, which includes alphaviral expression vectors have been used to study the structure and function of proteins and for protein production purposes. Attractive features of togaviral expression vectors are rapid and efficient gene expression, wide host range, and RNA genomes (Huang, 1996). Also, recombinant vaccines based on alphaviral expression vectors have been shown to induce a strong humoral and cellular immune response with good immunological memory and protective effects (Tubulekas *et al.,* 1997). Alphaviral expression vectors and their use are discussed, for example, in Lundstrom (1997).

In one study, Li and Garoff (1996) used Semliki Forest virus (SFV) expression vectors to express retroviral genes and to produce retroviral particles in BHK-21 cells. The particles produced by this method had protease and reverse transcriptase activity and were infectious. Furthermore, no helper virus could be detected in the virus stocks. Therefore, this system has features that are attractive for its use in gene therapy protocols.

Baculoviral expression vectors have traditionally been used to express heterologous proteins in insect cells. Examples of proteins include mammalian chemokine receptors (Wang *et al.,* 1997), reporter proteins such as green fluorescent protein (Wu *et al.,* 1997), and FLAG fusion proteins (Wu *et al.,* 1997; Koh *et al.,* 1997). Recent advances in baculoviral expression vector technology, including their use in virion display vectors and expression in mammalian cells is reviewed by Possee (1997). Other reviews on baculoviral expression vectors include Jones and Morikawa (1996) and O'Reilly (1997).

Other suitable viral expression systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA 86*:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci. 569*:86-103, 1989; Flexner et al., *Vaccine 8*:17-21, 1990; U.S. Patent

Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques 6*:616-627, 1988; Rosenfeld et al., *Science 252*:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA 91*:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA 90*:11498-11502, 1993; Guzman et al., *Circulation 88*:2838-2848, 1993; and Guzman et al., *Cir. Res. 73*:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. In other systems, the DNA may be introduced as "naked" DNA, as described, for example, in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

It will be apparent that a vaccine may comprise a polynucleotide and/or a polypeptide component, as desired. It will also be apparent that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and/or polypeptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts).While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or

dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, under select circumstances, the adjuvant composition may be designed to induce an immune response predominantly of the Th1 type or Th2 type. High levels of Th1-type cytokines (*e.g.*, IFN-γ, TNFα, IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science 273*:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.,* SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa Corporation; Seattle, WA), RC-529 (Corixa Corporation; Seattle, WA) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties.

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.,* a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g.*, Coombes et al., *Vaccine 14*:1429-1438, 1996) and

administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets *Chlamydia*-infected cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-*Chlamydia* effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392*:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic immunity (*see* Timmerman and Levy, *Ann. Rev. Med. 50*:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with

marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med. 4*:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNFα to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNFα, CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a *Chlamydial* protein (or portion or other variant thereof) such that the *Chlamydial* polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein.

Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology 75*:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the *Chlamydial* polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Routes and frequency of administration of pharmaceutical compositions and vaccines, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *Chlamydial* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier,

such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a *Chlamydial* protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

In another aspect, the present invention provides methods for using the polypeptides described above to diagnose Chlamydial infection. In this aspect, methods are provided for detecting Chlamydial infection in a biological sample, using one or more of the above polypeptides, either alone or in combination. For clarity, the term "polypeptide" will be used when describing specific embodiments of the inventive diagnostic methods. However, it will be clear to one of skill in the art that the fusion proteins of the present invention may also be employed in such methods.

As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient. The polypeptides are used in an assay, as described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample, relative to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to *Chlamydia* antigens which may be indicative of *Chlamydia*-infection.

In embodiments in which more than one polypeptide is employed, the polypeptides used are preferably complementary (*i.e.*, one component polypeptide will tend to detect infection in samples where the infection would not be detected by another component polypeptide). Complementary polypeptides may generally be identified by

using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *Chlamydia*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested.

A variety of assay formats are known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (*e.g.*, in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate, or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of techniques known to those of ordinary skill in the art. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to a well in a microtiter plate or to a membrane is preferred. In

such cases, adsorption may be achieved by contacting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging from about 10 ng to about 1 µg, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent assay (ELISA). This assay may be performed by first contacting a polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection reagent.

More specifically, once the polypeptide is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin (BSA) or Tween 20™ (Sigma Chemical Co., St. Louis, MO) may be employed. The immobilized polypeptide is then incubated with the sample, and antibody is allowed to bind to the antigen. The sample may be diluted with a suitable dilutent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of antibody within an HGE-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at

equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. Detection reagent may then be added to the solid support. An appropriate detection reagent is any compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the detection reagent contains a binding agent (such as, for example, Protein A, Protein G, immunoglobulin, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of binding agent to reporter group may be achieved using standard methods known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (*e.g.*, Zymed Laboratories, San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An appropriate amount of time may generally be determined from the manufacturer's instructions or by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*Chlamydia* antibodies in the sample, the signal detected from the reporter group that remains bound to the solid

support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for *Chlamydia*-infection. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for Chlamydial infection.

In a related embodiment, the assay is performed in a rapid flow-through or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (*e.g.*, protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The detection of bound detection reagent may then be performed as described above. In the strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-*Chlamydia* antibodies in the sample. Typically, the concentration of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide

immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 25 ng to about 1 μg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (*e.g.*, one drop) of patient serum or blood.

Of course, numerous other assay protocols exist that are suitable for use with the polypeptides of the present invention. The above descriptions are intended to be exemplary only. One example of an alternative assay protocol which may be usefully employed in such methods is a Western blot, wherein the proteins present in a biological sample are separated on a gel, prior to exposure to a binding agent. Such techniques are well known to those of skill in the art.

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a *Chlamydial* protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a *Chlamydial* protein if it reacts at a detectable level (within, for example, an ELISA) with a *Chlamydial* protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a *Chlamydial* infection using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a *Chlamydial* protein will generate a signal indicating the presence of a *Chlamydial* infection in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without infection. To determine whether a binding agent satisfies this requirement, biological

samples (*e.g.*, blood, sera, sputum urine and/or tissue biopsies) from patients with and without *Chlamydial* infection (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* *6*:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may

be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y, ^{123}I, ^{125}I, ^{131}I, ^{186}Re, ^{188}Re, ^{211}At, and ^{212}Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diptheria

toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in site-specific regions by appropriate methods. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density, and the rate of clearance of the antibody.

Antibodies may be used in diagnostic tests to detect the presence of *Chlamydia* antigens using assays similar to those detailed above and other techniques well known to those of skill in the art, thereby providing a method for detecting Chlamydial infection in a patient.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a

polymerase chain reaction (PCR) based assay to amplify *Chlamydia*-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a polypeptide of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a polypeptide of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect *Chlamydia*-specific sequences in biological samples. DNA probes or primers comprising oligonucleotide sequences described above may be used alone or in combination with each other.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

ISOLATION OF DNA SEQUENCES ENCODING *CHLAMYDIA* ANTIGENS

Chlamydia antigens of the present invention were isolated by expression cloning of a genomic DNA library of *Chlamydia trachomatis* LGV II essentially as described by Sanderson et al. (*J. Exp. Med.*, 1995, *182*:1751-1757) and were shown to induce PBMC proliferation and IFN-γ in an immunoreactive T cell line.

A *Chlamydia*-specific T cell line was generated by stimulating PBMCs from a normal donor with no history of chlamydial genital tract infection with elementary bodies of *Chlamydia trachomatis* LGV II. This T cell line, referred to as TCL-8, was found to recognize both *Chlamydia trachomatis* and *Chlamydia pneumonia* infected monocyte-derived dendritic cells.

A randomly sheared genomic library of *Chlamydia trachomatis* LGV II was constructed in Lambda ZAP (Stratagene, La Jolla, CA) and the amplified library plated out in 96 well microtiter plates at a density of 30 clones/well. Bacteria were induced to express recombinant protein in the presence of 2 mM IPTG for 3 h, then pelleted and resuspended in 200 μl of RPMI 10% FBS. 10 μl of the induced bacterial suspension was transferred to 96 well plates containing autologous monocyte-derived dendritic cells. After a 2 h incubation, dendritic cells were washed to remove free *E. coli* and *Chlamydia*-specific T cells were added. Positive *E. coli* pools were identified by determining IFN-γ production and proliferation of the T cells in response to the pools.

Four positive pools were identified, which were broken down to yield four pure clones (referred to as 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31), with insert sizes of 481 bp, 183 bp, 110 bp and 1400 bp, respectively. The determined DNA sequences for 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31 are provided in SEQ ID NO: 1-4, respectively. Clone 1-B1-66 is approximately in region 536690 of the *C. trachomatis* genome (NCBI *C. trachomatis* database). Within clone 1-B1-66, an open reading frame (ORF) has been identified (nucleotides 115 - 375) that encodes a previously identified 9 kDa protein (Stephens, et al. Genbank Accession No. AE001320), the sequence of which is provided in SEQ ID NO: 5). Clone 4-D7-28 is a smaller region of the same ORF (amino acids 22-82 of 1-B1-66). Clone 3-G3-10 is approximately in region 74559 of the *C. trachomatis* genome. The insert is cloned in the antisense orientation with respect to its orientation in the genome. The clone 10-C10-31 contains an open reading frame that corresponds to a previously published sequence for S13 ribosomal protein from *Chlamydia trachomatis* (Gu, L. et al. *J. Bacteriology*, *177*:2594-2601, 1995). The predicted protein sequences for 4-D7-28 and 10-C10-31 are provided in SEQ ID NO: 6 and 12, respectively. Predicted protein sequences for 3-G3-10 are provided in SEQ ID NO: 7-11.

In a related series of screening studies, an additional T cell line was used to screen the genomic DNA library of *Chlamydia trachomatis* LGV II described above. A *Chlamydia*-specific T cell line (TCT-1) was derived from a patient with a chlamydial genital tract infection by stimulating patient PBMC with autologous monocyte-derived dendritic cells infected with elementary bodies of *Chlamydia trachomatis* LGV II. One clone, 4C9-18 (SEQ ID NO: 21), containing a 1256 bp insert, elicited a specific immune response, as measured by standard proliferation assays, from the *Chlamydia*-specific T cell line TCT-1. Subsequent analysis revealed this clone to contain three known sequences: lipoamide dehydrogenase (Genbank Accession No. AE001326), disclosed in SEQ ID NO: 22; a hypothetical protein CT429 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 23; and part of an open reading frame of ubiquinone methyltransferase CT428 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 24.

In further studies involving clone 4C9-18 (SEQ ID NO: 21), the full-length amino acid sequence for lipoamide dehydrognase (SEQ ID NO: 22) from *C. trachomatis* (LGV II) was expressed in clone CtL2-LPDA-FL, as disclosed in SEQ ID NO: 90.

To further characterize the open reading frame containing the T cell stimulating epitope(s), a cDNA fragment containing nucleotides 1-695 of clone 4C9-18 with a cDNA sequence encoding a 6X-Histidine tag on the amino terminus was subcloned into the NdeI/EcoRI site of the pET17b vector (Novagen, Madison, WI), referred to as clone 4C9-18#2 BL21 pLysS (SEQ ID NO: 25, with the corresponding amino acid sequence provided in SEQ ID NO: 26) and transformed into *E. coli*. Selective induction of the transformed *E. coli* with 2 mM IPTG for three hours resulted in the expression of a 26 kDa protein from clone 4C9-18#2 BL21 pLysS, as evidenced by standard Coomassie-stained SDS-PAGE. To determine the immunogenicity of the protein encoded by clone 4C9-18#2 BL21 pLysS, *E. coli* expressing the 26 kDa protein were titered onto 1 x 10^4 monocyte-derived dendritic cells and incubated for two hours. The dendritic cell cultures were washed and 2.5 x 10^4 T cells (TCT-1) added and allowed to incubate for an additional 72 hours, at which time the level of IFN-γ in the culture supernatant was determined by ELISA. As shown in Fig. 1, the T-cell line TCT-1 was found to respond to induced cultures as measured by IFN-g, indicating a

Chlamydia-specific T-cell response against the lipoamide dehydrogenase sequence. Similarly, the protein encoded by clone 4C9-18#2 BL21 pLysS was shown to stimulate the TCT-1 T-cell line by standard proliferation assays.

Subsequent studies to identify additional *Chlamydia trachomatis* antigens using the above-described CD4+ T-cell expression cloning technique yielded additional clones. The TCT-1 and TCL-8 *Chlamydia*-specific T-cell lines, as well as the TCP-21 T-cell line were utilized to screen the *Chlamydia trachomatis* LGVII genomic library. The TCP-21 T-cell line was derived from a patient having a humoral immune response to *Chlamydia pnuemoniae.* The TCT-1 cell line identified 37 positive pools, the TCT-3 cell line identified 41 positive pools and the TCP-21 cell line identified 2 positive pools. The following clones were derived from 10 of these positive pools. Clone 11-A3-93 (SEQ ID NO: 64), identified by the TCP-21 cell line, is a 1339 bp genomic fragment sharing homology to the HAD superfamily (CT103). The second insert in the same clone shares homology with the fab I gene (CT104) present on the complementary strand. Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pnuemoniae*.

Clone 11-G10-46, (SEQ ID NO: 62), identified using the TCT-3 cell line, contains a 688 bp insert that shares homology to the hypothetical protein CT610. Clone 11-G1-34, (SEQ ID NO: 61), identified using the TCT-3 cell line, has two partial open reading frames (ORF) with an insert size of 1215 bp. One ORF shares homology to the malate dehydrogenase gene (CT376), and the other ORF shares homology to the glycogen hydrolase gene (CT042). Clone 11-H3-68, (SEQ ID NO: 60), identified using the TCT-3 cell line, has two ORFs with a total insert size of 1180 bp. One partial ORF encodes the plasmid-encoded PGP6-D virulence protein while the second ORF is a complete ORF for the L1 ribosomal gene (CT318). Clone 11-H4-28, (SEQ ID NO: 59), identified using the TCT-3 cell line, has an insert size of 552 bp and is part of the ORF for the dnaK gene (CT396). Clone 12-B3-95, (SEQ ID NO: 58), identified using the TCT-1 cell line, has an insert size of 463 bp and is a part of the ORF for for the lipoamide dehydrogenase gene (CT557). Clones 15-G1-89 and 12-B3-95 are identical, (SEQ ID NO: 55 and 58, respectively), identified using the TCT-1 cell line, has an insert size of 463 bp and is part of the ORF for the lipoamide dehydrogenase gene

(CT557). Clone 12-G3-83, (SEQ ID NO: 57), identified using the TCT-1 cell line, has an insert size of 1537 bp and has part of the ORF for the hypothetical protein CT622.

Clone 23-G7-68, (SEQ ID NO: 79), identified using the TCT-3 cell line, contains a 950 bp insert and contains a small part of the L11 ribosomal ORF, the entire ORF for L1 ribosomal protein and a part of the ORF for L10 ribosomal protein. In addition, this clone also identified the patient lines CT4, CT5, CT11, CT12, and CHH037. Clone 22-F8-91, (SEQ ID NO: 80), identified using the TCT-1 cell line, contains a 395 bp insert that contains a part of the pmpC ORF on the complementary strand of the clone. Clone 21-E8-95, (SEQ ID NO: 81), identified using the TCT-3 cell line, contains a 2,085 bp insert which contains part of CT613 ORF, the complete ORF for CT612, the complete ORF for CT611 and part of the ORF for CT610. Clone 19-F12-57, (SEQ ID NO: 82), identified using the TCT-3 cell line, contains a 405 bp insert which contains part of the CT 858 ORF and a small part of the recA ORF. Clone 19-F12-53, (SEQ ID NO: 83), identified using the TCT-3 cell line, contains a 379 bp insert that is part of the ORF for CT455 encoding glutamyl tRNA synthetase. Clone 19-A5-54, (SEQ ID NO: 84), identified using the TCT-3 cell line, contains a 715 bp insert that is part of the ORF3 (complementary strand of the clone) of the cryptic plasmid. Clone 17-E11-72, (SEQ ID NO: 85), identified using the TCT-1 cell line, contains a 476 bp insert that is part of the ORF for Opp_2 and pmpD. The pmpD region of this clone is covered by the pmpD region of clone 15-H2-76. Clone 17-C1-77, (SEQ ID NO: 86), identified using the the patient cell lines CT3, CT1, CT4, and CT12, contains a 1551 bp insert that is part of the CT857 ORF, as well as part of the CT858 ORF. Clone 15-H2-76, (SEQ ID NO: 87), identified using the TCT-1 cell line, contains a 3,031 bp insert that contains a large part of the pmpD ORF, part of the CT089 ORF, as well as part of the ORF for SycE. Clone 15-A3-26, (SEQ ID NO: 88), contains a 976 bp insert that contains part of the ORF for CT858. Clone 17-G4-36, (SEQ ID NO: 267), identified using the patient lines CL8, TCT-10, CT1, CT5, CT13, and CHH037, contains a 680 bp insert that is in frame with beta-gal in the plasmid and shares homology to part of the ORF for DNA-directed RNA polymerase beta subunit (CT315 in SerD).

Several of the clones described above share homology to various polymorphic membrane proteins. The genomic sequence of *Chlamydia trachomatis* contains a family of nine polymorphic membrane protein genes, referred to as pmp.

These genes are designated pmpA, pmpB, pmpC, pmpD, pmpE, pmpF, pmpG, pmpH and pmpI. Proteins expressed from these genes are believed to be of biological relevance in generating a protective immune response to a *Chlamydial* infection. In particular, pmpC, pmpD, pmpE and pmpI contain predictable signal peptides, suggesting they are outer membrane proteins, and therefore, potential immunological targets.

Based on the *Chlamydia trachomatis* LGVII serovar sequence, primer pairs were designed to PCR amplify the full-length fragments of pmpC, pmpD, pmpE, pmpG, pmpH and pmpI. The resulting fragments were subcloned into the DNA vaccine vector JA4304 or JAL, which is JA4304 with a modified linker (SmithKline Beecham, London, England). Specifically, PmpC was subcloned into the JAL vector using the 5' oligo GAT AGG CGC GCC GCA ATC ATG AAA TTT ATG TCA GCT ACT GCT G and the 3' oligo CAG AAC GCG TTT AGA ATG TCA TAC GAG CAC CGC A, as provided in SEQ ID NO: 197 and 198, respectively. PCR amplification of the gene under conditions well known in the art and ligation into the 5' ASCI/3' MluI sites of the JAL vector was completed after inserting the short nucleotide sequence GCAATC (SEQ ID NO: 199) upstream of the ATG to create a Kozak-like sequence. The resulting expression vector contained the full-length pmpC gene comprising 5325 nucleotides (SEQ ID NO: 173) containing the hypothetical signal sequence, which encodes a 187 kD protein (SEQ ID NO: 179). The pmpD gene was subcloned into the JA4304 vaccine vector following PCR amplification of the gene using the following oligos: 5' oligo-TGC AAT CAT GAG TTC GCA GAA AGA TAT AAA AAG C (SEQ ID NO: 200) and 3' oligo- CAG AGC TAG CTT AAA AGA TCA ATC GCA ATC CAG TAT TC (SEQ ID NO: 201). The gene was ligated into the a 5' blunted HIII/3' MluI site of the JA4304 vaccine vector using standard techniques well known in the art. The CAATC (SEQ ID NO: 202) was inserted upstream of the ATG to create a Kozak-like sequence. This clone is unique in that the last threonine of the HindIII site is missing due to the blunting procedure, as is the last glycine of the Kozak-like sequence. The insert, a 4593 nucleotide fragment (SEQ ID NO: 172) is the full-length gene for pmpD containing the hypothetical signal sequence, which encodes a 161 kD protein (SEQ ID NO: 178). PmpE was subcloned into the JA4304 vector using the 5' oligo- TGC AAT CAT GAA AAA AGC GTT TTT CTT TTT C (SEQ ID NO: 203), and the 3' oligo- CAG AAC

GCG TCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 204). Following PCR amplification, the gene was ligated into the 5' blunted HIII/3' MluI site of JA4304. To facilitate this, a short nucleotide sequence, TGCAATC (SEQ ID NO: 293), was added upstream of the initiation codon for creating a Kozak-like sequence and reconstituting the HindIII site. The insert is the full-length pmpE gene (SEQ ID NO: 171) containing the hypothetical signal sequence. The pmpE gene encodes a 105 kD protein (SEQ ID NO: 177). The pmpG gene was PCR amplified using the 5' oligo- GTG CAA TCA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 205), and the 3' oligo- CAG AAC GCG TTT AGA ACC GGA CTT TAC TTC C (SEQ ID NO: 206) and subcloned into the JA4304 vector. Similar cloning strategies were followed for the pmpI and pmpK genes. In addition, primer pairs were designed to PCR amplify the full-length or overlapping fragments of the pmp genes, which were then subcloned for protein expression in the pET17b vector (Novagen, Madison, WI) and transfected into E. coli BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Several of the genes encoding the recombinant proteins, as described below, lack the native signal sequence to facilitate expression of the protein. Full-length protein expression of pmpC was accomplished through expression of two overlapping fragments, representing the amino and carboxy termini. Subcloning of the pmpC-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 187, with the corresponding amino acid sequence provided in SEQ ID NO: 195) used the 5' oligo- CAG ACA TAT GCA TCA CCA TCA CCA TCA CGA GGC GAG CTC GAT CCA AGA TC (SEQ ID NO: 207), and the 3' oligo- CAG AGG TAC CTC AGA TAG CAC TCT CTC CTA TTA AAG TAG G (SEQ ID NO: 208) into the 5' NdeI/3' KPN cloning site of the vector. The carboxy terminus portion of the gene, pmpC-carboxy terminal fragment (SEQ ID NO: 186, with the corresponding amino acid sequence provided in SEQ ID NO: 194), was subcloned into the 5' NheI/3' KPN cloning site of the expression vector using the following primers: 5' oligo- CAG AGC TAG CAT GCA TCA CCA TCA CCA TCA CGT TAA GAT TGA GAA CTT CTC TGG C (SEQ ID NO: 209), and 3' oligo- CAG AGG TAC CTT AGA ATG TCA TAC GAG CAC CGC AG (SEQ ID NO: 210). PmpD was also expressed as two overlapping proteins. The pmpD-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 185, with the corresponding amino acid sequence provided in

SEQ ID NO: 193) contains the initiating codon of the pET17b and is expressed as a 80 kD protein. For protein expression and purification purposes, a six-histidine tag follows the initiation codon and is fused at the 28th amino acid (nucleotide 84) of the gene. The following primers were used, 5' oligo, CAG ACA TAT GCA TCA CCA TCA CCA TCA CGG GTT AGC (SEQ ID NO: 211), and the 3' oligo- CAG AGG TAC CTC AGC TCC TCC AGC ACA CTC TCT TC (SEQ ID NO: 212), to splice into the 5' NdeI/3' KPN cloning site of the vector. The pmpD-carboxy terminus portion (SEQ ID NO: 184) was expressed as a 92 kD protein (SEQ ID NO: 192). For expression and subsequent purification, an additional methionine, alanine and serine was included, which represent the initiation codon and the first two amino acids from the pET17b vector. A six-histidine tag downstream of the methionine, alanine and serine is fused at the 691st amino acid (nucleotide 2073) of the gene. The 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CGG TGC TAT TTC TTG CTT ACG TGG (SEQ ID NO: 213) and the 3' oligo- CAG AGG TAC TTn AAA AGA TCA ATC GCA ATC CAG TAT TCG (SEQ ID NO: 214) were used to subclone the insert into the 5' NheI/3' KPN cloning site of the expression vector. PmpE was expressed as a 106kD protein (SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191). The pmpE insert also lacks the native signal sequence. PCR amplification of the gene under conditions well known in the art was performed using the following oligo primers: 5' oligo- CAG AGG ATC CAC ATC ACC ATC ACC ATC ACG GAC TAG CTA GAG AGG TTC (SEQ ID NO: 215), and the 3' oligo- CAG AGA ATT CCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 216), and the amplified insert was ligated into a 5' BamHI/3' EcoRI site of JA4304. The short nucleotide sequence, as provided in SEQ ID NO: 217, was inserted upstream of the initiation codon for creating the Kozak-like sequence and reconstituting the HindIII site. The expressed protein contains the initiation codon and the downstream 21 amino acids from the pET17b expression vector, i.e., MASMTGGQQMGRDSSLVPSSDP (SEQ ID NO: 218). In addition, a six-histidine tag is included upstream of the sequence described above and is fused at the 28th amino acid (nucleotide 84) of the gene, which eliminates the hypothetical signal peptide. The sequences provided in SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191 do not include these additional sequences. The pmpG gene (SEQ ID NO: 182, with the corresponding

amino acid sequence provided in SEQ ID No; 190) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGG TAC CGC ATC ACC ATC ACC ATC ACA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 219), and the 3' oligo- CAG AGC GGC CGC TTA GAA CCG GAC TTT ACT TCC (SEQ ID NO: 220), and ligated into the 5' KPN/3' NotI cloning site of the expression vector. The expressed protein contains an additional amino acid sequence at the amino end, namely, MASMTGGQQNGRDSSLVPHHHHHH (SEQ ID NO: 221), which comprises the initiation codon and additional sequence from the pET17b expression vector. The pmpI gene (SEQ ID NO: 181, with the corresponding amino acid sequence provided in SEQ ID No; 189) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CCT CTT TGG CCA GGA TCC C (SEQ ID NO: 222), and the 3' oligo- CAG AAC TAG TCT AGA ACC TGT AAG TGG TCC (SEQ ID NO: 223), and ligted into the expression vector at the 5' NheI/3' SpeI cloning site. The 95 kD expressed protein contains the initiation codon plus an additional alanine and serine from the pET17b vector at the amino end of the protein. In addition, a six-histidine tag is fused at the 21st amino acid of the gene, which eliminates the hypothetical signal peptide.

Clone 14H1-4, (SEQ ID NO: 56), identified using the TCT-3 cell line, contains a complete ORF for the TSA gene, thiol specific antioxidant – CT603 (the CT603 ORF is a homolog of CPn0778 from *C. pnuemoniae*). The TSA open reading frame in clone 14-H1-4 was amplified such that the expressed protein possess an additional methionine and a 6x histidine tag (amino terminal end). This amplified insert was sub-cloned into the Nde/EcoRI sites of the pET17b vector. Upon induction of this clone with IPTG, a 22.6 kDa protein was purified by Ni-NTA agarose affinity chromatography. The determined amino acid sequence for the 195 amino acid ORF of clone 14-H1-4 encoding the TSA gene is provided in SEQ ID NO: 65. Further analysis yielded a full-length clone for the TSA gene, referred to as CTL2-TSA-FL, with the full-length amino acid sequence provided in SEQ ID NO: 92.

Further studies yielded 10 additional clones identified by the TCT-1 and TCT-3 T-cell lines, as described above. The clones identified by the TCT-1 line are: 16-D4-22, 17-C5-19, 18-C5-2, 20-G3-45 and 21-C7-66; clones identified by the TCT-3

cell line are: 17-C10-31, 17-E2-9, 22-A1-49 and 22-B3-53. Clone 21-G12-60 was recognized by both the TCT-1 and TCT-3 T cell lines. In addition, clone 20-G3-45, which contained sequence specific for pmpB, was identified against the patient lines CT1 and CT4. Clone 16-D4-22 (SEQ ID NO: 119), identified using the TCT-1 cell line contains a 953 bp insert that contains two genes, parts of open reading frame 3 (ORF3) and ORF4 of the *C. trachomatis* plasmid for growth within mammalian cells. Clone 17-C5-19 (SEQ ID NO: 118), contains a 951 bp insert that contains part of the ORF for DT431, encoding for clpP_1 protease and part of the ORF for CT430 (diaminopimelate epimerase). Clone 18-C5-2 (SEQ ID NO: 117) is part of the ORF for S1 ribosomal protein with a 446 bp insert that was identified using the TCT-1 cell line. Clone 20-G3-45 (SEQ ID NO: 116), identified by the TCT-1 cell line, contains a 437 bp insert that is part of the pmpB gene (CT413). Clone 21-C7-8 (SEQ ID NO: 115), identified by the TCT-1 line, contains a 995bp insert that encodes part of the dnaK like protein. The insert of this clone does not overlap with the insert of the TCT-3 clone 11-H4-28 (SEQ ID NO: 59), which was shown to be part of the dnaK gene CT396. Clone 17-C10-31 (SEQ ID NO: 114), identified by the TCT-3 cell line, contains a 976 bp insert. This clone contains part of the ORF for CT858, a protease containing IRBP and DHR domains. Clone 17-E2-9 (SEQ ID NO: 113) contains part of ORFs for two genes, CT611 and CT610, that span a 1142 bp insert. Clone 22-A1-49 (SEQ ID NO: 112), identified using the TCT-3 line, also contains two genes in a 698 bp insert. Part of the ORF for CT660 (DNA gyrase{gyrA_2}) is present on the top strand where as the complete ORF for a hypothetical protein CT659 is present on the complementary strand. Clone 22-B3-53 (SEQ ID NO: 111), identified by the TCT-1 line, has a 267 bp insert that encodes part of the ORF for GroEL (CT110). Clone 21-G12-60 (SEQ ID NO: 110), identified by both the TCT-1 and TCT-3 cell lines contains a 1461 bp insert that contains partial ORFs for hypothetical proteins CT875, CT229 and CT228.

Additional *Chlamydia* antigens were obtained by screening a genomic expression library of *Chlamydia trachomatis* (LGV II serovar) in Lambda Screen-1 vector (Novagen, Madison, WI) with sera pooled from several *Chlamydia*-infected individuals using techniques well known in the art. The following immuno-reactive clones were identified and the inserts containing *Chlamydia* genes sequenced: CTL2#1 (SEQ ID NO: 71); CTL2#2 (SEQ ID NO: 70); CTL2#3-5' (SEQ ID NO: 72, a first

determined genomic sequence representing the 5' end); CTL2#3-3' (SEQ ID NO: 73, a second determined genomic sequence representing the 3' end); CTL2#4 (SEQ ID NO: 53); CTL2#5 (SEQ ID NO: 69); CTL2#6 (SEQ ID NO: 68); CTL2#7 (SEQ ID NO: 67); CTL2#8b (SEQ ID NO: 54); CTL2#9 (SEQ ID NO: 66); CTL2#10-5' (SEQ ID NO: 74, a first determined genomic sequence representing the 5' end); CTL2#10-3' (SEQ ID NO: 75, a second determined genomic sequence representing the 3' end); CTL2#11-5' (SEQ ID NO: 45, a first determined genomic sequence representing the 5' end); CTL2#11-3' (SEQ ID NO: 44, a second determined genomic sequence representing the 3' end); CTL2#12 (SEQ ID NO: 46); CTL2#16-5' (SEQ ID NO: 47); CTL2#18-5' (SEQ ID NO: 49, a first determined genomic sequence representing the 5' end); CTL2#18-3' (SEQ ID NO: 48, a second determined genomic sequence representing the 3' end); CTL2#19-5' (SEQ ID NO: 76, the determined genomic sequence representing the 5' end); CTL2#21 (SEQ ID NO: 50); CTL2#23 (SEQ ID NO: 51; and CTL2#24 (SEQ ID NO: 52).

Additional *Chlamydia trachomatis* antigens were identified by serological expression cloning. These studies used sera pooled from several *Chlamydia*-infected individuals, as described above, but, IgA,and IgM antibodies were used in addition to IgG as a secondary antibody. Clones screened by this method enhance detection of antigens recognized by an early immune response to a *Chlamydial* infection, that is a mucosal humoral immune response. The following immunoreactive clones were characterized and the inserts containing *Chlamydia* genes sequenced: CTL2gam-1 (SEQ ID NO: 290), CTL2gam-2 (SEQ ID NO: 289), CTL2gam-5 (SEQ ID NO: 288), CTL2gam-6-3' (SEQ ID NO: 287, a second determined genomic sequence representing the 3' end), CTL2gam-6-5' (SEQ ID NO: 286, a first determined genomic sequence representing the 5' end), CTL2gam-8 (SEQ ID NO: 285), CTL2gam-10 (SEQ ID NO: 284), CTL2gam-13 (SEQ ID NO: 283), CTL2gam-15-3' (SEQ ID NO: 282, a second determined genomic sequence representing the 3' end), CTL2gam-15-5' (SEQ ID NO: 281, a first determined genomic sequence representing the 5' end), CTL2gam-17 (SEQ ID NO: 280), CTL2gam-18 (SEQ ID NO: 279), CTL2gam-21 (SEQ ID NO: 278), CTL2gam-23 (SEQ ID NO: 277), CTL2gam-24 (SEQ ID NO: 276), CTL2gam-26 (SEQ ID NO: 275), CTL2gam-27 (SEQ ID NO: 274), CTL2gam-28 (SEQ ID NO: 273), CTL2gam-30-3' (SEQ ID NO: 272, a second determined genomic sequence

representing the 3' end) and CTL2gam-30-5' (SEQ ID NO: 271, a first determined genomic sequence representing the 5' end).

EXAMPLE 2

INDUCTION OF T CELL PROLIFERATION AND INTERFERON-γ PRODUCTION BY *CHLAMYDIA TRACHOMATIS* ANTIGENS

The ability of recombinant *Chlamydia trachomatis* antigens to induce T cell proliferation and interferon-γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatograph (Webb et al., *J. Immunology 157*:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. trachomatis* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μg/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μl, 50 μl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 μCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN-γ is measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN-γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN-γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The

plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

Using the above methodology, recombinant 1B1-66 protein (SEQ ID NO: 5) as well as two synthetic peptides corresponding to amino acid residues 48-67 (SEQ ID NO: 13; referred to as 1-B1-66/48-67) and 58-77 (SEQ ID NO: 14, referred to as 1B1-66/58-77), respectively, of SEQ ID NO: 5, were found to induce a proliferative response and IFN-γ production in a Chlamydia-specific T cell line used to screen a genomic library of *C. trachomatis* LGV II.

Further studies have identified a *C. trachomatis*-specific T-cell epitope in the ribosomal S13 protein. Employing standard epitope mapping techniques well known in the art, two T-cell epitopes in the ribosomal S13 protein (rS13) were identified with a *Chlamydia*-specific T-cell line from donor CL-8 (T-cell line TCL-8 EB/DC). Fig. 8 illustrates that the first peptide, rS13 1-20 (SEQ ID NO: 106), is 100% identical with the corresponding *C. pneumoniae* sequence, explaining the cross-reactivity of the T-cell line to recombinant *C. trachomatis*- and *C. pneumoniae*-rS13. The response to the second peptide rS13 56-75 (SEQ ID NO: 108) is *C. trachomatis*-specific, indicating that the rS13 response in this healthy asymptomatic donor was elicited by exposure to *C. trachomatis* and not to *C. pneumoniae*, or any other microbial infection.

As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5×10^4 TCP-21 T-cells in the presence of 1×10^4 monocyte-derived dendritic cells

with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae,* or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 μg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae.*

To further define the epitope described above, an additional T-cell line, TCT-3, was used in epitope mapping experiments. The immunoassays were performed as described above, except that only peptides from *C. trachomatis* were tested. The T-cells gave a proliferative response to two peptides, CT-OMCB #152-171 and CT-OMCB #157-176 (SEQ ID NO: 246 and 247, respectively), thereby defining an additional immunogenic epitope in the cysteine rich outer membrane protein of *C. trachomatis*.

Clone 14H1-4, (SEQ ID NO: 56, with the corresponding full-length amino acid sequence provided in SEQ ID NO: 92), was identified using the TCT-3 cell line in the CD4 T-cell expression cloning system previously described, and was shown to contain a complete ORF for the, thiol specific antioxidant gene (CT603), referred to as TSA. Epitope mapping immunoassays were performed, as described above, to further define the epitope. The TCT-3 T-cells line exhibited a strong proliferative response to the overlapping peptides CT-TSA #96-115, CT-TSA #101-120 and CT-TSA #106-125 (SEQ ID NO: 254-256, respectively) demonstrating an immunoreactive epitope in the thiol specific antioxidant gene of *C. trachomatis* serovar LGVII.

EXAMPLE 3
PREPARATION OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugating or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 4
ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING *CHLAMYDIA* ANTIGENS USING RETROVIRAL EXPRESSION VECTOR SYSTEMS AND SUBSEQUENT IMMUNOLOGICAL ANALYSIS

A genomic library of *Chlamydia trachomatis* LGV II was constructed by limited digests using BamHI, BglII, BstYi and MboI restriction enzymes. The restriction digest fragments were subsequently ligated into the BamHI site of the retroviral vectors pBIB-KS1,2,3. This vector set was modified to contain a Kosak translation initiation site and stop codons in order to allow expression of proteins from short DNA genomic fragments, as shown in Fig. 2. DNA pools of 80 clones were prepared and transfected into the retroviral packaging line Phoenix-Ampho, as described in Pear, W.S., Scott, M.L. and Nolan, G.P., Generation of High Titre, Helper-free Retroviruses by Transient Transfection. Methods in Molecular Medicine: Gene

Therapy Protocols, Humana Press, Totowa, NJ, pp. 41-57. The *Chlamydia* library in retroviral form was then transduced into H2-Ld expressing P815 cells, which were then used as target cells to stimulate an antigen specific T-cell line.

A *Chlamydia*-specific, murine $H2^d$ restricted CD8+ T-cell line was expanded in culture by repeated rounds of stimulation with irradiated *C. trachomatis*-infected J774 cells and irradiated syngeneic spleen cells, as described by Starnbach, M., in *J. Immunol.*, 153:5183, 1994. This *Chlamydia*-specific T-cell line was used to screen the above *Chlamydia* genomic library expressed by the retrovirally-transduced P815 cells. Positive DNA pools were identified by detection of IFN-γ production using Elispot analysis (*SEE* Lalvani et al., *J. Experimental Medicine 186*:859-865, 1997).

Two positive pools, referred to as 2C7 and 2E10, were identified by IFN-γ Elispot assays. Stable transductants of P815 cells from pool 2C7 were cloned by limiting dilution and individual clones were selected based upon their capacity to elicit IFN-γ production from the *Chlamydia*-specific CTL line. From this screening process, four positive clones were selected, referred to as 2C7-8, 2C7-9, 2C7-19 and 2C7-21. Similarly, the positive pool 2E10 was further screened, resulting in an additional positive clone, which contains three inserts. The three inserts are fragments of the CT016, tRNA syntase and clpX genes (SEQ ID NO: 268-270, respectively).

Transgenic DNA from these four positive 2C7 clones were PCR amplified using pBIB-KS specific primers to selectively amplify the *Chlamydia* DNA insert. Amplified inserts were gel purified and sequenced. One immunoreactive clone, 2C7-8 (SEQ ID NO: 15, with the predicted amino acid sequence provided in SEQ ID NO: 32), is a 160 bp fragment with homology to nucleotides 597304-597145 of *Chlamydia trachomatis*, serovar D (NCBI, BLASTN search; SEQ ID NO: 33, with the predicted amino acid sequence provided in SEQ ID NO: 34). The sequence of clone 2C7-8 maps within two putative open reading frames from the region of high homology described immediately above, and in particular, one of these putative open reading frames, consisting of a 298 amino acid fragment (SEQ ID NO: 16, with the predicted amino acid sequence provided in SEQ ID NO: 17), was demonstrated to exhibit immunological activity.

Full-length cloning of the 298 amino acid fragment (referred to as CT529 and/or the Cap1 gene) from serovar L2 was obtained by PCR amplification using 5'-

ttttgaagcaggtaggtgaatatg (forward) (SEQ ID NO: 159) and 5'-ttaagaaatttaaaaaatccctta (reverse) (SEQ ID NO: 160) primers, using purified *C. trachomatis* L2 genomic DNA as template. This PCR product was gel-purified, cloned into pCRBlunt (Invitrogen, Carlsbad, CA) for sequencing, and then subcloned into the *Eco*RI site of pBIB-KMS, a derivative of pBIB-KS for expression. The *Chlamydia pnuemoniae* homlogue of CT529 is provided in SEQ ID NO: 291, with the corresponding amino acid sequence provided in SEQ ID NO: 292.

Full-length DNA encoding various CT529 serovars were amplified by PCR from bacterial lysates containing 10^5 IFU, essentially as described (Denamur, E., C. Sayada, A. Souriau, J. Orfila, A. Rodolakis and J. Elion. 1991. J. Gen. Microbiol. 137: 2525). The following serovars were amplified as described: Ba (SEQ ID NO: 134, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 135); E (BOUR) and E (MTW447) (SEQ ID NO: 122, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 123); F (NI1) (SEQ ID NO: 128, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 129); G; (SEQ ID NO: 126, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 127); Ia (SEQ ID NO: 124, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 125); L1 (SEQ ID NO: 130, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 131); L3 (SEQ ID NO: 132, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 133); I (SEQ ID NO: 263, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 264); K (SEQ ID NO: 265, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 266); and MoPn (SEQ ID NO: 136, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 137). PCR reactions were performed with Advantage Genomic PCR Kit (Clontech, Palo Alto, CA) using primers specific for serovar L2 DNA (external to the ORF). Primers sequences were 5'-ggtataatatctctctaaattttg (forward-SEQ ID NO: 161) and 5'-agataaaaaaggctgtttc' (reverse-SEQ ID NO: 162) except for MoPn which required 5'-ttttgaagcaggtaggtgaatatg (forward-SEQ ID NO: 163) and 5'-tttacaataagaaaagctaagcactttgt (reverse-SEQ ID NO: 164). PCR amplified DNA was purified with QIAquick PCR purification kit (Qiagen, Valencia, CA) and cloned in pCR2.1 (Invitrogen, Carlsbad, CA) for sequencing.

Sequencing of DNA derived from PCR amplified inserts of immunoreactive clones was done on an automated sequencer (ABI 377) using both a pBIB-KS specific forward primer 5'-ccttacacagtcctgctgac (SEQ ID NO: 165) and a reverse primer 3'-gtttccgggccctcacattg (SEQ ID NO: 166). PCRBlunt cloned DNA coding for CT529 serovar L2 and pCR2.1 cloned DNA coding for CT529 serovar Ba, E (BOUR), E (MTW447), F (NI1), G, Ia, K, L1, L3 and MoPn were sequenced using T7 promoter primer and universal M13 forward and M13 reverse primers.

To determine if these two putative open reading frames (SEQ ID NO: 16 and 20) encoded a protein with an associated immunological function, overlapping peptides (17-20 amino acid lengths) spanning the lengths of the two open reading frames were synthesized, as described in Example 3. A standard chromium release assay was utilized to determine the percent specific lysis of peptide-pulsed $H2^d$ restricted target cells. In this assay, aliquots of P815 cells ($H2^d$) were labeled at 37° C for one hour with 100 μCi of ^{51}Cr in the presence or absence of 1 μg/ml of the indicated peptides. Following this incubation, labeled P815 cells were washed to remove excess ^{51}Cr and peptide, and subsequently plated in duplicate in microculture plates at a concentration of 1,000 cells/well. Effector CTL (*Chlamydia*-specific CD8 T cells) were added at the indicated effector:target ratios. Following a 4 hour incubation, supernatants were harvested and measured by gamma-counter for release of ^{51}Cr into the supernatant. Two overlapping peptides from the 298 amino acid open reading frame did specifically stimulate the CTL line. The peptides represented in SEQ ID NO: 138-156 were synthesized, representing the translation of the L2 homologue of the serovar D open reading frame for CT529 (Capl gene) and 216 amino acid open reading frame. As shown in Fig. 3, peptides CtC7.8-12 (SEQ ID NO: 18, also referred to as Capl#132-147, SEQ ID NO: 139) and CtC7.8-13 (SEQ ID NO: 19, also referred to as Capl#138-155, SEQ ID NO: 140) were able to elicit 38 to 52% specific lysis, respectively, at an effector to target ratio of 10:1. Notably, the overlap between these two peptides contained a predicted $H2^d$ (K^d and L^d) binding peptide. A 10 amino acid peptide was synthesized to correspond to this overlapping sequence (SEQ ID NO: 31) and was found to generate a strong immune response from the anti-*Chlamydia* CTL line by elispot assay. Significantly, a search of the most recent Genbank database revealed no proteins have previously been described for this gene. Therefore, the putative open

reading frame encoding clone 2C7-8 (SEQ ID NO: 15) defines a gene which encompasses an antigen from *Chlamydia* capable of stimulating antigen-specific CD8+ T-cells in a MHC-I restricted manner, demonstrating this antigen could be used to develop a vaccine against *Chlamydia.*

To confirm these results and to further map the epitope, truncated peptides (SEQ ID NO: 138-156) were made and tested for recognition by the T-cells in an IFN-g ELISPOT assay. Truncations of either Ser139 (Cap1#140-147, SEQ ID NO: 146) or Leu147 (Cap1#138-146, SEQ ID NO: 147) abrogate T-cell recognition. These results indicate that the 9-mer peptide Cap1#139-147 (SFIGGITYL, SEQ ID NO: 145) is the minimal epitope recognized by the *Chlamydia*-specific T-cells.

Sequence alignments of Cap1 (CT529) from selected serovars of *C. trachomatis* (SEQ ID NO: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139) shows one of the amino acid differences is found in position 2 of the proposed epitope. The homologous serovar D peptide is SIIGGITYL (SEQ ID NO: 168). The ability of SFIGGITYL and SIIGGITYL to target cells for recognition by the *Chlamydia* specific T-cells was compared. Serial dilutions of each peptide were incubated with P815 cells and tested for recognition by the T-cells in a ^{51}Cr release assay, as described above. The *Chlamydia*-specific T-cells recognize the serovar L2 peptide at a minimum concentration of 1 nM and the serovar D peptide at a minimum concentration of 10 nM.

Further studies have shown that a Cap1#139-147-specific T-cell clone recognizes *C. trachomatis* infected cells. To confirm that $Cap1_{139\text{-}147}$ is presented on the surface of *Chlamydia* infected cells, Balb-3T3 (H-2^{d}) cells were infected with *C. trachomatis* serovar L2 and tested to determine whether these cells are recognized by a CD8+ T-cell clone specific for Cap1#139-147 epitope (SEQ ID NO: 145). The T-cell clone specific for Cap1#139-147 epitope was obtained by limiting dilution of the line 69 T-cells. The T-cell clone specifically recognized the *Chlamydia* infected cells. In these experiments, target cells were *C. trachomatis* infected (positive control) or uninfected Balb/3T3 cells, showing 45%, 36% and 30% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively; or Cap1#139-147 epitope (SEQ ID NO: 145) coated, or untreated P815 cells, showing 83%, 75% and 58% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively (negative controls having less than 5% lysis in all cases). This data suggests that the epitope is presented during infection.

In vivo studies show Cap1#139-147 epitope-specific T-cells are primed during murine infection with *C. trachomatis*. To determine if infection with *C. trachomatis* primes a Cap1#139-147 epitope-specific T-cell response, mice were infected i.p. with 10^8 IFU of *C. trachomatis* serovar L2. Two weeks after infection, the mice were sacrificed and spleen cells were stimulated on irradiated syngeneic spleen cells pulsed with Cap1#139-147 epitope peptide. After 5 days of stimulation, the cultures were used in a standard ^{51}Cr release assay to determine if there were Cap1#139-147 epitope-specific T-cells present in the culture. Specifically, spleen cells from a *C. trachomatis* serovar L2 immunized mouse or a control mouse injected with PBS after a 5 days culture with Cap1#139-147 peptide-coated syngeneic spleen cells and CD8+ T-cells able to specifically recognize Cap1#139-147 epitope gave 73%, 60% and 32% specific lysis at a30:1, 10:1 and 3:1 effector to target ratios, respectively. The control mice had a percent lysis of approximately 10% at a 30:1 effector to target ratio, and steadily declining with lowering E:T ratios. Target cells were Cap1#139-147 peptide-coated, or untreated P815 cells. These data suggest that Cap1#139-147 peptide-specific T-cells are primed during murine infection with *C. trachomatis*.

Ct529 Localization

Studies were performed demonstrating that Ct529 (referred to herein as Cap-1) localizes to the inclusion membrane of *C. trachomatis*-infected cells and is not associated with elementary bodies or reticulate bodies. As described above, Cap-1 was identified as a product from *Chlamydia* that stimulates CD8+ CTL. These CTL are protective in a murine model of infection, thus making Cap-1 a good vaccine candidate. Further, since these CTL are MHC-I restricted, the Cap-1 gene must have access to the cytosol of infected cells, which may be a unique characteristic of specific *Chlamydial* gene products. Therefore, determination of the cellular localization of the gene products would be useful in characterizing Cap-1 as a vaccine candidate. To detect the intracellular localization of Cap-1, rabbit polyclonal antibodies directed against a recombinant polypeptide encompassing the N-terminal 125 amino acids of Cap-1 (SEQ ID NO: 305, with the amino acid sequence including the N-terminal 6-His tag provided in SEQ ID NO: 304) were used to stain McCoy cells infected with *Chlamydiae*.

Rabbit-anti-Cap-1 polyclonal antibodies were obtained by hyper-immunization of rabbits with a recombinant polypeptide, rCt529c1-125 (SEQ ID NO: 305) encompassing the N-terminal portion of Cap-1. Recombinant rCt529e1-125 protein was obtained from *E. coli* transformed with a pET expression plasmid (as described above) encoding the nucleotides 1-375 encoding the N-terminal 1-125 amino acids of Cap-1. Recombinant protein was purified by Ni-NTA using techniques well known in the art. For a positive control antiserum, polyclonal antisera directed against elementary bodies were made by immunization of rabbits with purified *C. trachomatis* elementary bodies (Biodesign, Sacco, Maine). Pre-immune sera derived from rabbits prior to immunization with the Cap-1 polypeptide was used as a negative control.

Immunocytochemistry was performed on McCoy cell monolayers grown on glass coverslips inoculated with either *C. trachomatis* serovar L2 or *C. psitacci*, strain 6BC, at a concentration of 10^6 IFU (Inclusion Forming Units) per ml. After 2 hours, medium was aspirated and replaced with fresh RP-10 medium supplemented with cycloheximide (1.0 μg/ml). Infected cells were incubated at in 7% CO_2 for 24 hours and fixed by aspirating medium, rinsing cells once with PBS and methanol fixation for 5 minutes. For antigen staining, fixed cell monolayers were washed with PBS and incubated at 37°C for 2 hours with 1:100 dilutions of specific or control antisera. Cells were rinsed with PBS and incubated for 1 hour with fluorescein isothiocyanate (FITC)-labeled, anti-rabbit IgG (KPL, Gaithersburg) and stained with Evans blue (0.05%) in PBS. Fluorescence was observed with a 100X objective (Zeiss epifluorescence microscope), and photographed (Nikon UFX-11A camera).

Results from this study show Cap-1 localizes to the inclusion membrane of *C. trachomatis*-infected cells. Cap-1 specific antibody labeled the inclusion membranes of *C. trachomatis*-infected cells, but not *Chlamydial* elementary bodies contained in these inclusions or released by the fixation process. Conversely, the anti-elementary body antibody clearly labeled the bacterial bodies, not only within the inclusions, but those released by the fixation process. Specificity of the anti-Cap-1 antibody is demonstrated by the fact that it does not stain *C. psittaci*-infected cells. Specificity of the Cap-1 labeling is also shown by the absence of reactivity in pre-immune sera. These results suggest that Cap-1 is released from the bacteria and becomes associated with the *Chlamydial* inclusion membrane. Therefore, Cap-1 is a

gene product which may be useful for stimulating CD8+ T cells in the development of a vaccine against infections caused by *Chlamydia*.

The relevance of the Cap-1 gene as a potential CTL antigen in a vaccine against *Chlamydia* infection is further illustrated by two additional series of studies. First, CTL specific for the MHC-I epitope of Cap-1 CT529 #138-147 peptide of *C. trachomatis* (SEQ ID NO: 144) have been shown to be primed to a high frequency during natural infection. Specifically, Balb/C mice were inoculated with 10^6 I.F.U. of *C. trachomatis*, serova L2. After 2 weeks, spleens were harvested and quantified by Elispot analysis for the number of IFN-γ secreting cells in response to Cap-1 #138-147 peptide-pulsed antigen presenting cells. In two experiments, the number of IFN-γ-secreting cells in 10^5 splenocytes was about 1% of all CD8+ T-cells. This high frequency of responding CD8+ CTL to the MHC-1 epitope (Cap-1 CT529 #138-147 peptide) suggest that Cap-1 is highly immunogenic in infections.

Results from a second series of studies have shown that the Cap-1 protein is almost immediately accessible to the cytosol of the host cell upon infection. This is shown in a time-course of Cap-1 CT529 #138-147 peptide presentation. Briefly, 3T3 cells were infected with *C. trachomatis* serovar L2 for various lengths of time, and then tested for recognition by Cap-1 CT529 #138-147 peptide-specific CTL. The results show that *C. trachomatis*-infected 3T3 cells are targeted for recognition by the antigen-specific CTL after only 2 hours of infection. These results suggest that Cap-1 is an early protein synthesized in the development of *C. trachomatis* elementary bodies to reticulate bodies. A CD8+ CTL immune response directed against a gene product expressed early in infection may be particularly efficacious in a vaccine against *Chlamydia* infection.

EXAMPLE 5

GENERATION OF ANTIBODY AND T-CELL RESPONSES IN MICE IMMUNIZED WITH *CHLAMYDIA* ANTIGENS

Immunogenicity studies were conducted to determine the antibody and CD4+ T cell responses in mice immunized with either purified SWIB or S13 proteins formulated with Montanide adjuvant, or DNA-based immunizations with pcDNA-3 expression

vectors containing the DNA sequences for SWIB or S13. SWIB is also referred to as clone 1-B1-66 (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5), and S13 ribosomal protein is also referred to as clone 10-C10-31 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12). In the first experiment, groups of three C57BL/6 mice were immunized twice and monitored for antibody and CD4+ T-cell responses. DNA immunizations were intradermal at the base of the tail and polypeptide immunizations were administered by subcutaneous route. Results from standard ^{3}H-incorporation assays of spleen cells from immunized mice shows a strong proliferative response from the group immunized with purified recombinant SWIB polypeptide (SEQ ID NO: 5). Further analysis by cytokine induction assays, as previously described, demonstrated that the group immunized with SWIB polypeptide produced a measurable IFN-γ and IL-4 response. Subsequent ELISA-based assays to determine the predominant antibody isotype response in the experimental group immunized with the SWIB polypeptide were performed. Fig. 4 illustrates the SWIB-immunized group gave a humoral response that was predominantly IgG1.

In a second experiment, C3H mice were immunized three times with 10 μg purified SWIB protein (also referred to as clone 1-B1-66, SEQ ID NO: 5) formulated in either PBS or Montanide at three week intervals and harvested two weeks after the third immunization. Antibody titers directed against the SWIB protein were determined by standard ELISA-based techniques well known in the art, demonstrating the SWIB protein formulated with Montanide adjuvant induced a strong humoral immune response. T-cell proliferative responses were determined by a XTT-based assay (Scudiero, et al, *Cancer Research*, 1988, 48:4827). As shown in Fig. 5, splenocytes from mice immunized with the SWIB polypeptide plus Montanide elicited an antigen specific proliferative response. In addition, the capacity of splenocytes from immunized animals to secrete IFN-γ in response to soluble recombinant SWIB polypeptide was determined using the cytokine induction assay previously described. The splenocytes from all animals in the group immunized with SWIB polypeptide formulated with montanide adjuvant secreted IFN-γ in response to exposure to the SWIB Chlamydia antigen, demonstrating an *Chlamydia*-specific immune response.

In a further experiment, C3H mice were immunized at three separate time points at the base of the tail with 10 μg of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) formulated with the SBAS2 adjuvant (SmithKline Beecham, London, England). Antigen-specific antibody titers were measured by ELISA, showing both polypeptides induced a strong IgG response, ranging in titers from 1 $x10^{-4}$ to 1 $x10^{-5}$. The IgG1 and IgG2a components of this response were present in fairly equal amounts. Antigen-specific T-cell proliferative responses, determined by standard ^{3}H-incorporation assays on spleen cells isolated from immunized mice, were quite strong for SWIB (50,000 cpm above the negative control) and even stronger for s13 (100,000 cpm above the negative control). The IFNγ production was assayed by standard ELISA techniques from supernatant from the proliferating culture. *In vitro* restimulation of the culture with S13 protein induced high levels of IFNγ production, approximately 25 ng/ml versus 2 ng/ml for the negative control. Restimulation with the SWIB protein also induced IFNγ, although to a lesser extent.

In a related experiment, C3H mice were immunized at three separate time points with 10 μg of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) mixed with 10 μg of Cholera Toxin. Mucosal immunization was through intranasal inoculation. Antigen-specific antibody responses were determined by standard ELISA techniques. Antigen-specific IgG antibodies were present in the blood of SWIB-immunized mice, with titers ranging from 1 $x10^{-3}$ to 1 $x10^{-4}$, but non-detectable in the S13-immunized animals. Antigen-specific T-cell responses from isolated splenocytes, as measured by IFNγ production, gave similar results to those described immediately above for systemic immunization.

An animal study was conducted to determine the immunogenicity of the CT529 serovar LGVII CTL epitope, defined by the CT529 10mer consensus peptide (CSFIGGITYL – SEQ ID NO: 31), which was identified as an H2-Kd restricted CTL epitope. BALB/c mice (3 mice per group) were immunized three times with 25 μg of peptide combined with various adjuvants. The peptide was administered systemically at the base of the tail in either SKB Adjuvant System SBAS-2'', SBAS-7 (SmithKline

Beecham, London, England) or Montanide. The peptide was also administered intranasally mixed with 10ug of Cholera Toxin (CT). Naive mice were used as a control. Four weeks after the 3rd immunization, spleen cells were restimulated with LPS-blasts pulsed with 10ug/ml CT529 10mer consensus peptide at three different effector to LPS-blasts ratios : 6, 1.5 and 0.4 at $1x10^6$ cell/ml. After 2 restimulations, effector cells were tested for their ability to lyse peptide pulsed P815 cells using a standard chromium release assay. A non-relevant peptide from chicken egg ovalbumin was used as a negative control. The results demonstrate that a significant immune response was elicited towards the CT529 10mer consensus peptide and that antigen-specific T-cells capable of lysing peptide-pulsed targets were elicited in response to immunization with the peptide. Specifically, antigen-specific lytic activities were found in the SBAS-7 and CT adjuvanted group while Montanide and SBAS-2" failed to adjuvant the CTL epitope immunization.

EXAMPLE 6

EXPRESSION AND CHARACTERIZATION OF *CHLAMYDIA PNEUMONIAE* GENES

The human T-cell line, TCL-8, described in Example 1, recognizes *Chlamydia trachomatis* as well as *Chlamydia pneumonia* infected monocyte-derived dendritic cells, suggesting *Chlamydia trachomatis* and *pneumonia* may encode cross-reactive T-cell epitopes. To isolate the *Chlamydia pneumonia* genes homologous to *Chlamydia trachomatis* LGV II clones 1B1-66, also referred to as SWIB (SEQ ID NO: 1) and clone 10C10-31, also referred to as S13 ribosomal protein (SEQ ID NO: 4), HeLa 229 cells were infected with *C. pneumonia* strain TWAR (CDC/CWL-029). After three days incubation, the *C. pneumonia*-infected HeLa cells were harvested, washed and resuspended in 200 µl water and heated in a boiling water bath for 20 minutes. Ten microliters of the disrupted cell suspension was used as the PCR template.

C. pneumonia specific primers were designed for clones 1B1-66 and 10C10-31 such that the 5' end had a 6X-Histidine tag and a Nde I site inserted, and the 3' end had a stop codon and a BamHI site included (Fig. 6). The PCR products were amplified and sequenced by standard techniques well known in the art. The *C.*

pneumonia-specific PCR products were cloned into expression vector pET17B (Novagen, Madison, WI) and transfected into E. coli BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Two proteins from *C. pneumonia* were thus generated, a 10-11 kDa protein referred to as CpSWIB (SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively), a 15 kDa protein referred to as CpS13 (SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively).

EXAMPLE 7

INDUCTION OF T CELL PROLIFERATION AND INTERFERON-γ PRODUCTION BY *CHLAMYDIA PNEUMONIAE* ANTIGENS

The ability of recombinant *Chlamydia pneumoniae* antigens to induce T cell proliferation and interferon-γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatography (Webb et al., *J. Immunology 157*:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. pneumoniae* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μg/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μl, 50 μl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 μCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN-γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN-γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN-γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

A human anti-*Chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* was used to determine whether the expressed proteins described in the example above, (i.e., CpSWIB, SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively, and the 15 kDa protein referred to as CpS13 SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively), possessed T-cell epitopes common to both *C. trachomatis* and *C. pneumonia*. Briefly, *E. coli* expressing *Chlamydial* proteins were titered on 1 x 10^4 monocyte-derived dendritic cells. After two hours, the dendritic_cells cultures were washed and 2.5 x 10^4 T cells (TCL-8) added and allowed to incubate for an additional 72 hours. The amount of INF-γ in the culture supernatant was then determined by ELISA. As shown in Figs. 7A and 7B, the TCL-8 T-cell line specifically recognized the S13 ribosomal protein from both *C. trachomatis* and *C. pneumonia* as demonstrated by the antigen-specific induction of IFN-γ, whereas only the SWIB protein from *C. trachomatis* was recognized by the T-cell line. To

validate these results, the T cell epitope of *C. trachomatis* SWIB was identified by epitope mapping using target cells pulsed with a series of overlapping peptides and the T-cell line TCL-8. 3H-thymidine incorporation assays demonstrated that the peptide, referred to as C.t.SWIB 52-67, of SEQ ID NO: 39 gave the strongest proliferation of the TCL-8 line. The homologous peptides corresponding to the SWIB of *C. pneumoniae* sequence (SEQ ID NO: 40), the topoisomerase-SWIB fusion of *C. pneumoniae* (SEQ ID NO: 43) and *C. trachomatis* (SEQ ID NO: 42) as well as the human SWI domain (SEQ ID NO: 41) were synthesized and tested in the above assay. The T-cell line TCL-8 only recognized the *C. trachomatis* peptide of SEQ ID NO: 39 and not the corresponding *C. pneumoniae* peptide (SEQ ID NO: 40), or the other corresponding peptides described above (SEQ ID NO; 41-43).

Chlamydia-specific T cell lines were generated from donor CP-21 with a positive serum titer against *C. pneumoniae* by stimulating donor PBMC with either *C. trachomatis* or *C. pneumoniae*-infected monocyte-derived dendritic cells, respectively. T-cells generated against *C. pneumoniae* responded to recombinant *C. pneumoniae*-SWIB but not *C. trachomatis*-SWIB, whereas the T-cell line generated against *C. trachomatis* did not respond to either *C. trachomatis*- or *C. pneumoniae*-SWIB (see Fig. 9). The *C. pneumoniae*-SWIB specific immune response of donor CP-21 confirms the *C. pneumoniae* infection and indicates the elicitation of *C. pneumoniae*-SWIB specific T-cells during *in vivo C. pneumoniae* infection.

Epitope mapping of the T-cell response to *C. pneumoniae*-SWIB has shown that Cp-SWIB-specific T-cells responded to the overlapping peptides Cp-SWIB 32-51 (SEQ ID NO: 101) and Cp-SWIB 37-56 (SEQ ID NO: 102), indicating a *C. pneumoniae*-SWIB-specific T-cell epitope Cp-SWIB 37-51 (SEQ ID NO: 100).

In additional experiments, T-cell lines were generated from donor CP1, also a *C. pneumoniae* seropositive donor, by stimulating PBMC with non-infectious elementary bodies from *C. trachomatis* and *C. pneumoniae*, respectively. In particular, proliferative responses were determined by stimulating 2.5 x 10^4 T-cells in the presence of 1 x 10^4 monocyte-derived dendritic cells and non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae,* or either recombinant *C. trachomatis* or *C. pneumoniae* SWIB protein. The T-cell response against SWIB resembled the data obtained with T-cell lines from CP-21 in that *C. pneumoniae*-SWIB, but not *C.*

trachomatis-SWIB elicited a response by the *C. pneumoniae* T-cell line. In addition, the *C. trachomatis* T-cell line did not proliferate in response to either *C. trachomatis* or *C. pneumoniae* SWIB, though it did proliferate in response to both CT and CP elementary bodies.As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5 x 10^4 TCP-21 T-cells in the presence of 1 x 10^4 monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae,* or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 μg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae.*

EXAMPLE 8

IMMUNE RESPONSES OF HUMAN PBMC AND T-CELL LINES AGAINST *CHLAMYDIA* ANTIGENS

The examples provided herein suggest that there is a population of healthy donors among the general population that have been infected with *C. trachomatis* and generated a protective immune response controlling the *C. trachomatis* infection. These donors remained clinically asymptomatic and seronegative for *C. trachomatis*. To characterize the immune responses of normal donors against *chlamydial* antigens which had been identified by CD4 expression cloning, PBMC

obtained from 12 healthy donors were tested against a panel of recombinant *chlamydial* antigens including *C. trachomatis-, C. pneumoniae*-SWIB and *C. trachomatis-, C. pneumoniae*-S13. The data are summarized in Table I below. All donors were seronegative for *C. trachomatis*, whereas 6/12 had a positive *C. pneumoniae* titer. Using a stimulation index of >4 as a positive response, 11/12 of the subjects responded to *C. trachomatis* elementary bodies and 12/12 responded to *C. pneumoniae* elementary bodies. One donor, AD104, responded to recombinant *C. pneumoniae*-S13 protein, but not to recombinant *C. trachomatis*-S13 protein, indicating a *C. pneumoniae*-specific response. Three out of 12 donors had a *C. trachomatis*-SWIB, but not a *C. pneumoniae*-SWIB specific response, confirming a *C. trachomatis* infection. *C. trachomatis* and *C. pneumoniae*- S13 elicited a response in 8/12 donors suggesting a chlamydial infection. These data demonstrate the ability of SWIB and S13 to elicit a T-cell response in PBMC of normal study subjects.

Table I.

Immune response of normal study subjects against *Chlamydia*

Donor	Sex	*Chlamydia* IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
AD100	male	negative	++	+++	+	-	++	++	-	n.t.
AD104	female	negative	+++	++	-	-	-	++	-	n.t.
AD108	male	CP 1:256	++	++	+	+/-	+	+	+	n.t.
AD112	female	negative	++	++	+	-	+	-	+/-	n.t.
AD120	male	negative	-	+	-	-	-	-	-	n.t.
AD124	female	CP 1:128	++	++	-	-	-	-	-	n.t.
AD128	male	CP 1:512	+	++	-	-	++	+	++	-
AD132	female	negative	++	++	-	-	+	+	-	-
AD136	female	CP 1:128	+	++	-	-	+/-	-	-	-
AD140	male	CP 1:256	++	++	-	-	+	+	-	-
AD142	female	CP 1:512	++	++	-	-	+	+	+	-
AD146	female	negative	++	++	-	-	++	+	+	-

CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae;* EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein.Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3 x 10^5 PBMC with 1 x 10^4 monocyte-derived dendritic cells pre-incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^{3}H-thymidine pulse for the last 18h.

SI: Stimulation index

+/-:	SI ~	4
+:	SI >	4
++:	SI	10-30
+++:	SI >	30

In a first series of experiments, T-cell lines were generated from a healthy female individual (CT-10) with a history of genital exposure to *C. trachomatis* by stimulating T-cells with *C. trachomatis* LGV II elementary bodies as previously described. Although the study subject was exposed to *C. trachomatis*, she did not seroconvert and did not develop clinical symptoms, suggesting donor CT-10 may have developed a protective immune response against *C. trachomatis*. As shown in Fig. 10, a primary *Chlamydia*-specific T-cell line derived from donor CT-10 responded to *C. trachomatis*-SWIB, but not *C. pneumoniae*-SWIB recombinant proteins, confirming the exposure of CT-10 to *C. trachomatis*. Epitope mapping of the T-cell response to *C. trachomatis*-SWIB showed that this donor responded to the same epitope Ct-SWIB 52-67 (SEQ ID NO: 39) as T-cell line TCL-8, as shown in Fig. 11.

Additional T-cell lines were generated as described above for various *C. trachomatis* patients. A summary of the patients' clinical profile and proliferative responses to various *C. trachomatis* and *C. pneumoniae* elementary bodies and recombinant proteins are summarized in Table II as follows:

Proliferative response of *C. trachomatis* patients

Patients	Clinical manifestation	IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
CT-1	NGU	negative	+	+	-	-	++	++	++	+
CT-2	NGU	negative	++	++	-	-	+	+/-	-	-
CT-3	asymptomatic shed Eb Dx was HPV	Ct 1:512 Cp 1:1024 Cps 1:256	+	+	-	-	+	-	+	-
CT-4	asymptomatic shed Eb	Ct 1:1024	+	+	-	-	-	-	-	-
CT-5	BV	Ct 1:256 Cp 1:256	++	++	-	-	+	-	-	-
CT-6	perinial rash discharge	Cp 1:1024	+	+	-	-	-	-	-	-
CT-7	BV genital ulcer	Ct 1:512 Cp 1:1024	+	+	-	-	+	+	+	-
CT-8	Not known	Not tested	++	++	-	-	-	-	-	-
CT-9	asymptomatic	Ct 1:128 Cp 1:128	+++	++	-	-	++	+	+	-
CT-10	Itch mild vulvar	negative	++	++	-	-	-	-	-	-
CT-11	BV, abnormal pap	Ct 1: 512	+++	+++	-	-	+++	+/-	++	+
CT-12	asymptomatic	Cp 1: 512	++	++	-	-	++	+	+	-

NGU= Non-Gonococcal Urethritis; BV= Bacterial Vaginosis; CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae;* EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein

Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3 x 10^5 PBMC with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^{3}H-thymidine pulse for the last 18 hours.

SI: Stimulation index

+/-:	SI ~	4
+:	SI >	4
++:	SI	10-30
+++:	SI >	30

Using the panel of asymptomatic (as defined above) study subjects and *C. trachomatis* patients, as summarized in Tables I and II, a comprehensive study of the immune responses of PBMC derived from the two groups was conducted. Briefly, PBMCs from *C. pneumoniae* patients as well as from normal donors are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides, a panel of recombinant *chlamydial* antigens including *C. trachomatis-*, *C. pneumoniae*-SWIB and S13, as well as . *C. trachomatis* lpdA and TSA are added in duplicate at concentrations of 0.5 to 10 μg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μl, 50 μl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 μCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

Proliferative responses to the recombinant *Chlamydiae* antigens demonstrated that the majority of asymptomatic donors and *C. trachomatis* patients recognized the *C. trachomatis* S13 antigen (8/12) and a majority of the *C. trachomatis* patients recognized the *C. pneumonia* S13 antigen (8/12), with 4/12 asymptomatic donors also recognizing the *C. pneumonia* S13 antigen. Also, six out of twelve of the *C. trachomatis* patients and four out of twelve of the asymptomatic donors gave a proliferative response to the lpdA antigen of *C. trachomatis*. These results demonstrate that the *C. trachomatis* and *C. pneumonia* S13 antigen, *C. trachomatis* Swib antigen and the *C. trachomatis* lpdA antigen are recognized by the asymptomatic donors, indicating these antigens were recognized during exposure to *Chlamydia* and an immune response elicited against them. This implies these antigens may play a role in conferring protective immunity in a human host. In addition, the *C. trachomatis* and *C. pneumonia* S13 antigen is recognized equally well among the *C. trachomatis* patients, therefore indicating there may be epitopes shared between *C. trachomatis* and *C. pneumonia* in the S13 protein. Table III summarizes the results of these studies.

Table III.

Antigen	Normal Donors	C.t. Patients
C.t.-Swib	3/12	0/12
C.p.-Swib	0/12	0/12
C.t.-S13	8/12	8/12
C.p.-S13	4/12	8/12
lpdA	4/12	6/12
TSA	0/12	2/12

A series of studies were initiated to determine the cellular immune response to short-term T-cell lines generated from .asymptomatic donors and *C. trachomatis* patients. Cellular immune responses were measured by standard proliferation assays and IFN-γ, as described in Example 7. Specifically, the majority of the antigens were in the form of single *E. coli* clones expressing Chlamydial antigens, although some recombinant proteins were also used in the assays. The single *E. coli* clones were titered on 1×10^4 monocyte-derived dendritic cells and after two hours, the culture was washed and 2.5×10^4 T-cells were added. The assay using the recombinant proteins were performed as previously described. Proliferation was determined after four days with a standard ^{3}H-thymidine pulse for the last 18 hours. Induction of IFN-γ was determined from culture supernatants harvested after four days using standard ELISA assays, as described above. The results show that all the *C. trachomatis* antigens tested, except for C.T. Swib, elicited a proliferative response from one or more different T-cell lines derived form *C. trachomatis* patients. In addition, proliferative responses were elicited from both the *C. trachomatis* patients and asymptomatic donors for the following *Chlamydia* genes, CT622, groEL, pmpD, CT610 and rS13.

The 12G3-83 clone also contains sequences to CT734 and CT764 in addition to CT622, and therefore these gene sequence may also have immunoreactive epitopes. Similarly, clone 21G12-60 contains sequences to the hypothetical protein genes CT229 and CT228 in addition to CT875; and 15H2-76 also contains sequences

from CT812 and CT088, as well as sharing homology to the sycE gene. Clone 11H3-61 also contains sequences sharing homology to the PGP6-D virulence protein.

Table IV.

Clone	**C. t. Antigen** (putative*)	**TCL from Asymp. Donors**	**TCL from C. t. Patients**	**SEQ ID NO:**
1B1-66 (E. coli)	Swib	2/2	0/4	5
1B1-66 (protein)	Swib	2/2	0/4	5
12G3-83 (E. coli)	CT622*	2/2	4/4	57
22B3-53 (E. coli)	groEL	1/2	4/4	111
22B3-53 (protein)	groEL	1/2	4/4	111
15H2-76 (E. coli)	PmpD*	1/2	3/4	87
11H3-61 (E. coli)	rL1*	0/2	3/4	60
14H1-4 (E. coli)	TSA	0/2	3/4	56
14H1-4 (protein)	TSA	0/2	3/4	56
11G10-46 (E. coli)	CT610	1/2	1/4	62
10C10-17 (E. coli)	rS13	1/2	1/4	62
10C10-17 (protein)	rS13	1/2	1/4	62
21G12-60 (E. coli)	CT875*	0/2	2/4	110
11H4-32 (E. coli)	dnaK	0/2	2/4	59
21C7-8 (E. coli)	dnaK	0/2	2/4	115
17C10-31 (E. coli)	CT858	0/2	2/4	114

EXAMPLE 9

PROTECTION STUDIES USING *CHLAMYDIA* ANTIGENS

1. SWIB

Protection studies were conducted in mice to determine whether immunization with chlamydial antigens can impact on the genital tract disease resulting from chlamydial inoculation. Two models were utilized; a model of intravaginal inoculation

that uses a human isolate containing a strain of *Chlamydia psittaci* (MTW447), and a model of intrauterine inoculation that involves a human isolate identified as *Chlamydia trachomatis*, serovar F (strain NI1). Both strains induce inflammation in the upper genital tract, which resemble endometritis and salpingitis caused by *Chlamydia trachomatis* in women. In the first experiment, C3H mice (4 mice per group) were immunized three times with 100 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5). Inoculations were at the base of the tail for systemic immunization. Two weeks after the last immunization, animals were progesterone treated and infected, either thru the vagina or by injection of the inoculum in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored (from + for very mild, to +++++ for very severe). Scores attributed to each single oviduct /ovary were summed and divided by the number of organs examined to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control-immunized animals receiving empty vector showed consistent inflammation with an ovary /oviduct mean inflammation score of 6.12, in contrast to 2.62 for the DNA-immunized group. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 8.37, versus 5.00 for the DNA-immunized group. Also, in the later model, vaccinated mice showed no signs of tubal occlusion while negative control vaccinated groups had inflammatory cells in the lumen of the oviduct

In a second experiment, C3H mice (4 mice per group) were immunized three times with 50 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5) encapsulated in Poly Lactide co-Glycolide microspheres (PLG); immunizations were made intra-peritoneally. Two weeks after the last immunization, animal were progesterone treated and infected by inoculation of *C. psittaci* in the vagina. Two weeks after infection, mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored as previously described. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean of inflammation for the group. Negative control-

immunized animals receiving PLG-encapsulated empty vector showed consistent infammation with an ovary /oviduct mean inflammation score of 7.28, versus 5.71 for the PLG-encapsulated DNA immunized group. Inflammation in the peritoneum was 1.75 for the vaccinated group versus 3. 75 for the control.

In a third experiment, C3H mice (4 per group) were immunized three times with 10 µg of purified recombinant protein, either SWIB (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5, or S13 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12) mixed with Cholera Toxin (CT); the preparation was administred intranasally upon anaesthesia in a 20 uL volume. Two weeks after the last immunization, animal were progesterone treated and infected, either by vaginal inoculation of *C. psittaci* or by injection of *C. trachomatis* serovar F in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. The degree of inflammation was scored as described above. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control- immunized animals receiving cholera toxin alone showed an ovary /oviduct mean inflammation score of 4.25 (only 2 mice analyzed ; 2 other died) versus 5.00 for the s13 plus cholera toxin-immunized group, and 1.00 for the SWIB plus cholera toxin. Untreated infected animals had an ovary /oviduct mean inflammation score of 7. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 7.37 versus 6.75 for the s13 plus cholera toxin-immunized group and 5.37 for the SWIB plus cholera toxin-immunized group. Untreated infected animals had an ovary /oviduct mean inflammation score of 8.

The three experiments described above suggest that SWIB-specific protection is obtainable. This protective effect is more marked in the model of homologous infection but is still present when in a heterologous challenge infection with *C. psittaci*.

2. CT529/Capl

CT529/Cap1 was identified earlier as a product from Chlamydia that stimulates CD8+ CTL. In this example, we sought to confirm that immunization with Cap1 would be protective in an animal model of chlamydia infection.

To generate recombinant vaccinia virus for delivery of a Cap1 immunogenic fragment, a DNA fragment containing a modified Kozak sequence and base pairs 319-530 of the cap1 gene (CT529) was amplified from C. trachomatis L2 genomic DNA using PCR™ and ligated into pSC11ss (Earl PL, Koenig S, Moss B (1991) Biological and immunological properties of human immunodeficiency virus type 1 envelope glycoprotein: analysis of proteins with truncations and deletions expressed by recombinant vaccinia viruses. *J Virol.* 65:31-41). DNA digested with SalI and StuI. The portion of the cap1 gene ligated into pSC11ss encodes amino acids 107-176 of Cap1 protein, containing the previously identified CTL epitope of amino acids 139-147. The resulting plasmid was used to transfect CV-1 cells (ATCC# CCL-70; Jensen FC et al. (1964) Infection of human and simian tissue cultures with Rous Sarcoma Virus. Proc. Natl. Acad. Sci. USA 52: 53-59.) which were subsequently infected with wild-type vaccinia virus. Homologous recombination between the wild-type virus and plasmid DNA generated recombinant vaccinia viruses which were selected on the basis of both beta-galactosidase expression and the inactivation of thymidine kinase, as described previously (Chakrabarti et al, Mol Cell Biol. 1985, 5(12):3403-9). Recombinant virus was plaque purified three times and titered after growth in human TK-143B cells. Virus preparations were treated with equal volume of 0.25 mg/ml trypsin for 30 mins. at 37°C and diluted in PBS prior to immunization of mice. Groups of 5 mice were used for all experimental and control groups. The data presented below are representative of three independent experiments.

A group of mice was immunized with 10^6 of the recombinant vaccinia i.p. and was allowed to recover for 3 weeks. Negative control groups were immunized with either buffer alone or wild-type vaccinia. As a positive control, a group of mice was infected i.v. with 10^6 i.f.u. of C. trachomatis. The number of organisms given to the positive control group has been previously shown to be cleared within 2 weeks. After 3 weeks, animals in each of the groups were challenged i.v. with 10^6 i.f.u. of C.

trachomatis. Three days after challenge the mice were sacrificed and the number of i.f.u. per spleen was determined.

The mean number of organisms found in the spleens of animals immunized with the vaccinia virus expressing Cap1 (7.1×10^4) was 2.6-fold fewer ($p<0.01$; Wilcoxon's-Rank Sum analysis) than animals in the control groups immunized with either buffer (1.8×10^5) or wild-type vaccinia (1.9×10^5). Animals in the positive group had 77-fold fewer organisms (2.4x103) per spleen than animals in the negative control groups ($p<0.01$; Wilcoxon's-Rank Sum analysis). These data demonstrate that immunization with an immunogenic fragment of Cap1 can afford a statistically significant level of protection against C. trachomatis infection.

EXAMPLE 10

Pmp/Ra12 FUSION PROTEINS

Various Pmp/Ra12 fusion constructs were generated by first synthesizing PCR fragments of a Pmp gene using primers containing a Not I restriction site. Each PCR fragment was then ligated into the NotI restriction site of pCRX1. The pCRX1 vector contains the 6HisRa12 portion of the fusion. The Ra12 portion of the fusion construct encodes a polypeptide corresponding to amino acid residues 192-323 of *Mycobacterium tuberculosis* MTB32A, as described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference. The correct orientation of each insert was determined by its restriction enzyme pattern and its sequence was verified. Multiple fusion constructs were made for PmpA, PmpB, PmpC, PmpF and PmpH, as described further below:

PmpA Fusion Proteins

PmpA is 107 kD protein containing 982 aa and was cloned from serovar E. The PmpA protein was divided into 2 overlapping fragments, the PmpA(N-terminal) and (C-terminal) portions.

PmpA(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGTTTATAACAAAGGAACTTATG (SEQ ID NO: 306)

GAGAGCGGCCGCTTACTTAGGTGAGAAGAAGGGAGTTTC (SEQ ID NO: 307)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 308, encoding a 66 kD protein (619aa) expressing the segment 1-473 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 309.

PmpA(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCCATTCTATTCATTTCTTTGATCCTG (SEQ ID NO: 310)
GAGAGCGGCCGCTTAGAAGCCAACATAGCCTCC (SEQ ID NO: 311)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 312, encoding a 74 kD protein (691aa) expressing the segment 438-982 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 313.

PmpF Fusion Proteins

PmpF is 112 kD protein containing 1034 aa and was cloned from the serovar E. PmpF protein was divided into 2 overlapping fragments, the PmpF(N- term) and (C-term) portions.

PmpF(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGATTAAAAGAACTTCTCTATCC (SEQ ID NO: 314)

GAGAGCGGCCGCTTATAATTCTGCATCATCTTCTATGGC (SEQ ID NO: 315)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 316, encoding a 69 kD protein (646aa) expressing the segment 1-499 aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 317.

PmpF(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACATACGAACTCTGATGGG (SEQ ID NO: 318)

GAGAGCGGCCGCTTAAAAGACCAGAGCTCCTCC (SEQ ID NO: 319)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 320, encoding a 77 kD protein (715aa) expressing the segment 466-1034aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 321.

PmpH Fusion Proteins

PmpH is 108 kD protein containing 1016 aa and was cloned from the serovar E. PmpH protein was divided into 2 overlapping fragments, the PmpH(N-term)and (C-term)portions.

PmpH(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGCCTTTTTCTTTGAGATCTAC (SEQ ID NO: 322)
GAGAGCGGCCGCTTACACAGATCCATTACCGGACTG (SEQ ID NO: 323)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 324, encoding a 64 kD protein (631aa) expressing the segment 1-484 aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 325. The donor line CHH037 was found to be reactive against this protein.

PmpH(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCCTGTAGTACAAAATAATTCAGC (SEQ ID NO: 326)
GAGAGCGGCCGCTTAAAAGATTCTATTCAAGCC (SEQ ID NO: 327)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 328, encoding a 77 kD protein (715aa) expressing the segment 449-1016aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 329. The patient line CT12 was found to be reactive in response to this protein.

PmpB Fusion Proteins

PmpB is 183 kD protein containing 1750 aa and was cloned from the serovar E. PmpB protein was divided into 4 overlapping fragments, PmpB(1), (2), (3) and (4).

PmpB(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATGGCTGTCAGCTACTGCG (SEQ ID NO: 330)

GAGAGCGGCCGCTTACTTAATGCGAATTTCTTCAAG (SEQ ID NO: 331)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 332, and encodes is a 53 kD protein (518aa) expressing the segment 1-372 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 333.

PmpB(2) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGGTGACCTCTCAATTCAATCTTC (SEQ ID NO: 334)

GAGAGCGGCCGCTTAGTTCTCTGTTACAGATAAGGAGAC (SEQ ID NO: 335)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 336 and encodes a 60 kD protein (585aa) expressing the segment 330-767 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 337. Cell lines derived from patient lines CT1, CT3, CT4 responded to this recombinant pmpB protein.

PmpB(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACCAACTGAATATCTCTGAGAAC (SEQ ID NO: 338)

GAGCGGCCGCTTAAGAGACTACGTGGAGTTCTG (SEQ ID NO: 339)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 340 encodes a 67 kD protein (654aa) expressing the segment 732-1236 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 341

PmpB(4) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGGAACTATTGTGTTCTCTTCTG (SEQ ID NO: 342)

GAGAGCGGCCGCTTAGAAGATCATGCGAGCACCGC (SEQ ID NO: 343)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 344 encodes a 76 kD protein (700aa) expressing the segment 1160-1750 of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 345.

PmpC Fusion Proteins

PmpC is 187 kD protein containing 1774 aa and was cloned from the serovar E/L2. PmpC protein was divided into 3 overlapping fragments, PmpC(1), (2) and (3).

PmpC(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATTTATGTCAGCTACTGC (SEQ ID NO: 346)

GAGAGCGGCCGCTTACCCTGTAATTCCAGTGATGGTC (SEQ ID NO: 347)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 348 and encodes a 51 kD protein (487aa) expressing the segment 1-340 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 349.

PmpC(2) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATACACAAGTATCAGAATCACC (SEQ ID NO: 350)

GAGAGCGGCCGCTTAAGAGGACGATGAGACACTCTCG (SEQ ID NO: 351)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 352 and encodes a 60 kD protein (583aa) expressing the segment 305-741 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 353.

PmpC(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCAATCTAACGAAAACACAGACG (SEQ ID NO: 354)

GAGAGCGGCCGCTTAGACCAAAGCTCCATCAGCAAC (SEQ ID NO: 355)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 356 and encodes a 70 kD protein (683aa) expressing the segment 714-1250 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 357.

EXAMPE 11

IMMUNOGENICITY OF CT622

Chlamydia-specific T cells lines were generated from two patients with Chlamydia infections and the lines were designated CT1 and CT13. The T cell lines were either generated against monocyte-derived dendritic cells infected *C. trachomatis* serovar E for 72 hours (CT1-ERB) or against killed serovar E elementary bodies (EB) (CT13-EEB). Once generated, the lines were tested against the recombinant Chlamydia-specific protein, CT622 in a proliferation assay. Proliferation assays were performed by stimulating 2.5×10^4 T cells in the presence of 1×10^4 monocyte-derived dendritic cells with either recombinant CT antigens (2μg/ml) or Chlamydia EBs (1μg/ml). The assay was incubated for 4 days with a ^{3}H-thymidine pulse for the last 18 hours.

The cell line CT1-ERB demonstrated proliferative responses significantly above the media controls when stimulated with CT622, CT875, and CT EB. The cell line CT13-EEB demonstrated a proliferative response significantly above media controls when stimulated with CT622, CT875, and CT EB (see Figure 12).

EXAMPLE 12

CLONING AND EXPRESSION OF FULL LENGTH CHLAMYDIA TRACHOMATIS GENES CT611, ORF3 AND OppA1

Recombinant protein expression of the full-length open reading frames was performed for clones containing genes CT611, ORF-3, and oppA1. The clones that contained the genes of interest were CtL2-8 (SEQ ID NO:285) which encoded 4 ORFs (CT474, CT473, CT060, and CT139), CtL2-10 (SEQ ID NO:284) which encoded the ORFs of CT610 and CT611, and clones 16CtL2-16 (SEQ ID NO:47), 16-D4-22 (SEQ ID NO:119) and 19-A5-54 (SEQ ID NO:84) which all contained sequences related to ORF-3. Sequences within CtL2-10 (Ct-610) and CtL2-16 (ORF-3) were also independently identified by the T-cell expression cloning approach. The clone CtL2-8 was further investigated as this clone had stimulated the proliferative responses and IFN-gamma production by two T cell lines generated against serovar E.

Cloning and expression of clone sequences:

CtL2-10 was found to encode two open reading frames (ORFs), CT610 and CT611, and these were found organized adjacent to each other within the genomic clone. The full length ORF of CT610 (containing a PQQ synthesis domain) was previously expressed and demonstrated to stimulate the proliferative responses of T cell lines generated against Chlamydia. To determine whether the second ORF, CT611, was also recognized by T cells, the full-length sequence of CT611 was PCR amplified and engineered for protein expression. The nucleotide sequence is disclosed in SEQ ID NO:361 with the corresponding amino acid sequence disclosed in SEQ ID NO:365.

The second serological clone, CtL2-8, was found to contain 4 ORFs (CT474, CT473, CT060, and CT139). Overlapping peptides to the three smallest predicted ORFs (CT474, CT473, and CT060) did not stimulate the proliferative responses of T

cell lines. This suggested that the immunostimulatory antigen resides in the fourth ORF, CT139. The ORF of CT139 is approximately 450 nucleotides. The full-length nucleotide sequence is disclosed in SEQ ID NO:359 and the full-length amino acid sequence is disclosed in SEQ ID NO:363. Amino acid sequence comparison from Genbank revealed that it is an oligo-peptide binding protein (oppA1) as well as belonging to the peptide ABC transporter family. This protein is 462 amino acids long with a predicted size of 48.3kDa and appears to contain 2 trans-membrane regions.

To express the full-length sequence of oppA1, oligonucleotides were designed which specifically amplified sequences starting from amino acid residue 22 (devoid of the first transmembrane domain), the nucleotide sequence for which is disclosed in SEQ ID NO:358 and, the amino acid sequence of which is disclosed in SEQ ID NO:362. This was shown to express the protein in E. coli.

The full-length cloning and recombinant protein expression of ORF-3 was also achieved. The nucleotide and amino acid sequences are disclosed in SEQ ID NOs:360 and 364, respectively.

EXAMPLE 13

RECOMBINANT CHLAMYDIAL ANTIGENS RECOGNIZED BY T CELL LINES

Patient T cell lines were generated from the following donors: CT1, CT2, CT3, CT4, CT5, CT6, CT7, CT8, CT9, CT10, CT11, CT12, CT13, CT14, CT15, and CT16, some of which were discussed above. A summary of their details is included in Table V.

Table V: C. *trachomatis* patients

Patients	**Gender**	Age	**Clinical Manifestation**	**Serovar**	**IgG titer**	**Multiple Infections**
CT1	M	27	NGU	LCR	Negative	No
CT2	M	24	NGU	D	Negative	E
CT3	M	43	Asymptomatic	J	Ct 1:512	No

			Shed Eb Dx was HPV		Cp 1:1024 Cps 1:256	
CT4	F	25	Asymptomatic Shed Eb	J	Ct 1:1024	Y
CT5	F	27	BV	LCR	Ct 1:256 Cp 1:256	F/F
CT6	M	26	Perinial rash Discharge, dysuria	G	Cp 1:1024	N
CT7	F	29	BV Genital ulcer	E	Ct 1:512 Cp 1:1024	N
CT8	F	24	Not Known	LCR	Not tested	NA
CT9	M	24	asymptomatic	LCR	Ct 1:128 Cp 1:128	N
CT10	F	20	Mild itch vulvar	negative	negative	12/1/98
CT11	F	21	BV Abnormal pap smear	J	Ct 1:512	F/F/J/E/E PID 6/96
CT12	M	20	asymptomatic	LCR	Cp 1:512	N
CT13	F	18	BV, gonorrhea, Ct vaginal discharge, dysuria	G	Ct 1:1024	N
CT14	M	24	NGU	LCR	Ct 1:256	N

					Cp 1:256	
CT15	F	21	Muco-purulint cervicitis Vaginal discharge	culture	Ct 1:256 Ct IgM 1:320 Cp 1:64	N
CT16	M	26	Asymptomatic/ contact	LCR	NA	N
CL8	M	38	No clinical history of disease	negative	negative	N

NGU=Non-Gonococcal Urethritis; BV=Bacterial Vaginosis; CT=Chlamydia trachomatis; Cp=Chlamydia pneumoniae; Eb=Chlamydia elementary bodies; HPV=human papiloma virus; Dx=diagnosis; PID=pelvic inflammatory disease; LCR=Ligase chain reaction.

PBMC were collected from a second series of donors and T cell lines have been generated from a sub-set of these. A summary of the details for three such T cell lines is listed in the table below.

Table III: Normal Donors

Donor	Gender	Age	CT IgG Titer	CP IgG Titer
CHH011	F	49	1:64	1:16
CHH037	F	22	0	0
CHH042	F	25	0	1:16

Donor CHH011 is a heathly 49 year old female donor sero-negaitve for *C. trachomatis*. PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response. Donor CHH037 is a 22 year old healthy

female donor sero-negative for C. trachomatis. PBMC poruced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response. CHH042 is a 25 year old healthy female donor with an IgG titer of 1:16 to *C. pneumoniae.* PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response.

Recombinant proteins for several *Chlamydia trachomatis* genes were generated as described above. Sequences for MOMP was derived from serovar F. The genes CT875, CT622, pmp-B-2, pmpA, and CT529 were derived from serovar E and sequences for the genes gro-EL, Swib, pmpD, pmpG, TSA, CT610, pmpC, pmpE, S13, lpdA, pmpI, and pmpH-C were derived from LII.

Several of the patient and donor lines described above were tested against the recombinant Chlamydia proteins. Table IV summarizes the results of the T cell responses to these recombinant Chlamydia proteins.

Table VII: Recombinant Chlamydia Antigens Recognized By T Cell Lines

Antigen	Sero-var	#of hits	CL8 L2	CT10 E	CT1 E	CT3 E	CT4 L2	CT5 E	CT11 E	CT12 E	CT13 E	CHH-011 E	CHH-037 E
gro-EL (CT110)	L2	10	-	+	+	+	+	+	+	+	+	+	+
MompF (CT681)	F	10	-	+	+	+	+	+	+	+	+	+	+
CT875	E	8	-	+	+	-	+	+	+	+	+	-	+
SWIB (CT460)	L2	8	+	+	-	+	-	+	-	+	+	+	+
pmpD (CT812)	L2	5	-	+	+	+	+	-	-	+	+	-	-

pmpG (CT871)	L2	6	-	+	+	-	+	+	nt	-	+	+	-
TSA (CT603)	L2	6	-	-	+	+	+	+	-	-	+	-	+
CT622	E	3	-	-	+	-	+	-	-	-	+	-	-
CT610	L2	3	-	+	-	+	-	-	-	+	-	-	-
pmpB-2 (CT413)	E	3	-	-	+	+	+	-	-	-	-	-	-
pmpC (CT414)	L2	4	-	-	-	+	-	+	-	+	-	-	+
pmpE (CT869)	L2	3	-	+	+	-	-	-	-	-	+	-	-
S13 (CT509)	L2	2	+	-	-	-	+	-	-	-	-	-	-
lpdA (CT557)	L2	3	-	-	+	+	-	-	-	-	-	+	-
pmpI (CT874)	L2	2	-	-	+	-	-	-	-	-	-	+	-
pmpH-C (CT872)	L2	1	-	-	-	-	-	-	-	+	-	-	-
pmpA (CT412)	E	0	-	-	-	-	-	-	-	-	-	-	-
CT529	E	0	-	-	-	-	-	-	-	-	-	-	-

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

Claims

What is Claimed:

1. A composition for eliciting an immune response comprising a Chlamydia Cap1 protein or an immunogenic fragment thereof and an immunostimulant.

2. The composition of claim 1, wherein the immunogenic fragment comprises at least a CTL epitope consisting essentially of amino acids 139-147 of a Cap1 protein.

3. The composition of claim 1, wherein the Cap 1 protein comprises an amino acid sequence set forth in SEQ ID NO: 121 or a sequence having at least about 90% identity to the sequence set forth in SEQ ID NO: 121.

4. The composition of claim 1, wherein the Cap1 protein or immunogenic fragment thereof comprises a sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

5. The composition of claim 1, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein.

6. The composition of claim 5, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein having an amino acid sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

7. The composition of claim 1, wherein the immunogenic fragment is

immunologically reactive with a CD8+ T-cell of a Chlamydia-infected animal.

8. A method for stimulating a Chlamydia-specific T-cell response in an animal comprising administering to an animal an effective amount of a composition according to claim 1.

9. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to an animal an effective amount of a composition according to claim 1.

10. A composition for eliciting an immune response comprising an isolated polynucleotide that encodes a Chlamydia Cap1 protein or an immunogenic fragment thereof and an immunostimulant.

11. The composition of claim 10, wherein the immunogenic fragment comprises at least the CTL epitope sequence consisting essentially of amino acids 139-147 of a Cap1 protein.

12. The composition of claim 10, wherein the Cap 1 protein comprises an amino acid sequence set forth in SEQ ID NO: 121 or a sequence having at least about 90% identity to the sequence set forth in SEQ ID NO: 121.

13. The composition of claim 10, wherein the Cap1 protein or immunogenic fragment thereof comprises a sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

14. The composition of claim 10, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein.

15. The composition of claim 14, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein having an amino acid sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

16. The composition of claim 10, wherein the immunogenic fragment is immunologically reactive with a CD8+ T-cell of a Chlamydia-infected animal.

17. The composition of claim 10, wherein the isolated polynucleotide is operably linked within a viral delivery vector.

18. The composition of claim 17, wherein the viral delivery vector is a vaccinia virus delivery vector.

19. A method for stimulating a Chlamydia-specific T-cell response in an animal comprising administering to said animal an effective amount of a composition according to claim 10.

20. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to an animal said effective amount of a composition according to claim 10.

21. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to said animal an effective amount of a composition according to claim 18.

22. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO:358-361;

(b) complements of the sequences provided in SEQ ID NO:358-361;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:358-361;

(d) sequences that hybridize to a sequence provided in SEQ ID NO:358-361, under highly stringent conditions;

(e) sequences having at least 95% identity to a sequence of SEQ ID NO:358-361;

(f) sequences having at least 99% identity to a sequence of SEQ ID NO:358-361; and

(g) degenerate variants of a sequence provided in SEQ ID NO:358-361.

23. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences encoded by a polynucleotide of claim 22;

(b) sequences having at least 95% identity to a sequence encoded by a polynucleotide of claim 22; and

(c) sequences having at least 99% identity to a sequence encoded by a polynucleotide of claim 22.

24. An isolated polypeptide comprising at least an immunogenic fragment of a polypeptide sequence selected from the group consisting of:

(a) a polypeptide sequence set forth in SEQ ID NO:362-365,

(b) a polypeptide sequence having at least 95% identity with a sequence set forth in SEQ ID NO:362-365, and

(c) a polypeptide sequence having at least 99% identity with a sequence set forth in SEQ ID NO:362-365.

25. An expression vector comprising a polynucleotide of claim 22 operably linked to an expression control sequence.

26. A host cell transformed or transfected with an expression vector according to claim 25.

27. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of any one of claims 23 and 24.

28. A method for detecting the presence of Chlamydia in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of any one of claims 23 and 24;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of Chlamydia in the patient.

29. A fusion protein comprising at least one polypeptide according to claim 23 or claim 24.

30. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 358-361 under highly stringent conditions.

31. A method for stimulating and/or expanding T cells specific for a Chlamydia protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) a polypeptide according to claim 23 or claim 24;

(b) a polynucleotide according to claim 22; and

(c) an antigen-presenting cell that expresses a polynucleotide according to claim 22,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

32. An isolated T cell population, comprising T cells prepared according to the method of claim 31.

33. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

(a) a polypeptide according to claim 23 or claim 24;

(b) a polynucleotide according to claim 22;

(c) an antibody according to claim 27;

(d) a fusion protein according to claim 29;

(e) a T cell population according to claim 32; and

(f) an antigen presenting cell that expresses a polypeptide according to claim 23 or claim 24.

34. A method for stimulating an immune response in a patient, comprising administering to the patient a composition selected from the group consisting of;

(a) a composition of claim 33;

(b) a polynucleotide sequence of any one of SEQ ID NO:407-430, 525-559, and 582-598; and

(c) a polypeptide sequence of any one of SEQ ID NO:431-454 and 560-581.

35. A method for the treatment of Chlamydia infection in a patient, comprising administering to the patient a composition selected from the group consisting of;

(a) a composition of claim 33;

(b) a polynucleotide sequence of any one of SEQ ID NO: 407-430, 525-559, and 582-598; and

(d) a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581.

36. A method for determining the presence of Chlamydia in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide according to claim 30;

(c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefore determining the presence of the cancer in the patient.

37. A diagnostic kit comprising at least one oligonucleotide according to claim 30.

38. A diagnostic kit comprising at least one antibody according to claim 27 and a detection reagent, wherein the detection reagent comprises a reporter group.

39. A method for the treatment of Chlamydia in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to any one of claims 23 and 24;

(ii) a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581;

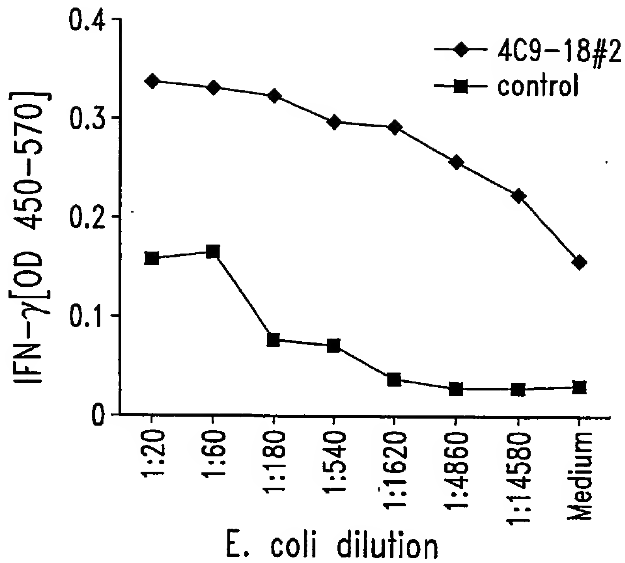
(iii) a polynucleotide according to claim 22;

(iv) a polynucleotide sequence of any one of SEQ ID NO: 407-430, 525-559 and 582-598;

(v) an antigen presenting cell that expresses a polypeptide sequence set forth in any one of claims 23 and 24;

(vi) an antigen presenting cell that expresses a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581, such that the T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells.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0.1
0
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control
1:20
1:60
1:180
1:540
1:1620
1:4860
1:14580
Medium
E. coli dilution

Fig. 1

Retroviral vector
pBIB-KS


```
      Kozak-Start
GA TCT GCC GCC ACC ATG GAA TTC GAT ATC GGA TCC CTG CAG
     A CGG CGG TGG TAC CTT AAG CTA TAG CCT AGG GAC GTC
(BglII)                 EcoRI         BamHI   PstI

AAG CTT GAG CTC GAG CGC GGC CGC TAA TTA GCT GAG              ReadingFrame 1
TTC GAA CTC GAG CTC GCG CCG GCG ATT AAT CGA CTC AGC T          KS1+
HinDIII     XhoI        NotI    Stop Stop Stop (SalI)

      Kozak-Start
GA TCT GCC GCC ACC ATG GGA ATT CGA TAT CGG ATC CCT GCA G
     A CGG CGG TGG TAC CCT TAA GCT ATA GCC TAG GGA CGT C
(BglII)                  EcoRI          BamHI   PstI

AA GCT TGA GCT CGA GCG CGG CCG CTA ATT AGC TGA G             ReadingFrame 1
TT CGA ACT CGA GCT CGC GCC GGC GAT TAA TCG ACT CAG CT          KS2+
HinDIII     XhoI        NotI    Stop Stop  Stop (SalI)

      Kozak-Start
GA TCT GCC GCC ACC ATG GGG AAT TCG ATA TCG GAT CCC TGC AG
     A CGG CGG TGG TAC CCC TTA AGC TAT AGC CTA GGG ACG TC
(BglII)                   EcoRI          BamHI   PstI

A AGC TTG AGC TCG AGC GCG GCC GCT AAT TAG CTG AG             ReadingFrame 3
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HinDIII     XhoI        NotI    Stop Stop  Stop (SalI)
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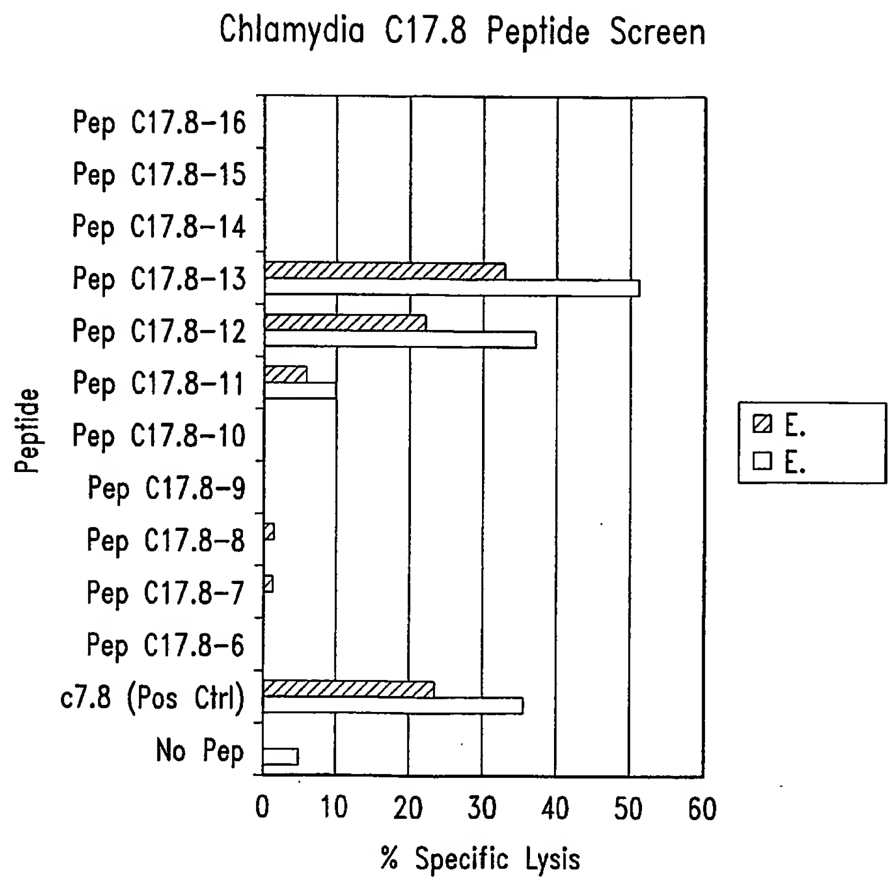
Fig. 2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Peptide
Pep C17.8-16
Pep C17.8-15
Pep C17.8-14
Pep C17.8-13
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Pep C17.8-11
Pep C17.8-10
Pep C17.8-9
Pep C17.8-8
Pep C17.8-7
Pep C17.8-6
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No Pep
0
10
20
30
40
50
60
% Specific Lysis
E.
E.

Fig. 3

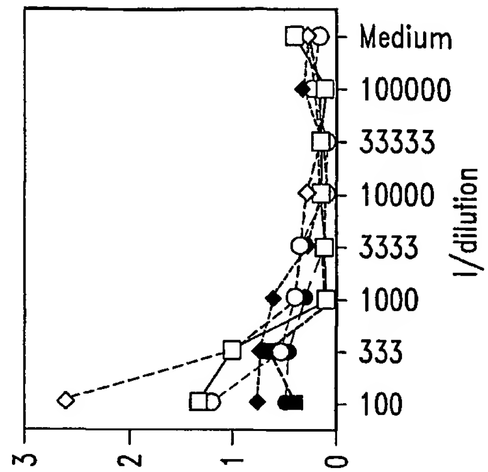


Fig. 4C

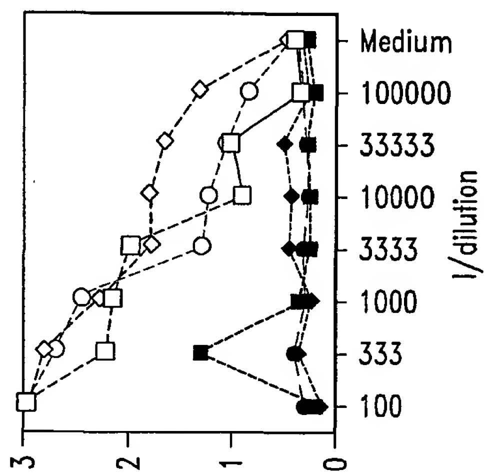


Fig. 4B

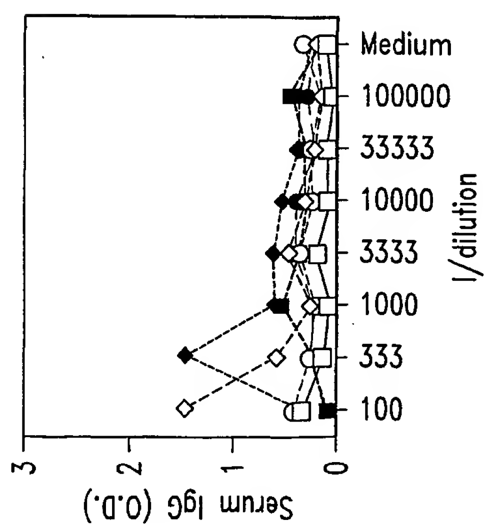
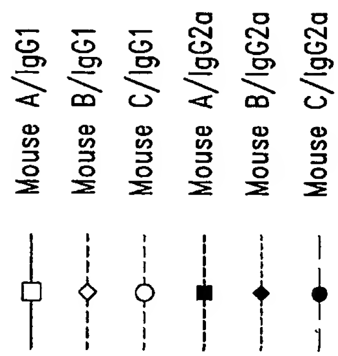
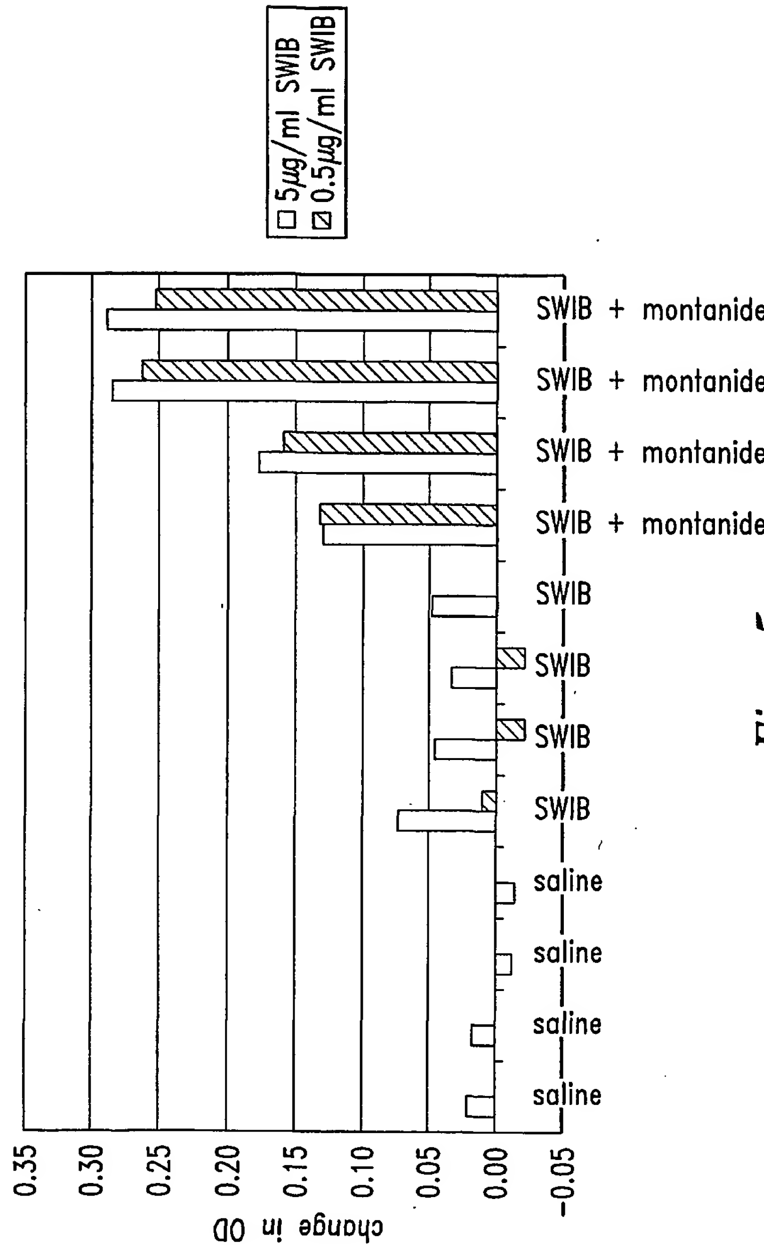


Fig. 4A





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0.5μg/ml SWIB
change in OD
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
-0.05
SWIB + montanide
SWIB + montanide
SWIB + montanide
SWIB + montanide
SWIB
SWIB
SWIB
SWIB
saline
saline
saline
saline

Fig. 5

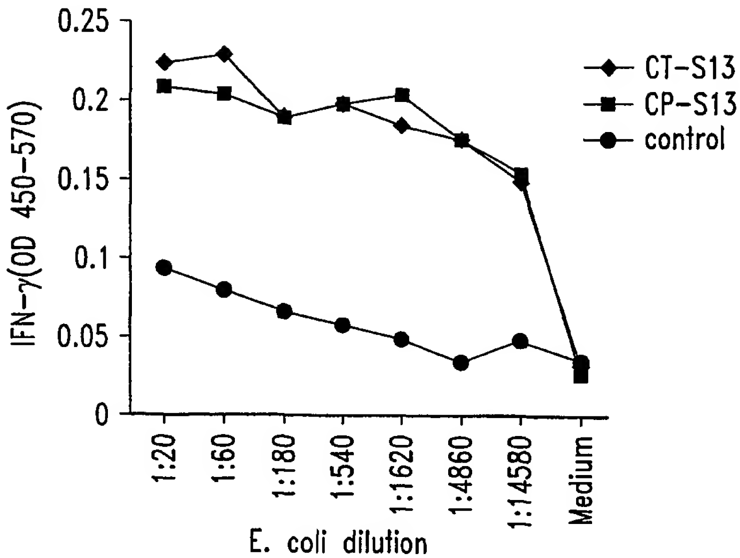
CP SWIB Nde (5' primer)
5' GATATACATATGCATCACCATCACCATCACATGAGTCAAAAAAATAAAAACTCT

CP SWIB EcoRI (3' primer)
5' CTCGAGGAATTCTTATTTTACAATATGTTTGGA

CP S13 Nde (5' primer)
5' GATATACATATGCATCACCATCACCATCACATGCCACGCATCATTGGAATGAT

CP S13 EcoRI (3' primer)
5' CTCGAGGAATTCTTATTTCTTCTTACCTGC

Fig. 6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0.1
0.05
0
IFN-γ(OD 450-570)
CT-S13
CP-S13
control
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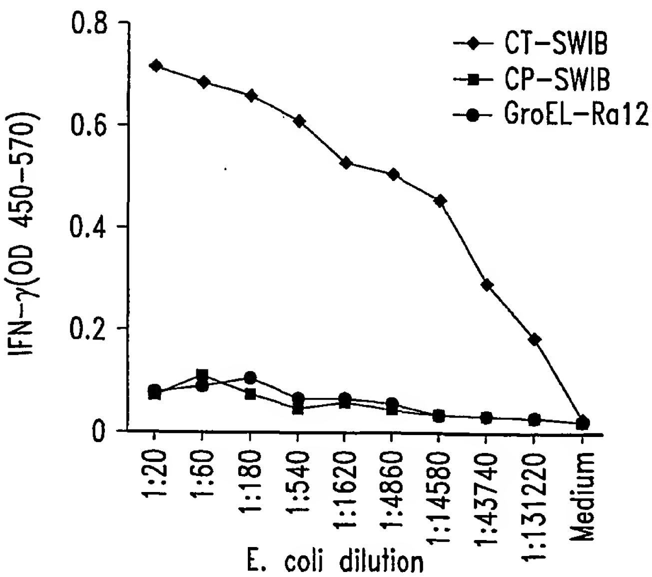
1:60
1:180
1:540
1:1620
1:4860
1:14580
Medium
E. coli dilution

Fig. 7A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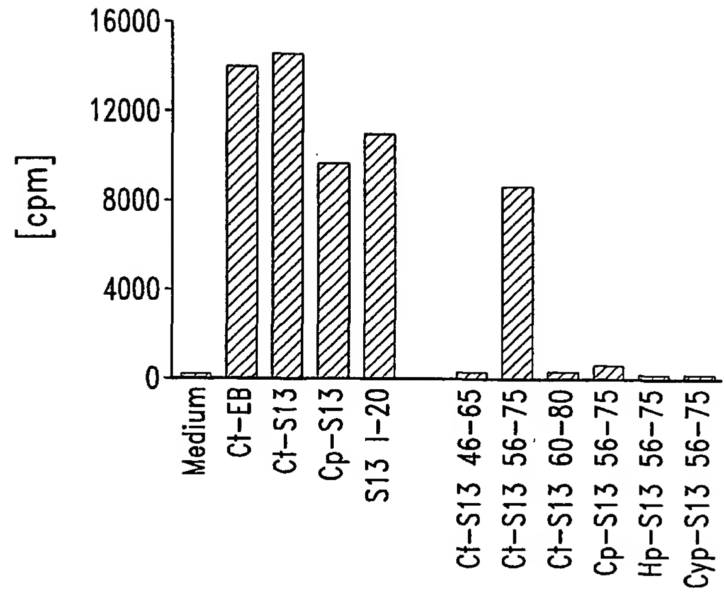
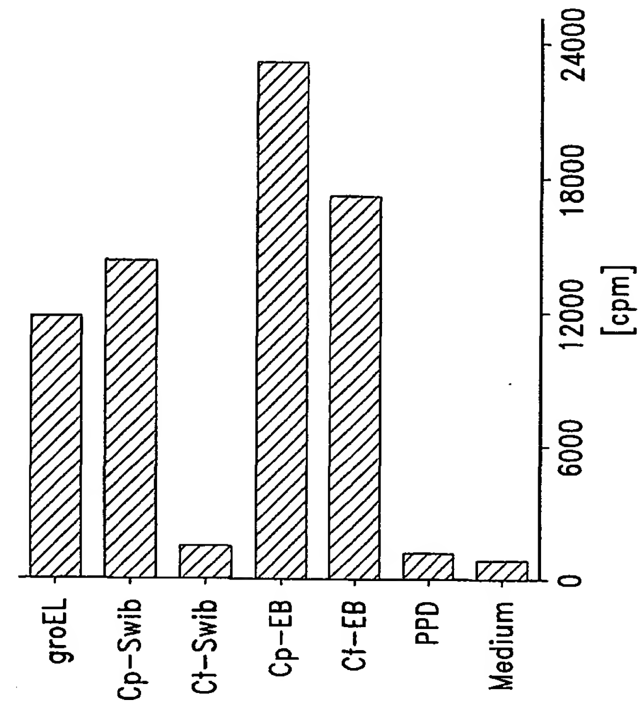
Medium
E. coli dilution

Fig. 7B



16000
12000
8000
4000
0
[cpm]
Medium
Ct-EB
Ct-S13
Cp-S13
S13 1-20
Ct-S13 46-65
Ct-S13 56-75
Ct-S13 60-80
Cp-S13 56-75
Hp-S13 56-75
Cyp-S13 56-75

Fig. 8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PPD
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6000
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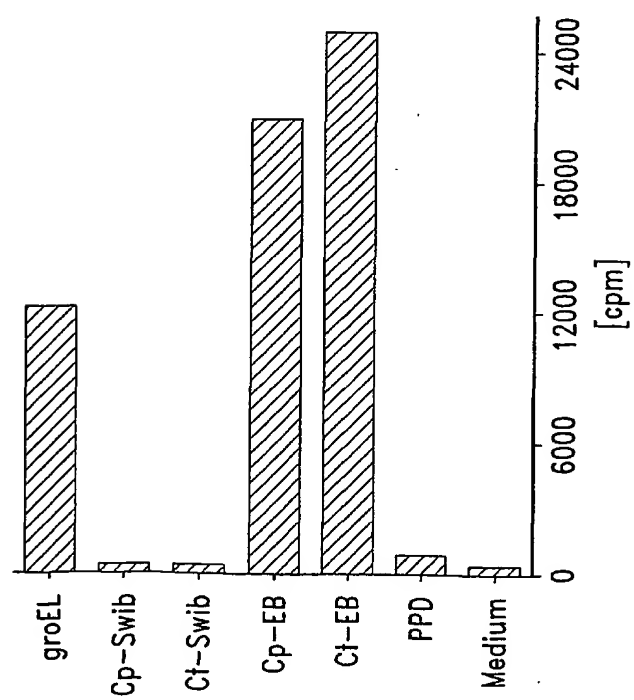
18000
24000
[cpm]

Fig. 9B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Ct–EB
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12000
18000
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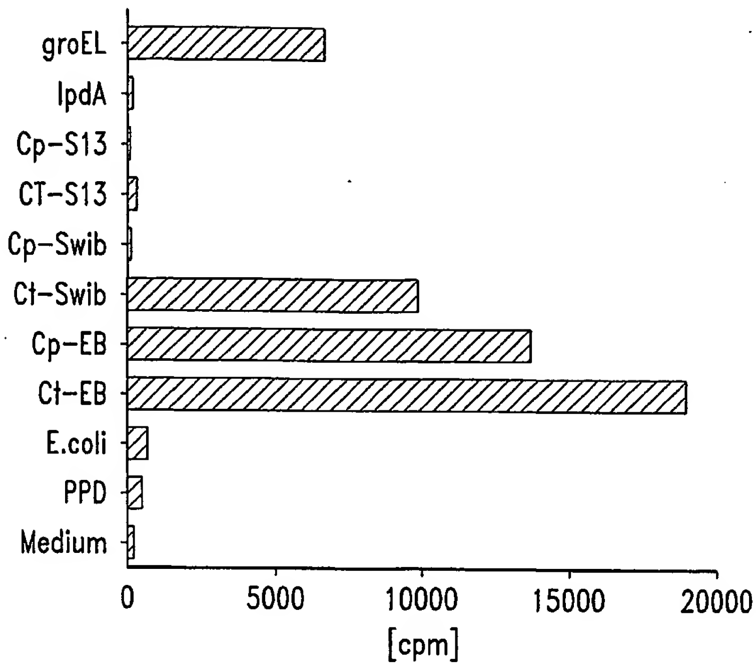
Fig. 9A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20000
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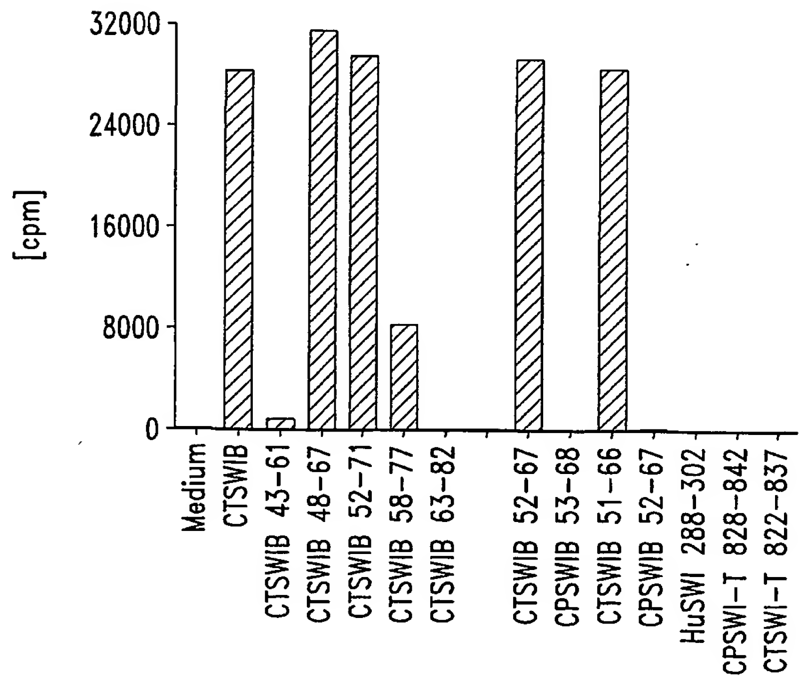
Fig. 10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CTSWIB 63-82
CTSWIB 52-67
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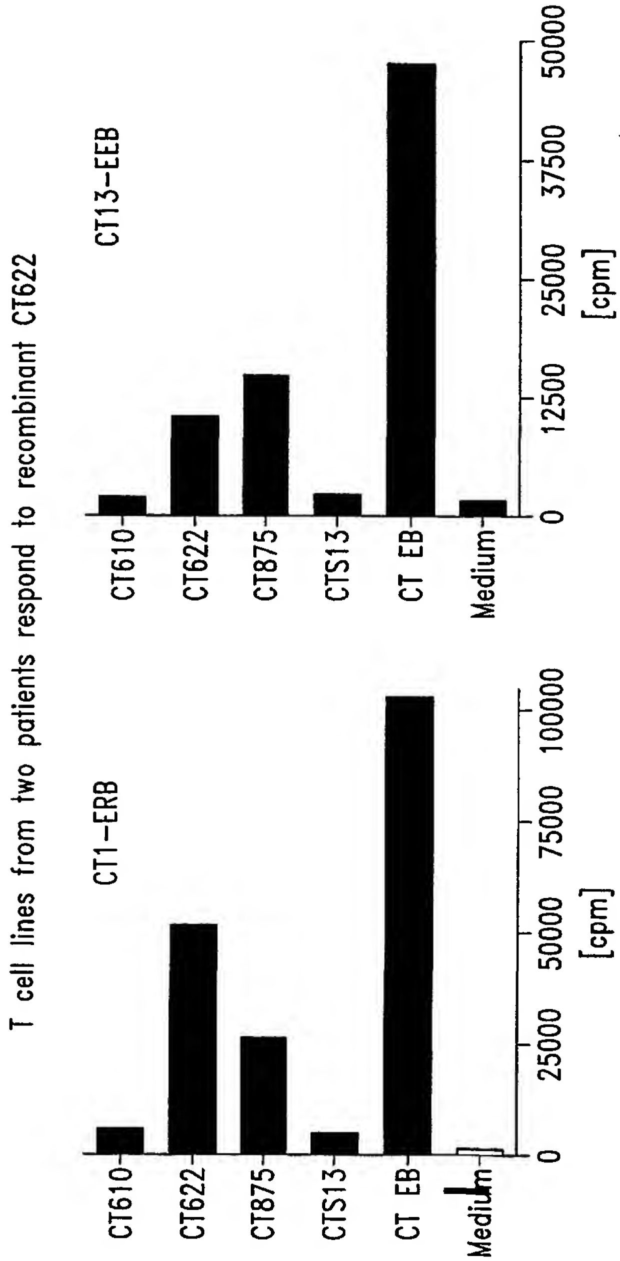
CTSWI-T 822-837

Fig. 11



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CT610
CT622
CT875
CTS13
CT EB
Medium
0
25000
50000
75000
100000
[cpm]
CT13-EEB
CT610
CT622
CT875
CTS13
CT EB
Medium
0
12500
25000
37500
50000
[cpm]

Fig. 12

SEQUENCE LISTING

<110> Corixa Corporation
Fling, Steven P.
Skeiky, Yasir A. W.
Probst, Peter
Bhatia, Ajay

<120> COMPOUNDS AND METHODS FOR TREATMENT AND
DIAGNOSIS OF CHLAMYDIAL INFECTION

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Ile Ile Lys Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp
        35                  40                  45
Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val
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            20                  25                  30
Gln Ser His Arg
        35
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35 40 45
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50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
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Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
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Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
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Ile Leu Trp Arg Leu Thr Met Gln Arg Leu Trp Trp Val Leu Asp Ser
65 70 75 80
Leu Ser Val Arg Lys Glu Gln Ile Ala Lys Pro Ala Ala Leu Val Leu
85 90 95
Arg Glu Lys Ser Arg Tyr Ser Lys Cys Arg Glu Arg Lys Met Leu Ala
100 105 110
Arg Arg Lys Ser Leu Glu Arg Lys Pro Arg Arg Ser Arg Ala Ser Ser
115 120 125
Met His Ser Ser Leu Cys Ser Arg Ser Phe Trp Asn Ala Leu Pro Thr
130 135 140
Phe Ser Asn Trp Cys Arg Cys Leu Leu Gln Trp Val Phe Val Arg Leu
145 150 155 160
Trp Leu Leu Asp Val Arg Ser Leu Leu Gln Leu Leu Asp Cys Ala Leu
165 170 175
Ser Ala Pro Glu His Lys Gly Phe Phe Lys Phe Leu Lys Lys Lys Ala
180 185 190
Val Ser Lys Lys Lys Gln Pro Phe Leu Ser Thr Lys Cys Leu Ala Phe
195 200 205
Leu Ile Val Lys Ile Val Phe Leu
210 215

<210> 21
<211> 1256
<212> DNA
<213> Chlamydia trachomatis

<400> 21
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tcggttgcga attcgcttcc ttattccata cgttaggctc cgaagtttct gtgatcgaag 120
caagctctca aatccttgct ttgaataatc cagatatttc aaaaaccatg ttcgataaat 180
tcacccgaca aggactccgt ttcgtactag aagcctctgt atcaaatatt gaggatatag 240
gagatcgcgt tcggttaact atcaatggga atgtcgaaga atacgattac gttctcgtat 300
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atgaacgcgg agtcatccct accgatgcca caatgcgcac aaacgtacct aacatttatg 420
ctattggaga tatcacagga aaatggcaac ttgcccatgt agcttctcat caaggaatca 480
ttgcagcacg gaatataggt ggccataaag aggaaatcga ttactctgct gtcccttctg 540
tgatctttac cttccctgaa gtcgcttcag taggcctctc cccaacagca gctcaacaac 600
atctccttct tcgcttactt tttctgaaaa atttgataca gaagaagaat tcctcgcaca 660
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tgattctttg cgagaattat ccgctaagct tggttacgat agcgatggag agactgggga 780
tttcttcaac gaggagtacg acgacgaaga agaggaaatc aaaccgaaga aaactacgaa 840
acgtggacgt aagaagagcc gttcataagc cttgctttta aggtttggta gttttacttc 900
tctaaaatcc aaatggttgc tgtgccaaaa agtagtttgc gtttccggat agggcgtaaa 960

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tgcgctgcat gaaagattgc ttcgagagcg gcatcgcgtg ggagatcccg gatactttct    1020
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agatttagat agagcttgtg tagcaggtaa actgggttat atgttgctgg gcgtgttagt    1140
tctagaatac ccaagtgtcc tccaggttgt aatactcgat acacttccct aagagcctct    1200
aatggatagg ataagttccg taatccatag gccatagaag ctaaacgaaa cgtatt        1256

<210> 22
<211> 601
<212> DNA
<213> Chlamydia trachomatis

<400> 22
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tcggttgcga attcgcttcc ttattccata cgttaggctc cgaagtttct gtgatcgaag     120
caagctctca aatccttgct ttgaataatc cagatatttc aaaaaccatg ttcgataaat     180
tcacccgaca aggactccgt ttcgtactag aagcctctgt atcaaatatt gaggatatag     240
gagatcgcgt tcggttaact atcaatggga atgtcgaaga atacgattac gttctcgtat     300
ctataggacg ccgtttgaat acagaaaata ttggcttgga taaagctggt gttatttgtg     360
atgaacgcgg agtcatccct accgatgcca caatgcgcac aaacgtacct aacatttatg     420
ctattggaga tatcacagga aaatggcaac ttgcccatgt agcttctcat caaggaatca     480
ttgcagcacg gaatataggt ggccataaag aggaaatcga ttactctgct gtcccttctg     540
tgatctttac cttccctgaa gtcgcttcag taggcctctc ccccaacagca gctcaacaac   600
a                                                                    601

<210> 23
<211> 270
<212> DNA
<213> Chlamydia trachomatis

<400> 23
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cacttgcgag gaggagggcg tctggaagac cagttgaatt tagctaagtt ttctgagcgt     120
tttgattctt tgcgagaatt atccgctaag cttggttacg atagcgatgg agagactggg     180
gatttcttca acgaggagta cgacgacgaa gaagaggaaa tcaaaccgaa gaaaactacg     240
aaacgtggac gtaagaagag ccgttcataa                                     270

<210> 24
<211> 363
<212> DNA
<213> Chlamydia trachomatis

<400> 24
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gcgtaaatgc gctgcatgaa agattgcttc gagagcggca tcgcgtggga gatcccggat     120
actttctttc agatacgaat aagcatagct gttcccagaa taaaaacggc cgacgctagg     180
aacaacaaga tttagataga gcttgtgtag caggtaaact gggttatatg ttgctgggcg     240
tgttagttct agaataccca agtgtcctcc aggttgtaat actcgataca cttccctaag     300
agcctctaat ggataggata agttccgtaa tccataggcc atagaagcta aacgaaacgt     360
att                                                                  363

<210> 25
<211> 696
<212> DNA
<213> Chlamydia trachomatis

<400> 25
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gcaagctctc aaatccttgc tttgaataat ccagatattt caaaaaccat gttcgataaa     180
ttcacccgac aaggactccg tttcgtacta gaagcctctg tatcaaatat tgaggatata     240
ggagatcgcg ttcggttaac tatcaatggg aatgtcgaag aatacgatta cgttctcgta     300
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tctataggac gccgtttgaa tacagaaaat attggcttgg ataaagctgg tgttatttgt     360
gatgaacgcg gagtcatccc taccgatgcc acaatgcgca caaacgtacc taacatttat     420
gctattggag atatcacagg aaaatggcaa cttgcccatg tagcttctca tcaaggaatc     480
attgcagcac ggaatatagg tggccataaa gaggaaatcg attactctgc tgtcccttct     540
gtgatcttta ccttccctga agtcgcttca gtaggcctct ccccaacagc agctcaacaa     600
catctccttc ttcgcttact ttttctgaaa aatttgatac agaagaagaa ttcctcgcac     660
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<210> 26
<211> 231
<212> PRT
<213> Chlamydia trachomatis

<400> 26

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Ala Arg Ala Gly Thr Ser Lys Glu Ile Pro Gln Lys Met Ala Ile Ile
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Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu
            20                  25                  30
Gly Ser Glu Val Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu
        35                  40                  45
Asn Asn Pro Asp Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln
    50                  55                  60
Gly Leu Arg Phe Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile
65                  70                  75                  80
Gly Asp Arg Val Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp
                85                  90                  95
Tyr Val Leu Val Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly
            100                 105                 110
Leu Asp Lys Ala Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr
        115                 120                 125
Asp Ala Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp
    130                 135                 140
Ile Thr Gly Lys Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile
145                 150                 155                 160
Ile Ala Ala Arg Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser
                165                 170                 175
Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly
            180                 185                 190
Leu Ser Pro Thr Ala Ala Gln Gln His Leu Leu Leu Arg Leu Leu Phe
        195                 200                 205
Leu Lys Asn Leu Ile Gln Lys Lys Asn Ser Ser His Thr Cys Glu Glu
    210                 215                 220
Glu Gly Val Trp Lys Thr Ser
225                 230
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<210> 27
<211> 264
<212> DNA
<213> Chlamydia pneumoniae

<400> 27

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tacattaaaa aacacaactg tcaggatcaa aaaaataaac gtaatatcct tcccgatgcg     180
aatcttgcca aagtctttgg ctctagtgat cctatcgaca tgttccaaat gaccaaagcc     240
ctttccaaac atattgtaaa ataa                                            264
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<210> 28
<211> 87
<212> PRT
<213> Chlamydia pneumoniae

<400> 28
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile
1 5 10 15
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
20 25 30
Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln
35 40 45
Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys
50 55 60
Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala
65 70 75 80
Leu Ser Lys His Ile Val Lys
85

<210> 29
<211> 369
<212> DNA
<213> Chlamydia pneumoniae

<400> 29
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cctgaggcaa gagcctctga attaactgaa gaagaagtag gacgactgaa ctctctgcta 180
caatcagaat ataccgtaga aggggatttg cgacgtcgtg ttcaatcgga tatcaaaaga 240
ttgatcgcca tccattctta tcgaggtcag agacatagac tttctttacc agtaagagga 300
caacgtacaa aaactaattc tcgtactcga aaaggtaaaa gaaaaacagt cgcaggtaag 360
aagaaataa 369

<210> 30
<211> 122
<212> PRT
<213> Chlamydia pneumoniae

<400> 30
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
1 5 10 15
Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu
20 25 30
Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu
35 40 45
Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr
50 55 60
Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
65 70 75 80
Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
85 90 95
Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
100 105 110
Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
115 120

<210> 31
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 31

Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 32
<211> 53
<212> PRT
<213> Chlamydia trachomatis

<400> 32
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe
1 5 10 15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
20 25 30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr
35 40 45
Lys Ala Asn Met Gly
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<210> 33
<211> 161
<212> DNA
<213> Chlamydia trachomatis

<400> 33
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ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac aaaatgctgg 120
caaaaccgtt tctttcttcc caaactaaag caaatatggg a 161

<210> 34
<211> 53
<212> PRT
<213> Chlamydia trachomatis

<400> 34
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile
1 5 10 15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
20 25 30
Leu Phe Val Asn Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr
35 40 45
Lys Ala Asn Met Gly
50

<210> 35
<211> 55
<212> DNA
<213> Chlamydia pneumoniae

<400> 35
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<210> 36
<211> 33
<212> DNA
<213> Chlamydia pneumoniae

<400> 36
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<210> 37
<211> 53

<212> DNA
<213> Chlamydia pneumoniae

<400> 37
gatatacata tgcatcacca tcaccatcac atgccacgca tcattggaat gat 53

<210> 38
<211> 30
<212> DNA
<213> Chlamydia pneumoniae

<400> 38
ctcgaggaat tcttatttct tcttacctgc 30

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 39
Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
1 5 10 15

<210> 40
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 40
Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser
1 5 10 15

<210> 41
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 41
Lys Glu Tyr Ile Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp
1 5 10 15

<210> 42
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 42
Lys Lys Ile Ile Ile Pro Asp Ser Lys Leu Gln Gly Val Ile Gly Ala

1 5 10 15

<210> 43
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 43
Lys Lys Leu Leu Val Pro Asp Asn Asn Leu Ala Thr Ile Ile Gly
1 5 10 15

<210> 44
<211> 509
<212> DNA
<213> Chlamydia

<400> 44
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cgccgtgggc gatttagcga aaaatgattc ttctattcaa gtacgcatca ctgcttatcg 180
tgctgcagcc gtgttggaga tacaagatct tgtgcctcat ttacgagttg tagtccaaaa 240
tacacaatta gatggaacgg aaagaagaga agcttggaga tctttatgtg ttcttactcg 300
gcctcatagt ggtgtattaa ctggcataga tcaagcttta atgacctgtg agatgttaaa 360
ggaatatcct gaaaagtgta cggaagaaca gattcgtaca ttattggctg cagatcatcc 420
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ttctataatg gaatcggttc tcgtgccgg 509

<210> 45
<211> 481
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 23
<223> n=A,T,C or G

<400> 45
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<210> 46
<211> 427
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 20
<223> n=A,T,C or G

<400> 46
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tctaagccct gacacattct ttgaacaacc ttatgcccgt gttcgggata agccaactct 180
cgcccccgaa acatacaaga aacctttact ttatttcctt tctcaataaa ggctctagct 240
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tacttcccgt agtccatgat tttgcacaca ggaggctctg agtttgaagc aacctcgtgc 420
cgaattc 427

<210> 47
<211> 600
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 522
<223> n=A,T,C or G

<400> 47
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<210> 48
<211> 600
<212> DNA
<213> Chlamydia

<400> 48
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aactgttatc ctctaatttt tcaagaacag gagagtctgg gaataatcct aaagagtttt 480
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<210> 49
<211> 600
<212> DNA
<213> Chlamydia

<400> 49
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gatagtacag tccaagatat tttagacaaa atcacaacag acccttctct aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcactccc 240
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agctctggga gcatgttctt agtctcagca gatattattg catcaagaat ggaaggcggc 360

gttgttctag ctttggtacg agaaggtgat tctaagccct acgcgattag ttatggatac 420
tcatcaggcg ttcctaattt atgtagtcta agaaccagaa ttattaatac aggattgact 480
ccgacaacgt attcattacg tgtaggcggt ttagaaagcg gtgtggtatg ggttaatgcc 540
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<210> 50
<211> 406
<212> DNA
<213> Chlamydia

<400> 50
gatccgaatt cggcacgagt tcttagcttg cttaattacg taattaacca aactaaaggg 60
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tcctatgttc ttcagctata aaaatacttc ttaaaacttg atatgctgta atcaaatcat 180
cattaaccac aacataatca aattcgctag cggcagcaat ttcgacagcg ctatgctcta 240
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<210> 51
<211> 602
<212> DNA
<213> Chlamydia

<400> 51
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cccaggaaca ttgaaacttt attaggagga actgaaatag gaaaattcac agtcacaccc 180
aaaagctctg ggagcatgtt cttagtctca gcagatatta ttgcatcaag aatggaaggc 240
ggcgttgttc tagctttggt acgagaaggt gattctaagc cctacgcgat tagttatgga 300
tactcatcag gcgttcctaa tttatgtagt ctaagaacca gaattattaa tacaggattg 360
actccgacaa cgtattcatt acgtgtaggc ggtttagaaa gcggtgtggt atgggttaat 420
gccctttcta atggcaatga tattttagga ataacaaata cttctaatgt atcttttttg 480
gaggtaatac ctcaaacaaa cgcttaaaca atttttattg gatttttctt ataggtttta 540
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tc 602

<210> 52
<211> 145
<212> DNA
<213> Chlamydia

<400> 52
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aacattttca gctcgtgccg aattc 145

<210> 53
<211> 450
<212> DNA
<213> Chlamydia

<400> 53
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gatcaaaccc acacttggga caagtaccta caacataacg gtccgctaaa aacttccctt 120
cttcctcaga atacagctgt tcggtcacct gattctctac cagtccgcgt tcctgcaagt 180
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attcttgata ccccatgcct gccaactctg cattaagggt aattgcgatt ccgtattcat 360
cagaaccaca aatatacaaa acctctttgc cttgtagtct ctgaaaacgc gcataaacat 420
ctgcaggcaa ataagcctcg tgccgaattc 450

<210> 54
<211> 716
<212> DNA
<213> Chlamydia

<400> 54
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ccatccaaaa ggaaaaactg gtgaagcaag ctttaggaac acaatatcga gtagctgaaa 480
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aaaaatgatc gacaaggagc acgctaaatt tgtacatacc ccaaaatcaa tcagccatct 660
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<210> 55
<211> 463
<212> DNA
<213> Chlamydia trachomatis

<400> 55
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cgcgttcggt taactatcaa tgggaatgtc gaagaatacg attacgttct cgtatctata 180
ggacgccgtt tgaatacaga aaatattggc ttggataaag ctggtgttat ttgtgatgaa 240
cgcggagtca tccctaccga tgccacaatg cgcacaaacg tacctaacat ttatgctatt 300
ggagatatca caggaaaatg gcaacttgcc catgtagctt ctcatcaagg aatcattgca 360
gcacggaata taggtggcca taaagaggaa atcgattact ctgctgtccc ttctgtgatc 420
tttaccttcc ctgaagtcgc ttcagtaggc ctctccccaa cag 463

<210> 56
<211> 829
<212> DNA
<213> Chlamydia trachomatis

<400> 56
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gaatggtgcc ttctgaagag ggattaaaag aatacttcca gacgatggat taagcatctt 600
tgaaagtaag aaagtcgtac agatcttgat ctgaaaagag aagaaggctt tttaattttc 660
tgcagagagc cagcgaggct tcaataatgt tgaagtctcc gacaccaggc aatgctaagg 720
cgacgatatt agttagtgaa gtctgagtat taaggaaatg aaggccaaag aaatagctat 780
caataaagaa gccttcttcc ttgactctaa agaatagtat gtcgtatcc 829

<210> 57
<211> 1537
<212> DNA
<213> Chlamydia trachomatis

<400> 57
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tgggtcagct gcttccgcag gaagtgcggc aggagcgttg aaatcctcta acaattcagg 180
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ttttacagcc ggcatccggc ttctcgcgaa gtataac 1537

<210> 58
<211> 463
<212> DNA
<213> Chlamydia trachomatis

<400> 58
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tttaccttcc ctgaagtcgc ttcagtaggc ctctccccaa cag 463

<210> 59
<211> 552
<212> DNA
<213> Chlamydia trachomatis

<400> 59
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ttgaagcaag ctctggatta aaagaagatg aaattcaaca aatgatccgc gatgcagagc 180
ttcataaaga ggaagacaaa caacgaaaag aagcttctga tgtgaaaaat gaagccgatg 240
gaatgatctt tagagccgaa aaagctgtga aagattacca cgacaaaatt cctgcagaac 300
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ccacaacagc tatcaaagca gcttctgatg agttgagtac tcgtatgcaa aaaatcggag 420
aagctatgca ggctcaatcc gcatccgcag cagcatcttc tgcagcgaat gctcaaggag 480
ggccaaacat taactccgaa gatctgaaaa aacatagttt cagcacacga cctccagcag 540
gaggaagcgc ct 552

<210> 60

<211> 1180
<212> DNA
<213> Chlamydia trachomatis

<400> 60
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cttttaggag aaaaaatcta taatgctaga aaaatcctga gtaaggatca cttctcctca 120
acaacttttt catcttggat agagttagtt tttagaacta agtcttctgc ttacaatgct 180
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<210> 61
<211> 1215
<212> DNA
<213> Chlamydia trachomatis

<400> 61
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aaatggggag attgttgcta cgcaaggaaa agctttgaac acaacagcca agcgggatgc 180
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catacaggct ttgaa 1215

<210> 62
<211> 688
<212> DNA
<213> Chlamydia trachomatis

<400> 62
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ctaacacttt atcagcgtca tctttgagaa gcatctcaat gagcgctttt tcttctctag 120
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atccaaagta ctcagtcaat ccacgaattt tctctctagc gatacgtgga atttgactct 240
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gaatcgcaga taaatattta ggaaaggctt tgatatgtaa ataatagtct ttggcacgag 540
cctgtaattg ctctttagta agctccccct tcgaccattt cacataaaac gtgtgttcta 600
gcatatgctt attttgaata attaaatcta actgatctaa aaaattcata aacacctcca 660
tcatttcttt tcttgactcc acgtaacc 688

<210> 63
<211> 269
<212> DNA
<213> Chlamydia trachomatis

<400> 63
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tttggaaaat tgaccgctta ggacaaggcg aaaagagtaa aattactgta tgggtaaaac 240
ctcttaaaga aggttgctgc tttacagct 269

<210> 64
<211> 1339
<212> DNA
<213> Chlamydia trachomatis

<400> 64
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gatagtattc actcggactc cccaacgtcg gccggcttcc caagccagta cttttgtatc 480
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tatgtttatt ttaaaataat ttgttttaac aactgtttaa tagttttaat ttttaaagtg 1320
tgaaaaacag gttttatat 1339

<210> 65
<211> 195
<212> PRT
<213> Chlamydia trachomatis

<400> 65
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             20                  25                  30
Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val Cys
        35                  40                  45
Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu Glu
    50                  55                  60
His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr His
 65                  70                  75                  80
Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly Thr
                 85                  90                  95
Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe
            100                 105                 110
Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu
        115                 120                 125
Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro
    130                 135                 140
Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu Ile
145                 150                 155                 160
Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser Gly
                165                 170                 175
Glu Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe Gln
            180                 185                 190
Thr Met Asp
        195

      <210> 66
      <211> 520
      <212> DNA
      <213> Chlamydia

      <400> 66
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tgatgtaaat tagcgcaatt agagggggat gaggttactt ggaaatataa ggagcgaagc 180
gatgaaggag atgtatttgc tctggaagca aaggtttctg aagctaacag aacattgcgt 240
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tcatcgaacg aatttttcaa tcctcgaaaa tcttctccag agacttcgga aagatcttct 480
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      <210> 67
      <211> 276
      <212> DNA
      <213> Chlamydia

      <400> 67
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caagggcact atcaggaccc aagagcttca gattatgacc tcccacgtgc tagcgactat 180
gatttgccta gaagcccata tcctactcca cctttgcctt ctagatatca gctacagaat 240
atggatgtag aagcagggtt ccgtgaggca gtttat 276

<210> 68
<211> 248
<212> DNA
<213> Chlamydia

<400> 68
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tatgaaactt cttctgaaag cgattctgag gcataagaag catttagttt tattcggttt 180
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tcttattg 248

<210> 69
<211> 715
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 34
<223> n=A,T,C or G

<400> 69
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<210> 70
<211> 323
<212> DNA
<213> Chlamydia

<400> 70
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<210> 71
<211> 715
<212> DNA
<213> Chlamydia

<400> 71

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<210> 72
<211> 641
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 550,559,575,583,634,638
<223> n=A,T,C or G

<400> 72
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tcagcgtatt cggactgatg ccctaaagat cccnggangt t 641

<210> 73
<211> 584
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 460,523,541,546
<223> n=A,T,C or G

<400> 73
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gacttattac ggaacgagta aggcggagat ttctagagtt ctgcaaaagg gtaagcactg 180
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aagtattttt atagctgaag aacataggat gagtcatggn tagaaaagat cgtttaacta 480
atgaaagact gaataagcta tttgatagcc cctttagttt ggntaattac gtaattaagc 540
nagctnagaa caaaattgct agaggagatg ttcgttcttc taac 584

<210> 74
<211> 465
<212> DNA

<213> Chlamydia

<400> 74
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<210> 75
<211> 545
<212> DNA
<213> Chlamydia

<400> 75
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taagc 545

<210> 76
<211> 797
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 788,789
<223> n=A,T,C or G

<400> 76
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<210> 77
<211> 399
<212> DNA
<213> Chlamydia

<400> 77

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atcattaaaa agttgaagtt agatcctgag gcaagagcct ctgaattaac tgaagaagaa 180
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<210> 78
<211> 285
<212> DNA
<213> Chlamydia

<400> 78
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attgtaaaga aagtttggga atacattaaa aaacacaact gtcaggatca aaaaaataaa 180
cgtaatatcc ttcccgatgc gaatcttgcc aaagtctttg gctctagtga tcctatcgac 240
atgttccaaa tgaccaaagc cctttccaaa catattgtaa aataa 285

<210> 79
<211> 950
<212> DNA
<213> Chlamydia

<400> 79
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<210> 80
<211> 395
<212> DNA
<213> Chlamydia

<400> 80
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<210> 81
<211> 2085
<212> DNA
<213> Chlamydia

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<210> 82
<211> 405
<212> DNA
<213> Chlamydia

<400> 82
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gcaaaaaata aattagctcc tccattccga actgcagaat ttgat 405

<210> 83
<211> 379
<212> DNA
<213> Chlamydia

<400> 83
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<210> 84
<211> 715
<212> DNA
<213> Chlamydia

<400> 84
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<210> 85
<211> 476
<212> DNA
<213> Chlamydia

<400> 85
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<210> 86
<211> 1551
<212> DNA
<213> Chlamydia

<400> 86
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<210> 87
<211> 3031
<212> DNA
<213> Chlamydia

<400> 87
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<210> 88
<211> 976
<212> DNA
<213> Chlamydia

<400> 88
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<210> 89
<211> 94
<212> PRT
<213> Chlamydia

<400> 89
Met His His His His His His Met Ser Gln Lys Asn Lys Asn Ser Ala
5 10 15

Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly
20 25 30

Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr
35 40 45

Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
50 55 60

Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp
65 70 75 80

Met Phe Gln Met Thr Lys Ala Leu Ser Lys His Ile Val Lys
85 90

<210> 90
<211> 474
<212> PRT
<213> Chlamydia

<400> 90

Met Ala Ser His His His His His His Met Asn Glu Ala Phe Asp Cys
5 10 15

Val Val Ile Gly Ala Gly Pro Gly Gly Tyr Val Ala Ala Ile Thr Ala
20 25 30

Ala Gln Ala Gly Leu Lys Thr Ala Leu Ile Glu Lys Arg Glu Ala Gly
35 40 45

Gly Thr Cys Leu Asn Arg Gly Cys Ile Pro Ser Lys Ala Leu Leu Ala
50 55 60

Gly Ala Glu Val Val Thr Gln Ile Arg His Ala Asp Gln Phe Gly Ile
65 70 75 80

His Val Glu Gly Phe Ser Ile Asn Tyr Pro Ala Met Val Gln Arg Lys
85 90 95

Asp Ser Val Val Arg Ser Ile Arg Asp Gly Leu Asn Gly Leu Ile Arg
100 105 110

Ser Asn Lys Ile Thr Val Phe Ser Gly Arg Gly Ser Leu Ile Ser Ser
115 120 125

Thr Glu Val Lys Ile Leu Gly Glu Asn Pro Ser Val Ile Lys Ala His
130 135 140

Ser Ile Ile Leu Ala Thr Gly Ser Glu Pro Arg Ala Phe Pro Gly Ile
145 150 155 160

Pro Phe Ser Ala Glu Ser Pro Arg Ile Leu Cys Ser Thr Gly Val Leu
165 170 175

Asn Leu Lys Glu Ile Pro Gln Lys Met Ala Ile Ile Gly Gly Gly Val
180 185 190

Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu Gly Ser Glu Val
195 200 205

Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu Asn Asn Pro Asp
210 215 220

Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln Gly Leu Arg Phe
225 230 235 240

Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile Gly Asp Arg Val
245 250 255

Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp Tyr Val Leu Val
260 265 270

Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly Leu Asp Lys Ala
275 280 285

Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr Asp Ala Thr Met
290 295 300

Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp Ile Thr Gly Lys
305 310 315 320

Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile Ile Ala Ala Arg
325 330 335

Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser Ala Val Pro Ser
340 345 350

Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly Leu Ser Pro Thr
355 360 365

Ala Ala Gln Gln Gln Lys Ile Pro Val Lys Val Thr Lys Phe Pro Phe
370 375 380

Arg Ala Ile Gly Lys Ala Val Ala Met Gly Glu Ala Asp Gly Phe Ala
385 390 395 400

Ala Ile Ile Ser His Glu Thr Thr Gln Gln Ile Leu Gly Ala Tyr Val
405 410 415

Ile Gly Pro His Ala Ser Ser Leu Ile Ser Glu Ile Thr Leu Ala Val
420 425 430

Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr Ile His Ala His
435 440 445

Pro Thr Leu Ala Glu Val Trp Ala Glu Ser Ala Leu Leu Ala Val Asp
450 455 460

Thr Pro Leu His Met Pro Pro Ala Lys Lys
465 470

<210> 91
<211> 129
<212> PRT
<213> Chlamydia

<400> 91
Met His His His His His His Met Pro Arg Ile Ile Gly Ile Asp Ile
5 10 15

Pro Ala Lys Lys Lys Leu Lys Ile Ser Leu Thr Tyr Ile Tyr Gly Ile
20 25 30

Gly Ser Ala Arg Ser Asp Glu Ile Ile Lys Lys Leu Lys Leu Asp Pro
35 40 45

Glu Ala Arg Ala Ser Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn
50 55 60

Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg Arg Arg
65 70 75 80

Val Gln Ser Asp Ile Lys Arg Leu Ile Ala Ile His Ser Tyr Arg Gly
85 90 95

Gln Arg His Arg Leu Ser Leu Pro Val Arg Gly Gln Arg Thr Lys Thr
100 105 110

Asn Ser Arg Thr Arg Lys Gly Lys Arg Lys Thr Val Ala Gly Lys Lys
115 120 125

Lys

<210> 92
<211> 202
<212> PRT
<213> Chlamydia

<400> 92
Met His His His His His His Met Gly Ser Leu Val Gly Arg Gln Ala
1   5   10   15

Pro Asp Phe Ser Gly Lys Ala Val Val Cys Gly Glu Glu Lys Glu Ile
            20   25   30

Ser Leu Ala Asp Phe Arg Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro
        35   40   45

Lys Asp Phe Thr Tyr Val Cys Pro Thr Glu Leu His Ala Phe Gln Asp
    50   55   60

Arg Leu Val Asp Phe Glu Glu His Gly Ala Val Val Leu Gly Cys Ser
65   70   75   80

Val Asp Asp Ile Glu Thr His Ser Arg Trp Leu Thr Val Ala Arg Asp
                85   90   95

Ala Gly Gly Ile Glu Gly Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser
            100   105   110

Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
        115   120   125

Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His
    130   135   140

Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu
145   150   155   160

Arg Ile Leu Asp Ser Leu Ile Phe Phe Glu Asn His Gly Met Val Cys
                165   170   175

Pro Ala Asn Trp Arg Ser Gly Glu Arg Gly Met Val Pro Ser Glu Glu
            180   185   190

Gly Leu Lys Glu Tyr Phe Gln Thr Met Asp
        195   200

<210> 93
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> made in a lab

<400> 93

Glu Asn Ser Leu Gln Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp
1 5 10 15
Asp Lys Leu

<210> 94
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 94
Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys
1 5 10 15
Val Phe Gly Thr
20

<210> 95
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 95
Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
1 5 10 15
Glu Lys Pro Ile
20

<210> 96
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 96
Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met
1 5 10 15
Phe Gln Met Thr
20

<210> 97
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 97
Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met Phe Gln Met Thr Lys
1 5 10 15
Met Val Ser Gln
20

<210> 98
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 98
Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly
1 5 10 15
Thr Glu Lys Pro
20

<210> 99
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 99
Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly
1 5 10 15

<210> 100
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 100
Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp Pro Thr
1 5 10 15

<210> 101
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 101
Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys
1 5 10 15
Gln Asp Gln Lys
20

<210> 102
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 102

Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn
1 5 10 15
Lys Arg Asn Ile
20

<210> 103
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 103
Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys
1 5 10 15

<210> 104
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 104
Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
1 5 10 15
Ser Asp Tyr Val
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<210> 105
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 105
Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln
1 5 10 15
Ser Asp Ile Lys Arg
20

<210> 106
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 106
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
1 5 10 15
Ile Ser Leu Thr
20

<210> 107
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 107
Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
1 5 10 15
Ser Asp Tyr Val
20

<210> 108
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 108
Leu Asn Ala Leu Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg
1 5 10 15
Arg Arg Val Gln
20

<210> 109
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 109
Leu Asn Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg
1 5 10 15
Arg Arg Val Gln
20

<210> 110
<211> 1461
<212> DNA
<213> Chlamydia

<400> 110
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tgcctagaag cccatatcct actccacctt tgccttctag atatcagcta cagaatatgg 180
atgtagaagc agggttccgt gaggcagttt atgcttcttt tgtagcagga atgtacaatt 240
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gtgatatgct taccaacggg tcacagacat ttagcaacct gatgcagcgt tgggatagag 360
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ggacagatta gagaaaaatg agcaagcttt attgtccgat gtgcgcttag ttttatctag 1440
ctacacaaga tggttggata g 1461

<210> 111
<211> 267
<212> DNA
<213> Chlamydia

<400> 111
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acagaattcg tggaggattc cgggtttgcg cagttaaagc tccaggcttt ggagatagaa 120
gaaaagctat gttggaagac atcgctatct taactggcgg tcaactcatt agcgaagagt 180
tgggcatgaa attagaaaac gctaacttag ctatgttagg taaagctaaa aaagttatcg 240
tttctaaaga agacacgacc atcgtcg 267

<210> 112
<211> 698
<212> DNA
<213> Chlamydia

<400> 112
tgataagcaa gcaaccgctc aactagcagc tctaactatt aaaaaaatcc tctgttttga 60
tgaaaattcc tacgagaagg agctggcatg cttagaaaag aaacgcagta gcgtacaaaa 120
agatctgagc caactgaaaa aatacacagt tctctacatc aagaagctgc tcgaaaccta 180
cagacaactc gggcatcgaa agacaaaaat tgcaaaattt gatgacctac ctaccgagag 240
agtctccgct cataagaaag caaaagaact cgctgcgctc gatcaagaag agaacttcta 300
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cgataatttt accgatatct ccccttagcaa cagtcaattc gtagataatc gtattggttc 600
cctgcacctc tttcagatgc acttcctctg gcttatcaac aagatttttt acaatgtacg 660
ctaaaaactc tttcatgcga agcaaatcct acacaagc 698

<210> 113
<211> 1142
<212> DNA
<213> Chlamydia

<400> 113
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aacgaaaaaa gaaggtattt tgattccttc tgcagggatt gatgaatcga atacggacca 180
gccttttgtt ttatatccta aagatatttt gggatcgtgt aatcgcatcg gagaatggtt 240
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ttaattattc aaaataagca tatgctagaa cacacgtttt atgtgaaatg gtcgaagggg 720
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cagtttgtgt ttgctctagg agttactcca gaagagttag aggctcatga gcctagtgaa 960
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ca 1142

<210> 114
<211> 976
<212> DNA
<213> Chlamydia

<400> 114
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ggactgcagc tgaagagtcg gctgctttaa gaacactatt ttctcgcatg gcctctttag 120
ggcacaaagt accttctggg cgcactactt taaagattcg tcgtcctttt ggtactacga 180
gagaagttcg tgtgaaatgg cgttatgttc ctgaaggtgt aggagatttg gctaccatag 240
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atgatgcgtt tcatcggtct agttcgctat tctactctcc aatggttccg catttttggg 360
cagagcttcg caatcattat gcaacgagtg gtttgaaaag cgggtacaat attgggagta 420
ccgatgggtt tctccctgtc attgggcctg ttatatggga gtcggagggt cttttccgcg 480
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aaacgaacaa cccaggtggt agtgtccttt atctttatgc actgctttcc atgttgacag 720
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tgggagacaa catggaagga tatactgtgg atctacaggt tgccgagtat ttaaaaagct 900
ttggacgtca agtattgaat tgttggagta aaggggatat cgagttatca acacctattc 960
ctctttttgg ttttga 976

<210> 115
<211> 995
<212> DNA
<213> Chlamydia

<400> 115
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agtttttgaa gttctctcaa ccaacgggga tactcacttg ggaggagacg acttcgacgg 720
agtcatcatc aactggatgc ttgatgaatt caaaaaacaa gaaggcattg atctaagcaa 780
agataacatg gctttgcaaa gattgaaaga tgctgctgaa aaagcaaaaa tagaattgtc 840
tggtgtatcg tctactgaaa tcaatcagcc attcatcact atcgacgcta atggacctaa 900
acatttggct ttaactctaa ctcgcgctca attcgaacac ctagcttcct ctctcattga 960
gcgaaccaaa caaccttgtg ctcaggcttt aaaag 995

<210> 116
<211> 437
<212> DNA
<213> Chlamydia

<400> 116
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ggaaccctta cttgtaaaaa ctctcaccgt ctacaatttt tgaaaaactc ttccgataaa 180
caaggtggag gaatctacgg agaagacaac atcaccctat ctaatttgac agggaagact 240
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aaagctctta caatgacagg actggatagt ttctgtttaa ttaataacac atcagaaaaa 360
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acaattccag gaatcac 437

<210> 117
<211> 446
<212> DNA
<213> Chlamydia

<400> 117
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agggacaaat tacccgaaaa gttaagggtg gtttgatcgt agatattggt atggaagcct 180
tccttccagg atcccaaata gacaataaga agatcaagaa cttagatgat tacgtaggca 240
aggtttgtga gttcaaaatt ctcaaaatca acgtggatcg tcggaacgtt gttgtatcta 300
gaagagaact tctcgaagct gaacgcattt ctaagaaagc agagttgatc gagcaaatca 360
ctatcggtga acgtcgcaaa ggtatcgtta agaatatcac agatttcgga gtattcttgg 420
atcttgatgg cattgacggc ctactc 446

<210> 118
<211> 951
<212> DNA
<213> Chlamydia

<400> 118
agtattgcga aatattactg tgagaagcaa tgctgagagc ggttctagta aaagtgaggg 60
gagagctgtc agaagggatc gctcaggaag cgagacaacg tgtggctgat ttattaggaa 120
gattccctct ttatcctgaa atcgatctgg aaacgctagt ttagtgggag actctatgcc 180
tgaaggggaa atgatgcata agttgcaaga tgtcatagat agaaagttgt tggattctcg 240
tcgtattttc ttctccgaac ctgtaacgga gaaaagtgct gcagaagcca tcaaaaagct 300
ttggtatttg gaactcacca atcctgggca gccaattgta tttgtcatta atagccctgg 360
agggtctgtt gatgctgggt ttgctgtttg ggaccaaatt aaaatgatct cttctccttt 420
gactacagtt gttacaggtt tagcagcatc tatgggatct gtattgagtt tgtgtgctgt 480
tccaggaaga cgttttgcta cgcctcatgc gcgcattatg attcaccagc cttctattgg 540
aggaaccatt actggtcaag ccacggactt ggatattcat gctcgtgaaa ttttaaaaac 600
aaaagcacgc attattgatg tgtatgtcga ggcaactgga caatctccag aggtgataga 660
gaaagctatc gatcgagata tgtggatgag tgcaaatgaa gcaatggagt ttggactgtt 720
agatgggatt ctcttctctt ttaacgactt gtagatatct tttatattct ggagcaggaa 780
acagtttcat tttgggagaa tcgatgcctt ctcttgagga tgttctgttt ttatgccagg 840
aagagatggt tgatgggttt ttatgtgtag agtcttctga aatagcagat gctaaactca 900
ctgtttttaa tagtgatgga tctatcgcgt ctatgtgcgg gaatgggttg c 951

<210> 119
<211> 953
<212> DNA
<213> Chlamydia

<400> 119
atatcaaagt tgggcaaatg acagagccgc tcaaggacca gcaaataatc cttgggacaa 60
catcaacacc tgtcgcagcc aaaatgacag cttctgatgg aatatcttta acagtctcca 120
ataatccatc aaccaatgct tctattacaa ttggtttgga tgcggaaaaa gcttaccagc 180
ttattctaga aaagttggga gatcaaattc ttggtggaat tgctgatact attgttgata 240
gtacagtcca agatatttta gacaaaatca caacagaccc ttctctaggt ttgttgaaag 300
cttttaacaa ctttccaatc actaataaaa ttcaatgcaa cgggttattc actcccagga 360
acattgaaac tttattagga ggaactgaaa taggaaaatt cacagtcaca cccaaaagct 420

ctgggagcat gttcttagtc tcagcagata ttattgcatc aagaatggaa ggcggcgttg 480
ttctagcttt ggtacgagaa ggtgattcta agccctacgc gattagttat ggatactcat 540
caggcgttcc taatttatgt agtctaagaa ccagaattat taatacagga ttgactccga 600
caacgtattc attacgtgta ggcggtttag aaagcggtgt ggtatgggtt aatgcccttt 660
ctaatggcaa tgatatttta ggaataacaa atacttctaa tgtatctttt ttggaggtaa 720
tacctcaaac aaacgcttaa acaattttta ttggattttt cttataggtt ttatatttag 780
agaaaaaagt tcgaattacg gggtttgtta tgcaaaataa aagcaaagtg agggacgatt 840
ttattaaaat tgttaaagat tcctggtatc ggtctgcgat tccgactcgt ccaacatcaa 900
tacaacctat taatttcccc tcgtcaaaaa taaggttatc aagtgagaaa tca 953

<210> 120
<211> 897
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 395
<223> n = A,T,C or G

<400> 120
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact 120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggatgagggg 360
ctcgtagcag atctttgtgt gtctcataag cgcanagcgg ctgcggctgt ctgtagcttc 420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg cgcaaccgtt tctttcttcc caaattaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tttgtggtgg gttctggact cgctatcagt 600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc 660
gaattgtcgg gagaggaaaa tgcttgcgag aggagagtcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc 780
gacgttttca aattggtgcc gttgcctatt acaatgggta ttcgtgcaat tgtggctgcg 840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcgccag agcataa 897

<210> 121
<211> 298
<212> PRT
<213> Chlamydia

<400> 121
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
100 105 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile

```
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
            180                 185                 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
        275                 280                 285
Ile Gly Leu Trp Thr Phe Cys Ala Arg Ala
    290                 295

      <210> 122
      <211> 897
      <212> DNA
      <213> Chlamydia

      <400> 122
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtggcttc     420
atcggaggaa ttacctacct cgcgacattc ggagttatcc gtccgattct gtttgtcaac     480
aaaatgctgg tgaacccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgtcgg gagaggaaaa tgcttgcgag aagagagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897

      <210> 123
      <211> 298
      <212> PRT
      <213> Chlamydia

      <400> 123
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1               5                  10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
```

```
                        85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                 185                 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                 280                 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295
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<210> 124
<211> 897
<212> DNA
<213> Chlamydia

<400> 124

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atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
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<210> 125
<211> 298
<212> PRT
<213> Chlamydia

<400> 125

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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1               5                  10                  15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
```

```
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                 185                 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                 280                 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295
```

<210> 126
<211> 897
<212> DNA
<213> Chlamydia

<400> 126

```
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
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<210> 127
<211> 298
<212> PRT
<213> Chlamydia

<400> 127

```
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1               5                   10                  15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                 185                 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                 280                 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295
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<210> 128
<211> 897
<212> DNA
<213> Chlamydia

<400> 128

```
atggcttcta tatgtggacg tttagggtct ggtacaggga atgctctaaa agcttttttt     60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact    120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc    180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacgaga    240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg    300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg    360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtggcttc    420
atcggaggaa ttacctacct cgcgacattc ggagttatcc gtccgattct gtttgtcaac    480
aaaatgctgg tgaacccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt    540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt    600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc    660
gaagtgtcgg gagaggaaaa tgcttgcgag aagagagtcg ctggagagaa agccaagacg    720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc    780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct    840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa       897
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<210> 129
<211> 298
<212> PRT
<213> Chlamydia

<400> 129
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
65 70 75 80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100 105 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180 185 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
210 215 220
Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275 280 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290 295

<210> 130
<211> 897
<212> DNA
<213> Chlamydia

<400> 130
atggctgcta tatgtggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact 120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggatgagggg 360
ctcgtagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcttc 420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg cgcaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540

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agctatatta tggcggctaa ccatgcagcg tttgtggtgg gttctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc     660
gaattgtcgg gagaggaaaa tgcttgcgag aggggagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gttgcctatt acaatgggta ttcgtgcaat tgtggctgcg     840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcaacag agtataa        897
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      <210> 131
      <211> 298
      <212> PRT
      <213> Chlamydia

      <400> 131
Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1               5                  10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
            180                 185                 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Arg Gly Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
        275                 280                 285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
    290                 295

      <210> 132
      <211> 897
      <212> DNA
      <213> Chlamydia

      <400> 132
atggctgcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
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```
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggatgagggg     360
ctcgtagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcttc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg cgcaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tttgtggtgg gttctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc     660
gaattgtcgg gagaggaaaa tgcttgtgag aggagagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gttgcctatt acaatgggta ttcgtgcaat tgtggctgcg     840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcaacag agtataa        897
```

```
<210> 133
<211> 298
<212> PRT
<213> Chlamydia

<400> 133
Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1               5                   10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
            180                 185                 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
        275                 280                 285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
    290                 295

<210> 134
<211> 897
<212> DNA
```

<213> Chlamydia

<400> 134
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact 120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg 360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc 420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt 600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc 660
gaaatgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc 780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct 840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa 897

<210> 135
<211> 298
<212> PRT
<213> Chlamydia

<400> 135
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100 105 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180 185 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Met Pro Gly
210 215 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275 280 285

```
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295

      <210> 136
      <211> 882
      <212> DNA
      <213> Chlamydia

      <400> 136
atggcttctg tatgtgggcg attaagtgct ggggtgggga acagatttaa cgcatttttc      60
acgcgtcccg gtaacaagct atcacggttt gtaaatagcg caaaaggatt agacagatca     120
ataaaggttg ggaagtctgc tgctgaatta acggcgagta ttttagagca aactgggggg     180
gcagggactg atgcacatgt tacggcggcc aaggtgtcta aagcacttgg ggacgcgcga     240
acagtaatgg ctctagggaa tgtcttcaat gggtctgtgc cagcaaccat tcaaagtgcg     300
cgaagctgtc tcgcccattt acgagcggcc ggcaaagaag aagaaacatg ctccaaggtg     360
aaagatctct gtgtttctca tagacgaaga gctgcggctg aggcttgtaa tgttattgga     420
ggagcaactt atattacaac tttcggagcg attcgtccga cattactcgt taacaagctt     480
cttgccaaac cattcctttc ctcccaagcc aaagaagggt tgggagcttc tgttggttat     540
atcatggcag cgaaccatgc ggcatctgtg cttgggtctg ctttaagtat tagcgcagaa     600
agagcagact gtgaagagcg gtgtgatcgc attcgatgta gtgaggatgg tgaaatttgc     660
gaaggcaata aattaacagc tatttcggaa gagaaggcta gatcatggac tctcattaag     720
tacagattcc ttactatgat agaaaaacta tttgagatgg tggcggatat cttcaagtta     780
attcctttgc caatttcgca tggaattcgt gctattgttg ctgcgggatg tacgttgact     840
tctgcagtta ttggcttagg tactttttgg tctagagcat aa                        882

      <210> 137
      <211> 293
      <212> PRT
      <213> Chlamydia

      <400> 137
Met Ala Ser Val Cys Gly Arg Leu Ser Ala Gly Val Gly Asn Arg Phe
 1               5                  10                  15
Asn Ala Phe Phe Thr Arg Pro Gly Asn Lys Leu Ser Arg Phe Val Asn
            20                  25                  30
Ser Ala Lys Gly Leu Asp Arg Ser Ile Lys Val Gly Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Ser Ile Leu Glu Gln Thr Gly Gly Ala Gly Thr Asp
    50                  55                  60
Ala His Val Thr Ala Ala Lys Val Ser Lys Ala Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Met Ala Leu Gly Asn Val Phe Asn Gly Ser Val Pro Ala Thr
                85                  90                  95
Ile Gln Ser Ala Arg Ser Cys Leu Ala His Leu Arg Ala Ala Gly Lys
            100                 105                 110
Glu Glu Glu Thr Cys Ser Lys Val Lys Asp Leu Cys Val Ser His Arg
        115                 120                 125
Arg Arg Ala Ala Ala Glu Ala Cys Asn Val Ile Gly Gly Ala Thr Tyr
    130                 135                 140
Ile Thr Thr Phe Gly Ala Ile Arg Pro Thr Leu Leu Val Asn Lys Leu
145                 150                 155                 160
Leu Ala Lys Pro Phe Leu Ser Ser Gln Ala Lys Glu Gly Leu Gly Ala
                165                 170                 175
Ser Val Gly Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val Leu Gly
            180                 185                 190
Ser Ala Leu Ser Ile Ser Ala Glu Arg Ala Asp Cys Glu Glu Arg Cys
        195                 200                 205
Asp Arg Ile Arg Cys Ser Glu Asp Gly Glu Ile Cys Glu Gly Asn Lys
    210                 215                 220
Leu Thr Ala Ile Ser Glu Glu Lys Ala Arg Ser Trp Thr Leu Ile Lys
225                 230                 235                 240
```

```
Tyr Arg Phe Leu Thr Met Ile Glu Lys Leu Phe Glu Met Val Ala Asp
                245                 250                 255
Ile Phe Lys Leu Ile Pro Leu Pro Ile Ser His Gly Ile Arg Ala Ile
            260                 265                 270
Val Ala Ala Gly Cys Thr Leu Thr Ser Ala Val Ile Gly Leu Gly Thr
        275                 280                 285
Phe Trp Ser Arg Ala
    290
```

<210> 138
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 138

```
Asp Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser
 1               5                  10                  15
```

<210> 139
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 139

```
Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
 1               5                  10                  15
```

<210> 140
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 140

```
Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile
 1               5                  10                  15
Arg Pro
```

<210> 141
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 141

```
Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn Lys
 1               5                  10                  15
Met Leu
```

<210> 142
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 142
Arg Pro Ile Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser
1 5 10 15
Ser Gln

<210> 143
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 143
Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met Gly
1 5 10 15
Ser

<210> 144
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 144
Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 145
Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 146
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 146

Phe Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 147
Cys Ser Phe Ile Gly Gly Ile Thr Tyr
1 5

<210> 148
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 148
Cys Ser Phe Ile Gly Gly Ile Thr
1 5

<210> 149
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 149
Cys Ser Ile Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 150
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 150
Cys Gly Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 151
Gly Phe Ile Gly Gly Ile Thr Tyr Leu

1 5

<210> 152
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 152
Gln Ile Phe Val Cys Leu Ile Ser Ala Glu Arg Leu Arg Leu Arg Leu
1 5 10 15
Ser Val Ala Ser
20

<210> 153
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 153
Glu Arg Leu Arg Leu Arg Leu Ser Val Ala Ser Ser Glu Glu Leu Pro
1 5 10 15
Thr Ser Arg His
20

<210> 154
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 154
Ala Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val
1 5 10 15
Arg Phe Cys Leu
20

<210> 155
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 155
Arg His Ser Glu Leu Ser Val Arg Phe Cys Leu Ser Thr Lys Cys Trp
1 5 10 15
Arg Asn Arg Phe
20

<210> 156
<211> 20
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 156

```
Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys Leu Lys
 1               5                  10                  15
Gln Ile Trp Asp
            20
```

<210> 157
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 157

```
Ile Phe Val Cys Leu Ile Ser Ala Glu Arg Leu Arg Leu Ser Val Ala
 1               5                  10                  15
Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val Arg
            20                  25                  30
Phe Cys Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys
        35                  40                  45
Leu Lys Gln Ile Trp
    50
```

<210> 158
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 158

```
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe
 1               5                  10                  15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
            20                  25                  30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile
        35                  40                  45
Lys Ala Asn Met
    50
```

<210> 159
<211> 24
<212> DNA
<213> Chlamydia

<400> 159

```
ttttgaagca ggtaggtgaa tatg                                          24
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<210> 160
<211> 24
<212> DNA
<213> Chlamydia

<400> 160

ttaagaaatt taaaaaatcc ctta 24

<210> 161
<211> 24
<212> DNA
<213> Chlamydia

<400> 161
ggtataatat ctctctaaat tttg 24

<210> 162
<211> 19
<212> DNA
<213> Chlamydia

<400> 162
agataaaaaa ggctgtttc 19

<210> 163
<211> 24
<212> DNA
<213> Chlamydia

<400> 163
ttttgaagca ggtaggtgaa tatg 24

<210> 164
<211> 29
<212> DNA
<213> Chlamydia

<400> 164
tttacaataa gaaaagctaa gcactttgt 29

<210> 165
<211> 20
<212> DNA
<213> Chlamydia

<400> 165
ccttacacag tcctgctgac 20

<210> 166
<211> 20
<212> DNA
<213> Chlamydia

<400> 166
gtttccgggc cctcacattg 20

<210> 167
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 167
Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 168
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 168
Ser Ile Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 169
<211> 2643
<212> DNA
<213> Chlamydia

<400> 169
```
gcaatcatgc gacctgatca tatgaacttc tgttgtctat gtgctgctat tttgtcatcc      60
acagcggtcc tctttggcca ggatccctta ggtgaaaccg ccctcctcac taaaaatcct     120
aatcatgtcg tctgtacatt ttttgaggac tgtaccatgg agagcctctt tcctgctctt     180
tgtgctcatg catcacaaga cgatcctttg tatgtacttg gaaattccta ctgttggttc     240
gtatctaaac tccatatcac ggaccccaaa gaggctcttt ttaaagaaaa aggagatctt     300
tccattcaaa actttcgctt cctttccttc acagattgct cttccaagga aagctctcct     360
tctattattc atcaaaagaa tggtcagtta tccttgcgca ataatggtag catgagtttc     420
tgtcgaaatc atgctgaagg ctctggagga gccatctctg cggatgcctt ttctctacag     480
cacaactatc ttttcacagc ttttgaagag aattcttcta aaggaaatgg cggagccatt     540
caggctcaaa ccttctcttt atctagaaat gtgtcgccta tttctttcgc ccgtaatcgt     600
gcggatttaa atggcggcgc tatttgctgt agtaatctta tttgttcagg gaatgtaaac     660
cctctctttt tcactggaaa ctccgccacg aatggaggcg ctatttgttg tatcagcgat     720
ctaaacacct cagaaaaagg ctctctctct cttgcttgta accaagaaac gctatttgca     780
agcaattctg ctaaagaaaa aggcggggct atttatgcca agcacatggt attgcgttat     840
aacggtcctg tttccttcat taacaacagc gctaaaatag gtggagctat cgccatccag     900
tccggaggga gtctctctat ccttgcaggt gaaggatctg ttctgttcca gaataactcc     960
caacgcacct ccgaccaagg tctagtaaga aacgccatct acttaragaa agatgcgatt    1020
ctttcttcct tagaagctcg caacggagat attcttttct ttgatcctat tgtacaagaa    1080
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ccagccaccg catctccttt agttattcag acaagtgcaa accgttcagt gattttctcg    1200
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cctatcgaac tgaaatccgg acgcttagtt ttaaaagatc gcgctgtcct ttccgcgcct    1320
tctctctctc aggatcctca agctctcctc attatggaag cgggaacttc tttaaaaact    1380
tcctctgatt tgaagttagc tacgctaagt attccccttc attccttaga tactgaaaaa    1440
agcgtaacta tccacgcccc taatctttct atccaaaaga tcttcctctc taactctgga    1500
gatgagaatt tttatgaaaa tgtagagctt ctcagtaaag agcaaaacaa tattcctctc    1560
cttactctcc ctaaagagca atctcattta catcttcctg atgggaacct ctcttctcac    1620
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attgctaatt ggacgcctaa aaactatgtg cctcatccag aacgtcaatc tacactcgtt    1740
gcgaacactc tttggaacac ctattccgat atgcaagctg tgcagtcgat gattaataca    1800
acagcgcacg gaggagccta tctatttgga acgtggggat ctgctgtttc taatttattc    1860
tatgttcacg acagctctgg gaaacctatc gataattggc atcatagaag ccttggctac    1920
ctattcggta tcagtactca cagtttagat gaccattctt tctgcttggc tgcaggacaa    1980
ttactcggga aatcgtccga ttcctttatt acgtctacag aaacgacctc ctatatagct    2040
actgtacaag cgcaactcgc tacctctcta atgaaaatct ctgcacaggc atgctacaat    2100
gaaagtatcc atgagctaaa aacaaaatat cgctccttct ctaaagaagg attcggatcc    2160
tggcatagcg ttgcagtatc cggagaagtg tgcgcatcga ttcctattgt atccaatggt    2220
tccggactgt tcagctcctt ctctattttc tctaaactgc aaggattttc aggaacacag    2280
gacggttttg aggagagttc gggagagatt cggtcctttt ctgccagctc tttcagaaat    2340
atttcacttc ctataggaat aacatttgaa aaaaaatccc aaaaaacacg aacctactat    2400
tactttctag gagcctacat ccaagacctg aaacgtgatg tggaatcggg acctgtagtg    2460
ttactcaaaa atgccgtctc ctgggatgct cctatggcga acttggattc acgagcctac    2520
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atgttccggc ttacgaatca aagagctcta cacagacttc agacgctgtt aaatgtgtct    2580
tgtgtgctgc gtgggcaaag ccatagttac tccctggatc tggggaccac ttacaggttc    2640
tag                                                                  2643

<210> 170
<211> 2949
<212> DNA
<213> Chlamydia

<400> 170
atgattcctc aaggaattta cgatggggag acgttaactg tatcatttcc ctatactgtt      60
ataggagatc cgagtgggac tactgttttt tctgcaggag agttaacatt aaaaaatctt     120
gacaattcta ttgcagcttt gcctttaagt tgttttggga acttattagg gagttttact     180
gttttaggga gaggacactc gttgactttc gagaacatac ggacttctac aaatggggca     240
gctctaagta atagcgctgc tgatggactg tttactattg agggttttaa agaattatcc     300
ttttccaatt gcaattcatt acttgccgta ctgcctgctg caacgactaa taagggtagc     360
cagactccga cgacaacatc tacaccgtct aatggtacta tttattctaa aacagatctt     420
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<212> DNA
<213> Chlamydia

<400> 174

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<210> 175
<211> 880
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 336
<223> Xaa = Any Amino Acid

<400> 175
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            20                  25                  30
Thr Ala Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr Phe Phe
        35                  40                  45
Glu Asp Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala His Ala
    50                  55                  60
Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys Trp Phe
65                  70                  75                  80
Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe Lys Glu
                85                  90                  95
Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe Thr Asp
            100                 105                 110
Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys Asn Gly
        115                 120                 125
Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg Asn His
    130                 135                 140
Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser Leu Gln
145                 150                 155                 160
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His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys Gly Asn
                165                 170                 175
Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser
            180                 185                 190
Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile
        195                 200                 205
Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu Phe Phe
    210                 215                 220
Thr Gly Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp
225                 230                 235                 240
Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu
                245                 250                 255
Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr
            260                 265                 270
Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn
        275                 280                 285
Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser
    290                 295                 300
Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser
305                 310                 315                 320
Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr Leu Xaa
                325                 330                 335
Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp Ile Leu
            340                 345                 350
Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser Pro Leu
        355                 360                 365
Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala
    370                 375                 380
Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser
385                 390                 395                 400
Ser Glu Arg Leu Ser Glu Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser
                405                 410                 415
Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys
            420                 425                 430
Asp Arg Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala
        435                 440                 445
Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser Asp Leu
    450                 455                 460
Lys Leu Ala Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu Lys
465                 470                 475                 480
Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe Leu
                485                 490                 495
Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu Leu Ser
            500                 505                 510
Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu Gln Ser
        515                 520                 525
His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr Gln
    530                 535                 540
Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser Leu
545                 550                 555                 560
Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg Gln
                565                 570                 575
Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met Gln
            580                 585                 590
Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala Tyr Leu
        595                 600                 605
Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val His Asp
    610                 615                 620
Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu Gly Tyr
625                 630                 635                 640
Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe Cys Leu
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                645                 650                 655
Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile Thr Ser
            660                 665                 670
Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu Ala Thr
        675                 680                 685
Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser Ile His
    690                 695                 700
Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe Gly Ser
705                 710                 715                 720
Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile Pro Ile
                725                 730                 735
Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe Ser Lys
            740                 745                 750
Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser Ser Gly
        755                 760                 765
Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser Leu Pro
    770                 775                 780
Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr
785                 790                 795                 800
Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser
                805                 810                 815
Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met
            820                 825                 830
Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg
        835                 840                 845
Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg
    850                 855                 860
Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe
865                 870                 875                 880
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<210> 176
<211> 982
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 981
<223> Xaa = Any Amino Acid

<400> 176

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            20                  25                  30
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro
        35                  40                  45
Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg
    50                  55                  60
Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala
65                  70                  75                  80
Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe
                85                  90                  95
Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro
            100                 105                 110
Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr Ser Thr
        115                 120                 125
Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Leu Asn
    130                 135                 140
Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly
145                 150                 155                 160
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Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys
165 170 175
Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val
180 185 190
Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val
195 200 205
Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp
210 215 220
Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val
225 230 235 240
Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg
245 250 255
Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn
260 265 270
Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala
275 280 285
Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn Asn Tyr
290 295 300
Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Gly Ser
305 310 315 320
Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe
325 330 335
Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys
340 345 350
Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn Ile Ala
355 360 365
Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu
370 375 380
Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr
385 390 395 400
Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln
405 410 415
Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys
420 425 430
Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly
435 440 445
Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly
450 455 460
Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu
465 470 475 480
Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys
485 490 495
Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr
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Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu
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Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr
545 550 555 560
Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr
565 570 575
Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp
580 585 590
Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile
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Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro
610 615 620
Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly
625 630 635 640
Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr

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Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu
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Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp
            675                     680                     685
Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser
        690                     695                     700
Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His
705                     710                     715                     720
Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr
                    725                     730                     735
Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala
                740                     745                     750
Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser
            755                     760                     765
Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala
        770                     775                     780
Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr
785                     790                     795                     800
Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu
                    805                     810                     815
Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala
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Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu
            835                     840                     845
Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe
        850                     855                     860
Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu
865                     870                     875                     880
Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr
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His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr
                900                     905                     910
Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr
            915                     920                     925
Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg
        930                     935                     940
Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His
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Gly Ser Lys Val Xaa Phe
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<210> 177
<211> 964
<212> PRT
<213> Chlamydia

<400> 177
Met Lys Lys Ala Phe Phe Phe Phe Leu Ile Gly Asn Ser Leu Ser Gly
 1               5                   10                  15
Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val
                20                  25                  30
Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly
            35                  40                  45
Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile
        50                  55                  60
Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile
65                  70                  75                  80
Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe
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                85                  90                  95
Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser
            100                 105                 110
Pro Asn Ser Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile
        115                 120                 125
Phe Glu Asn Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr
    130                 135                 140
Ala Ala Asp Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu
145                 150                 155                 160
Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser
                165                 170                 175
Tyr Val Gln Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser
            180                 185                 190
Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr
        195                 200                 205
Asn Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser
    210                 215                 220
Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys
225                 230                 235                 240
Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg
                245                 250                 255
Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr
            260                 265                 270
Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg
        275                 280                 285
Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile
    290                 295                 300
Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val
305                 310                 315                 320
Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly
                325                 330                 335
Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp
            340                 345                 350
Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn
        355                 360                 365
Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile
    370                 375                 380
Thr Val Ala Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser
385                 390                 395                 400
Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val
                405                 410                 415
Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe
            420                 425                 430
Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln
        435                 440                 445
Thr Lys Thr Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile
    450                 455                 460
Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly
465                 470                 475                 480
Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly
                485                 490                 495
Thr Gly Asp Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly
            500                 505                 510
Leu Asn Leu Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu
        515                 520                 525
Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala
    530                 535                 540
Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr
545                 550                 555                 560
Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser
                565                 570                 575
```

Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser
580 585 590
Glu Asn Ile Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln
595 600 605
Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala
610 615 620
Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg
625 630 635 640
Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys
645 650 655
His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu
660 665 670
Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His
675 680 685
Pro Phe Trp Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln
690 695 700
Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr
705 710 715 720
Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe
725 730 735
Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val
740 745 750
Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln
755 760 765
Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp
770 775 780
His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln
785 790 795 800
Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu
805 810 815
Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu
820 825 830
Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly
835 840 845
Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu
850 855 860
Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro
865 870 875 880
Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln
885 890 895
Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe
900 905 910
Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser
915 920 925
Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His
930 935 940
Gly Phe Tyr Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile
945 950 955 960
Ala Leu Arg Phe

<210> 178
<211> 1530
<212> PRT
<213> Chlamydia

<400> 178
Met Ser Ser Glu Lys Asp Ile Lys Ser Thr Cys Ser Lys Phe Ser Leu
1 5 10 15
Ser Val Val Ala Ala Ile Leu Ala Ser Val Ser Gly Leu Ala Ser Cys
20 25 30

Val Asp Leu His Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val
35 40 45
Gly Pro Gln Ala Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val
50 55 60
Gly Ser Lys Asp Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly
65 70 75 80
Asp Pro Ser Ser Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys
85 90 95
Val Glu Gln Ser Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln
100 105 110
Gly Val Asp Gln Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser
115 120 125
Phe Thr Ser Ser Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu
130 135 140
Gly Ile Ala Phe Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr
145 150 155 160
Asp Val Lys Ala Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp
165 170 175
Leu Ile Phe Glu Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser
180 185 190
Ser Leu Glu Gln Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His
195 200 205
Asp Cys Gln Gly Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala
210 215 220
Glu Gly Ser Ser Ala Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe
225 230 235 240
Phe Val Thr Gly Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala
245 250 255
Gly Asp Met Val Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly
260 265 270
Asn Ser Ala Asn Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys
275 280 285
Val Leu Phe Val Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg
290 295 300
Ala Leu Ser Gly Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln
305 310 315 320
Asn Cys Ala Glu Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu
325 330 335
Asp Lys Gly Ser Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val
340 345 350
Leu Leu Gln Gly Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala
355 360 365
Ser Gln Gly Gly Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn
370 375 380
Glu Gly Pro Val Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly
385 390 395 400
Ala Ile Ala Ala Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly
405 410 415
Ile Ser Phe Glu Gly Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys
420 425 430
Gly Ser Phe Ser Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp
435 440 445
Ile Ser Lys Asn Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr
450 455 460
Thr Ser Asp Leu Gly Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe
465 470 475 480
Gly Glu Asn Ile Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys
485 490 495
Asp Asn Ile Val Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly
500 505 510
Gly Ala Ile Leu Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly

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        515                 520                 525
Gly Ile Ser Phe Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr
    530                 535                 540
Gln Glu Glu Phe Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser
545                 550                 555                 560
Ser Gly Tyr Ser Gly Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile
                565                 570                 575
Leu His Asn Ala Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser
            580                 585                 590
Glu Glu Glu Ala Thr Leu Leu Gly Cys Cys Gly Gly Gly Ala Val His
        595                 600                 605
Gly Met Asp Ser Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly
    610                 615                 620
Asn Asn Tyr Ala Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser
625                 630                 635                 640
Lys Thr Val Gln Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn
                645                 650                 655
Ile Ala Ser Leu Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys
            660                 665                 670
Glu Leu Val Asp Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg
        675                 680                 685
Val Tyr Gly Gly Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser
    690                 695                 700
Gly Asn Lys Gly Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu
705                 710                 715                 720
Tyr Val Glu Glu Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro
                725                 730                 735
Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln
            740                 745                 750
Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly
        755                 760                 765
Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg
    770                 775                 780
Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala Lys Arg Val Arg Ile Val
785                 790                 795                 800
Asp Asn Gln Glu Ala Val Val Phe Ser Asn Asn Phe Ser Asp Ile Tyr
                805                 810                 815
Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg Glu Glu Asp Lys Leu Asp
            820                 825                 830
Gly Gln Ile Pro Glu Val Leu Ile Ser Gly Asn Ala Gly Asp Val Val
        835                 840                 845
Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu His Leu Pro His Thr Gly
    850                 855                 860
Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr Ile Ser Gln Asn Thr Gly
865                 870                 875                 880
Asn Val Leu Phe Tyr Asn Asn Val Ala Cys Ser Gly Gly Ala Val Arg
                885                 890                 895
Ile Glu Asp His Gly Asn Val Leu Leu Glu Ala Phe Gly Gly Asp Ile
            900                 905                 910
Val Phe Lys Gly Asn Ser Ser Phe Arg Ala Gln Gly Ser Asp Ala Ile
        915                 920                 925
Tyr Phe Ala Gly Lys Glu Ser His Ile Thr Ala Leu Asn Ala Thr Glu
    930                 935                 940
Gly His Ala Ile Val Phe His Asp Ala Leu Val Phe Glu Asn Leu Lys
945                 950                 955                 960
Glu Arg Lys Ser Ala Glu Val Leu Leu Ile Asn Ser Arg Glu Asn Pro
                965                 970                 975
Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu Ala Glu Ser Lys Val Pro
            980                 985                 990
Gln Cys Ile His Val Gln Gln Gly Ser Leu Glu Leu Leu Asn Gly Ala
        995                 1000                1005
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Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp Ala Gly Ala Lys Leu Val
    1010                1015                1020
Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu Asp Ser Gly Thr Pro Val
1025                1030                1035                1040
Gln Gly His Ala Ile Ser Lys Pro Glu Ala Glu Ile Glu Ser Ser Ser
                1045                1050                1055
Glu Pro Glu Gly Ala His Ser Leu Trp Ile Ala Lys Asn Ala Gln Thr
            1060                1065                1070
Thr Val Pro Met Val Asp Ile His Thr Ile Ser Val Asp Leu Ala Ser
        1075                1080                1085
Phe Ser Ser Ser Gln Gln Glu Gly Thr Val Glu Ala Pro Gln Val Ile
    1090                1095                1100
Val Pro Gly Gly Ser Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu
1105                1110                1115                1120
Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn
                1125                1130                1135
Glu Ala Lys Val Pro Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala
            1140                1145                1150
Ser Ala Glu Ile Ser Asn Leu Ser Val Ser Asp Leu Gln Ile His Val
        1155                1160                1165
Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp
    1170                1175                1180
Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro
1185                1190                1195                1200
Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn
                1205                1210                1215
Ala Leu Trp Glu Glu Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg
            1220                1225                1230
Phe Ala His Asn Leu Thr Ala Gln Arg Met Glu Phe Asp Tyr Ser Thr
        1235                1240                1245
Asn Val Trp Gly Phe Ala Phe Gly Gly Phe Arg Thr Leu Ser Ala Glu
    1250                1255                1260
Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly Ala Tyr Gly Gly Ala Ser
1265                1270                1275                1280
Ala Gly Val Asp Ile Gln Leu Met Glu Asp Phe Val Leu Gly Val Ser
                1285                1290                1295
Gly Ala Ala Phe Leu Gly Lys Met Asp Ser Gln Lys Phe Asp Ala Glu
            1300                1305                1310
Val Ser Arg Lys Gly Val Val Gly Ser Val Tyr Thr Gly Phe Leu Ala
        1315                1320                1325
Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser Leu Gly Glu Thr Gln Asn
    1330                1335                1340
Asp Met Lys Thr Arg Tyr Gly Val Leu Gly Glu Ser Ser Ala Ser Trp
1345                1350                1355                1360
Thr Ser Arg Gly Val Leu Ala Asp Ala Leu Val Glu Tyr Arg Ser Leu
                1365                1370                1375
Val Gly Pro Val Arg Pro Thr Phe Tyr Ala Leu His Phe Asn Pro Tyr
            1380                1385                1390
Val Glu Val Ser Tyr Ala Ser Met Lys Phe Pro Gly Phe Thr Glu Gln
        1395                1400                1405
Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala Ser Leu Thr Asn Ile Thr
    1410                1415                1420
Ile Pro Leu Gly Met Lys Phe Glu Leu Ala Phe Ile Lys Gly Gln Phe
1425                1430                1435                1440
Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr Ala Trp Glu Ala Tyr Arg
                1445                1450                1455
Lys Val Glu Gly Gly Ala Val Gln Leu Leu Glu Ala Gly Phe Asp Trp
            1460                1465                1470
Glu Gly Ala Pro Met Asp Leu Pro Arg Gln Glu Leu Arg Val Ala Leu
        1475                1480                1485
Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe Ser Thr Val Leu Gly Leu
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1490 1495 1500
Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr Asp Ser Lys Leu Gly Tyr
1505 1510 1515 1520
Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
1525 1530

<210> 179
<211> 1776
<212> PRT
<213> Chlamydia

<400> 179
Ala Ile Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val Leu
1 5 10 15
Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr
20 25 30
Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe Thr
35 40 45
Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val
50 55 60
Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His Leu
65 70 75 80
Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser
85 90 95
Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser Ser
100 105 110
Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly Ile
115 120 125
Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu
130 135 140
Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Phe Gly Glu
145 150 155 160
Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala
165 170 175
Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu
180 185 190
Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala Lys
195 200 205
Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn
210 215 220
Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu
225 230 235 240
Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala
245 250 255
Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu Thr
260 265 270
Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu
275 280 285
Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu Thr
290 295 300
Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro Asp
305 310 315 320
Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser Leu Thr
325 330 335
Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile Ala Thr
340 345 350
Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys Thr Asn
355 360 365
Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His Gly Gly
370 375 380
Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr Ser Glu

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385                 390                 395                 400
Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser Glu Asn
                405                 410                 415
Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys Leu Ser Leu
            420                 425                 430
Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys Glu Ser
        435                 440                 445
Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr Asp Thr
    450                 455                 460
Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser Thr Pro Glu
465                 470                 475                 480
Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Glu
                485                 490                 495
Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln
            500                 505                 510
Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn
        515                 520                 525
Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly
    530                 535                 540
Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu
545                 550                 555                 560
Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys Leu Thr
                565                 570                 575
Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn
            580                 585                 590
Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val Thr Leu
        595                 600                 605
Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala
    610                 615                 620
Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu
625                 630                 635                 640
Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr Glu Gly
                645                 650                 655
Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp
            660                 665                 670
Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr
        675                 680                 685
Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn
    690                 695                 700
Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn Glu Asn
705                 710                 715                 720
Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser
                725                 730                 735
Val Ser Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly
            740                 745                 750
Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn
        755                 760                 765
Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val
    770                 775                 780
Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp Asn Pro Asp
785                 790                 795                 800
Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly Pro Thr Glu
                805                 810                 815
Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile Gly Gly Gly
            820                 825                 830
Ala Ile Tyr Gly Glu Thr Val Lys Ile Glu Asn Phe Ser Gly Gln Gly
        835                 840                 845
Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser
    850                 855                 860
Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe
865                 870                 875                 880
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Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr Phe Ser Gly Asn
                885                 890                 895
Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala Gly Gly Ala Ile
            900                 905                 910
Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val Phe Ser Lys Asn
        915                 920                 925
Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr Gln Arg Lys Asp
    930                 935                 940
Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val Ser Leu Ser Gly
945                 950                 955                 960
Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly Ser Ala Ile Gly
                965                 970                 975
Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys Leu Glu Ser Gly
            980                 985                 990
Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr
        995                 1000                1005
Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn
    1010                1015                1020
Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser
1025                1030                1035                1040
Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Leu Val Thr Pro
                1045                1050                1055
Thr Leu Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp
            1060                1065                1070
Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn
        1075                1080                1085
Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly
    1090                1095                1100
Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr
1105                1110                1115                1120
Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val Lys Leu Thr Met
                1125                1130                1135
Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr
            1140                1145                1150
Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp
        1155                1160                1165
Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser Ala Phe Thr Gly
    1170                1175                1180
Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro
1185                1190                1195                1200
Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu Lys Pro Asn Thr
                1205                1210                1215
Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly Ser Ser Leu Val
            1220                1225                1230
Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val Ala Asp Gly Ala
        1235                1240                1245
Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser Val Glu Lys Asn
    1250                1255                1260
Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile
1265                1270                1275                1280
Asp Thr Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser Thr Asp Ser Glu
                1285                1290                1295
Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn Asn Asn Asp Ala
            1300                1305                1310
Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser Pro Ala Val Ala
        1315                1320                1325
Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala Ala Thr Ala
    1330                1335                1340
Thr Pro Thr Thr Thr Pro Thr Ala Thr Thr Thr Thr Ser Asn Gln Val
1345                1350                1355                1360
Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe
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                1365                1370                1375
Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser Leu Leu Val Leu
            1380                1385                1390
Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile Val Leu Thr Gly
        1395                1400                1405
Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro
    1410                1415                1420
Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp Lys Phe Asp Ser
1425                1430                1435                1440
Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His Phe Tyr Ala Asn
                1445                1450                1455
Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val Lys Gln Gly Leu
            1460                1465                1470
Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu Val Ser Tyr Asn
        1475                1480                1485
Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser Gln Val Gly Thr
    1490                1495                1500
Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly Ala Ser Val Ala
1505                1510                1515                1520
Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly Ala Ala Phe Ser
                1525                1530                1535
Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu Asn Asn Tyr Thr
            1540                1545                1550
His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys
        1555                1560                1565
Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys Ser Leu Pro Leu
    1570                1575                1580
Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys His Asp Thr Val
1585                1590                1595                1600
Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly Glu Trp Glu Asp
                1605                1610                1615
Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val Leu Arg Thr Pro
            1620                1625                1630
Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr
        1635                1640                1645
Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu Tyr Asp Pro Arg
    1650                1655                1660
Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile Pro Met Gly Leu
1665                1670                1675                1680
Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu Met Tyr Asn Arg
                1685                1690                1695
Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn Ser Pro Thr Cys
            1700                1705                1710
Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Gly Glu Ile Ile Cys Gly
        1715                1720                1725
Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser Thr Gln Leu Tyr
    1730                1735                1740
Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr Ile Glu Ala Asp
1745                1750                1755                1760
Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala Arg Met Thr Phe
                1765                1770                1775
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<210> 180
<211> 1752
<212> PRT
<213> Chlamydia

<400> 180

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Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser
 1               5                  10                  15
Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
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```
            20                  25                  30
Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile Gly Glu Ala
        35                  40                  45
Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
    50                  55                  60
Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser Asn Ser Ser
65                  70                  75                  80
Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
                85                  90                  95
Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr Asn Ala His
            100                 105                 110
Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
        115                 120                 125
Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Gly Ala Ile Phe Ser
    130                 135                 140
Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr Ile Gln Asn
145                 150                 155                 160
Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Gly Ser Thr Ile
                165                 170                 175
Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn Ser Ala Glu
            180                 185                 190
Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
        195                 200                 205
Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
    210                 215                 220
Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn Leu Gln Ser
225                 230                 235                 240
His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
                245                 250                 255
Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
            260                 265                 270
Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
        275                 280                 285
Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val
    290                 295                 300
Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
305                 310                 315                 320
Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
                325                 330                 335
Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly
            340                 345                 350
Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu Glu Glu Ile
        355                 360                 365
Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
    370                 375                 380
Leu Pro Ser Leu Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp
385                 390                 395                 400
Ala Ser Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asp
                405                 410                 415
Ser Gly Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val
            420                 425                 430
Pro Val Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser
        435                 440                 445
Ile Thr Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr
    450                 455                 460
Asp Val Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn
465                 470                 475                 480
Ser His Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly
                485                 490                 495
Gly Ile Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys
            500                 505                 510
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Thr Leu Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe
        515                 520                 525
Ile Lys Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe
    530                 535                 540
Cys Leu Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val
545                 550                 555                 560
Thr Lys Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro
                565                 570                 575
Gly Ile Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser
            580                 585                 590
Thr Gly Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser
        595                 600                 605
Asn Leu Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly
    610                 615                 620
Gly Gly Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala
625                 630                 635                 640
Glu Gln Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala
                645                 650                 655
Pro Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser
            660                 665                 670
Leu Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn
        675                 680                 685
Lys Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr
    690                 695                 700
Val Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly
705                 710                 715                 720
Ile Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile
                725                 730                 735
Ser Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu
            740                 745                 750
Ser Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu
        755                 760                 765
Val Gly Lys Glu Gly Gly Gly Leu His Ala Lys Thr Val Asn Ile Ser
    770                 775                 780
Asn Leu Lys Ser Gly Phe Ser Phe Ser Asn Asn Lys Ala Asn Ser Ser
785                 790                 795                 800
Ser Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala
                805                 810                 815
Ser Leu Gln Ala Ala Ala Ala Ala Ala Pro Ser Ser Pro Ala Thr Pro
            820                 825                 830
Thr Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr
        835                 840                 845
Phe Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile
    850                 855                 860
Asp Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile
865                 870                 875                 880
Tyr Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser
                885                 890                 895
Tyr Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr
            900                 905                 910
Gly Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn
        915                 920                 925
Cys Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Ile Ala Thr Pro Lys
    930                 935                 940
Thr Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile
945                 950                 955                 960
Gly Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg
                965                 970                 975
Phe Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala
            980                 985                 990
Asn Ala Asn Thr Pro Ser Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr
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        995                 1000                1005
Glu Lys Ile Thr Leu Glu Asn Gly Ser Phe Ile Phe Glu Arg Asn Gln
    1010                1015                1020
Ala Asn Lys Arg Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly
1025                1030                1035                1040
Asn Asn Ile Thr Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala
                1045                1050                1055
Ile Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu
            1060                1065                1070
Phe Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser
        1075                1080                1085
Gly Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp
    1090                1095                1100
Pro Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu
1105                1110                1115                1120
Ala Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn
                1125                1130                1135
Gln Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val
            1140                1145                1150
Lys Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp
        1155                1160                1165
Cys Val His Thr Ser Thr Lys Lys Thr Gly Ser Thr Gln Asn Val Tyr
    1170                1175                1180
Glu Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly
1185                1190                1195                1200
Thr Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro
                1205                1210                1215
Gln Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr
            1220                1225                1230
Glu Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile
        1235                1240                1245
Met Glu Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala
    1250                1255                1260
Leu Ala Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro
1265                1270                1275                1280
Gln Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr
                1285                1290                1295
Thr Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr
            1300                1305                1310
Asn Pro Lys Arg Ile Ser Ala Ala Val Pro Ser Gly Ser Ala Ala Thr
        1315                1320                1325
Thr Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr Gly Asp Leu Thr
    1330                1335                1340
Leu Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser
1345                1350                1355                1360
Asp Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val
                1365                1370                1375
Gln Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly
            1380                1385                1390
Tyr Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu
        1395                1400                1405
Gln Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro
    1410                1415                1420
Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser
1425                1430                1435                1440
Met Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala
                1445                1450                1455
Arg Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly
            1460                1465                1470
Thr Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr
        1475                1480                1485
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Tyr Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp
    1490                1495                1500
Phe Ile Leu Gly Ala Ala Phe Ser Lys Ile Val Gly Lys Thr Lys Ala
1505                1510                1515                1520
Ile Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr
                1525                1530                1535
Gln Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys
            1540                1545                1550
Gln His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr
        1555                1560                1565
Gly His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro Ser Ile His Glu
    1570                1575                1580
Arg Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu Ala Asp Leu Arg
1585                1590                1595                1600
Ile Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile
                1605                1610                1615
Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe
            1620                1625                1630
Thr Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg
        1635                1640                1645
Asn Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn
    1650                1655                1660
Cys Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser
1665                1670                1675                1680
Ile Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn
                1685                1690                1695
Glu Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg
            1700                1705                1710
Ala Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr
        1715                1720                1725
Gly Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu Ser Gln Met Thr
    1730                1735                1740
Ser Cys Gly Ala Arg Met Ile Phe
1745                1750
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<210> 181
<211> 2601
<212> DNA
<213> Chlamydia

<400> 181

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agcctctttc ctgctctttg tgctcatgca tcacaagacg atcctttgta tgtacttgga     180
aattcctact gttggttcgt atctaaactc catatcacgg accccaaaga ggctcttttt     240
aaagaaaaag gagatctttc cattcaaaac tttcgcttcc tttccttcac agattgctct     300
tccaaggaaa gctctccttc tattattcat caaaagaatg gtcagttatc cttgcgcaat     360
aatggtagca tgagtttctg tcgaaatcat gctgaaggct ctggaggagc catctctgcg     420
gatgcctttt ctctacagca caactatctt ttcacagctt ttgaagagaa ttcttctaaa     480
ggaaatggcg gagccattca ggctcaaacc ttctctttat ctagaaatgt gtcgcctatt     540
tctttcgccc gtaatcgtgc ggatttaaat ggcggcgcta tttgctgtag taatcttatt     600
tgttcaggga atgtaaaccc tctctttttc actggaaact ccgccacraa tggaggcsct     660
atttgttgta tcagcgatct aaacacctca gaaaaaggct ctctctctct tgcttgtaac     720
caaraaacgc tatttgcaag caattctgct aaagaaaaag gcggggctat ttatgccaag     780
cacatggtat tgcgttataa cggtcctgtt tccttcatta acaacagcgc taaaataggt     840
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ctgttccaga ataactccca acgcacctcc gaccaaggtc tagtaagaaa cgccatctac     960
ttagagaaag atgcgattct ttcttcctta gaagctcgca acggagatat tcttttcttt    1020
gatcctattg tacaagaaag tagcagcaaa gaatcgcctc ttccctcctc tttgcaagcc    1080
agcgtgactt ctcccacccc agccaccgca tctcctttag ttattcagac aagtgcaaac    1140
cgttcagtga ttttctcgag cgaacgtctt tctgaagaag aaaaaactcc tgataacctc    1200
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acttcccaac tacagcagcc tatcgaactg aaatccggac gcttagtttt aaaagatcgc   1260
gctgtccttt ccgsgccttc tctctctcag gatcctcaag ctctcctcat tatggaagcg   1320
ggaacttctt taaaaacttc ctytgatttg aagttagsta cgstaagtat tccccttcat   1380
tccttagata ctgaaaaaag cgtaactatc cacgccccta atctttctat ccaaaagatc   1440
ttcctctcta actctggaga tgagaatttt tatgaaaatg tagagcttct cagtaaagag   1500
caaaacaata ttcctctcct tactctccct aaagagcaat ctcatttaca tcttcctgat   1560
gggaacctct cttctcactt tggatatcaa ggagattgga ctttttcttg gaaagattct   1620
gatgaagggc attctctgat tgctaattgg acgcctaaaa actatgtgcc tcatccagaa   1680
cgtcaatcta cactcgttgc gaacactctt tggaacacct attccgatat gcaagctgtg   1740
cagtcgatga ttaatacaac agcgcacgga ggagcctatc tatttggaac gtggggatct   1800
gctgtttcta atttattcta tgttcacgac agctctggga aacctatcga taattggcat   1860
catagaagcc ttggctacct attcggtatc agtactcaca gtttagatga ccattctttc   1920
tgcttggctg caggacaatt actcgggaaa tcgtccgatt cctttattac gtctacagaa   1980
acgacctcct atatagctac tgtacaagcg caactcgcta cctctctaat gaaaatctct   2040
gcacaggcat gctacaatga aagtatccat gagctaaaaa caaaatatcg ctccttctct   2100
aaagaaggat tcggatcctg gcatagcgtt gcagtatccg gagaagtgtg cgcatcgatt   2160
cctattgtat ccaatggttc cggactgttc agctccttct ctatttctc taaactgcaa   2220
ggattttcag gaacacagga cggttttgag gagagttcgg gagagattcg gtccttttct   2280
gccagctctt tcagaaatat ttcacttcct ataggaataa catttgaaaa aaaatcccaa   2340
aaaacacgaa cctactatta ctttctagga gcctacatcc aagacctgaa acgtgatgtg   2400
gaatcgggac ctgtagtgtt actcaaaaat gccgtctcct gggatgctcc tatggcgaac   2460
ttggattcac gagcctacat gttccggctt acgaatcaaa gagctctaca cagacttcag   2520
acgctgttaa atgtgtcttg tgtgctgcgt gggcaaagcc atagttactc cctggatctg   2580
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<210> 182
<211> 3021
<212> DNA
<213> Chlamydia

<400> 182

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ccctatactg ttataggaga tccgagtggg actactgttt tttctgcagg agagttaaca    180
ttaaaaaatc ttgacaattc tattgcagct ttgcctttaa gttgttttgg gaacttatta    240
gggagtttta ctgttttagg gagaggacac tcgttgactt tcgagaacat acggacttct    300
acaaatgggg cagctctaag taatagcgct gctgatggac tgtttactat tgagggtttt    360
aaagaattat cctttccaa ttgcaattca ttacttgccg tactgcctgc tgcaacgact    420
aataagggta gccagactcc gacgacaaca tctacaccgt ctaatggtac tatttattct    480
aaaacagatc ttttgttact caataatgag aagttctcat tctatagtaa tttagtctct    540
ggagatgggg gagctataga tgctaagagc ttaacggttc aaggaattag caagctttgt    600
gtcttccaag aaaatactgc tcaagctgat gggggagctt gtcaagtagt caccagtttc    660
tctgctatgg ctaacgaggc tcctattgcc tttgtagcga atgttgcagg agtaagaggg    720
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gatccagtag taagtttttc cagaaatact gcggtagagt ttgatgggaa cgtagcccga    840
gtaggaggag ggatttactc ctacgggaac gttgctttcc tgaataatgg aaaaaccttg    900
tttctcaaca atgttgcttc tcctgtttac attgctgcta agcaaccaac aagtggacag    960
gcttctaata cgagtaataa ttacggagat ggaggagcta tcttctgtaa gaatggtgcg   1020
caagcaggat ccaataactc tggatcagtt tcctttgatg gagagggagt agttttcttt   1080
agtagcaatg tagctgctgg gaaaggggga gctatttatg ccaaaaagct ctcggttgct   1140
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gcaaaattat cagtgaattc tctaagtcag acaggtggga gtctgtatat ggaagctggg   1620
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atcacgcttt ccaatctgca tttgtctctt tcttctttgt tagcaaacaa tgcagttacg   1740
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actaagcccc cagctaatgc cccatcagat ttgactctag ggaatgagat gcctaagtat    1980
ggctatcaag gaagctggaa gcttgcgtgg gatcctaata cagcaaataa tggtccttat    2040
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ttggttccaa atagtttatg ggatccatt ttagatatac gatctgcgca ttcagcaatt    2160
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tccttaggag caaactccta ctttggatca tcgatgtttg gtctagcatt taccgaagta    2340
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ggacatctcc taaatctatc agttcctgtt ggagtgaagt ttgatcgatg ttctagtaca    2760
catcctaata aatatagctt tatggcggct tatatctgtg atgcttatcg caccatctct    2820
ggtactgaga caacgctcct atcccatcaa gagacatgga caacagatgc ctttcattta    2880
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<210> 183
<211> 2934
<212> DNA
<213> Chlamydia

<400> 183

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atgcccaact cagttccaga tcctacgaaa gagtcgctat caaataaaat tagtttgaca     180
ggagacactc acaatctcac taactgctat ctcgataacc tacgctacat actggctatt     240
ctacaaaaaa ctcccaatga aggagctgct gtcacaataa cagattacct aagctttttt     300
gatacacaaa aagaaggtat ttattttgca aaaaatctca cccctgaaag tggtggtgcg     360
attggttatg cgagtcccaa ttctcctacc gtggagattc gtgatacaat aggtcctgta     420
atctttgaaa ataatacttg ttgcagacta tttacatgga gaaatcctta tgctgctgat     480
aaaataagag aaggcggagc cattcatgct caaaatcttt acataaatca taatcatgat     540
gtggtcggat ttatgaagaa cttttcttat gtccaaggag gagccattag taccgctaat     600
acctttgttg tgagcgagaa tcagtcttgt ttctctttta tggacaacat ctgtattcaa     660
actaatacag caggaaaagg tggcgctatc tatgctggaa cgagcaattc ttttgagagt     720
aataactgcg atctcttctt catcaataac gcctgttgtg caggaggagc gatcttctcc     780
cctatctgtt ctctaacagg aaatcgtggt aacatcgttt tctataacaa tcgctgcttt     840
aaaaatgtag aaacagcttc ttcagaagct tctgatggag gagcaattaa agtaactact     900
cgcctagatg ttacaggcaa tcgtggtagg atctttttta gtgacaatat cacaaaaaat     960
tatggcggag ctatttacgc tcctgtagtt accctagtgg ataatggccc tacctacttt    1020
ataaacaata tcgccaataa taagggggc gctatctata tagacggaac cagtaactcc    1080
aaaatttctg ccgaccgcca tgctattatt tttaatgaaa atattgtgac taatgtaact    1140
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aacaaaatga agtctagaaa agcttgtggt gtagctgttg gtgcaacgtt aatcgacgct     1500
gacaaatggt caatcactgg tgaagcacgc ttaatcaatg aaagagctgc tcacatgaat     1560
gcacaattcc gcttctaa                                                    1578
```

<210> 189
<211> 866
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 220, 242, 425, 448, 453, 455
<223> Xaa = Any Amino Acid

<400> 189

```
Met Ala Ser His His His His His His Leu Phe Gly Gln Asp Pro Leu
 1               5                  10                  15
Gly Glu Thr Ala Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr
            20                  25                  30
Phe Phe Glu Asp Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala
        35                  40                  45
His Ala Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys
    50                  55                  60
Trp Phe Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe
65                  70                  75                  80
Lys Glu Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe
                85                  90                  95
Thr Asp Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys
            100                 105                 110
Asn Gly Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg
        115                 120                 125
Asn His Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser
    130                 135                 140
Leu Gln His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys
145                 150                 155                 160
Gly Asn Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn
                165                 170                 175
Val Ser Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly
            180                 185                 190
Ala Ile Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu
        195                 200                 205
Phe Phe Thr Gly Asn Ser Ala Thr Asn Gly Gly Xaa Ile Cys Cys Ile
    210                 215                 220
Ser Asp Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn
225                 230                 235                 240
Gln Xaa Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala
                245                 250                 255
Ile Tyr Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe
            260                 265                 270
Ile Asn Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly
        275                 280                 285
Gly Ser Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn
    290                 295                 300
Asn Ser Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr
305                 310                 315                 320
Leu Glu Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp
                325                 330                 335
Ile Leu Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser
```

```
            340                 345                 350
Pro Leu Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala
        355                 360                 365
Thr Ala Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile
    370                 375                 380
Phe Ser Ser Glu Arg Leu Ser Glu Glu Glu Lys Thr Pro Asp Asn Leu
385                 390                 395                 400
Thr Ser Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val
                405                 410                 415
Leu Lys Asp Arg Ala Val Leu Ser Xaa Pro Ser Leu Ser Gln Asp Pro
            420                 425                 430
Gln Ala Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Xaa
        435                 440                 445
Asp Leu Lys Leu Xaa Thr Xaa Ser Ile Pro Leu His Ser Leu Asp Thr
    450                 455                 460
Glu Lys Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile
465                 470                 475                 480
Phe Leu Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu
                485                 490                 495
Leu Ser Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu
            500                 505                 510
Gln Ser His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly
        515                 520                 525
Tyr Gln Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His
    530                 535                 540
Ser Leu Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu
545                 550                 555                 560
Arg Gln Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp
                565                 570                 575
Met Gln Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala
            580                 585                 590
Tyr Leu Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val
        595                 600                 605
His Asp Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu
    610                 615                 620
Gly Tyr Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe
625                 630                 635                 640
Cys Leu Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile
                645                 650                 655
Thr Ser Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu
            660                 665                 670
Ala Thr Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser
        675                 680                 685
Ile His Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe
    690                 695                 700
Gly Ser Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile
705                 710                 715                 720
Pro Ile Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe
                725                 730                 735
Ser Lys Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser
            740                 745                 750
Ser Gly Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser
        755                 760                 765
Leu Pro Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr
    770                 775                 780
Tyr Tyr Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val
785                 790                 795                 800
Glu Ser Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala
                805                 810                 815
Pro Met Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn
            820                 825                 830
```

Gln Arg Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val
835 840 845
Leu Arg Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr
850 855 860
Arg Phe
865

<210> 190
<211> 1006
<212> PRT
<213> Chlamydia

<400> 190
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
1 5 10 15
Val Pro His His His His His His Met Ile Pro Gln Gly Ile Tyr Asp
20 25 30
Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro
35 40 45
Ser Gly Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu
50 55 60
Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu
65 70 75 80
Gly Ser Phe Thr Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn
85 90 95
Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp
100 105 110
Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys
115 120 125
Asn Ser Leu Leu Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser
130 135 140
Gln Thr Pro Thr Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser
145 150 155 160
Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser
165 170 175
Asn Leu Val Ser Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr
180 185 190
Val Gln Gly Ile Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln
195 200 205
Ala Asp Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala
210 215 220
Asn Glu Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly
225 230 235 240
Gly Gly Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser
245 250 255
Thr Ser Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val
260 265 270
Glu Phe Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr
275 280 285
Gly Asn Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn
290 295 300
Val Ala Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln
305 310 315 320
Ala Ser Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys
325 330 335
Lys Asn Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe
340 345 350
Asp Gly Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys
355 360 365
Gly Gly Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro
370 375 380

```
Val Gln Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu
385                 390                 395                 400
Gly Glu Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile
                405                 410                 415
Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val
            420                 425                 430
Asn Gly Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly
        435                 440                 445
Lys Ile Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn
    450                 455                 460
Asp Pro Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser
465                 470                 475                 480
Lys Leu Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val
                485                 490                 495
Phe Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln
            500                 505                 510
Gly Arg Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu
        515                 520                 525
Ser Gln Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Leu Asp
    530                 535                 540
Phe Val Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu
545                 550                 555                 560
Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn
                565                 570                 575
Asn Ala Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His
            580                 585                 590
Pro Ala Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly
        595                 600                 605
Pro Ile Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp
    610                 615                 620
Trp Leu Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly
625                 630                 635                 640
Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu
                645                 650                 655
Met Pro Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro
            660                 665                 670
Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys
        675                 680                 685
Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val Ala Ser Leu Val Pro Asn
    690                 695                 700
Ser Leu Trp Gly Ser Ile Leu Asp Ile Arg Ser Ala His Ser Ala Ile
705                 710                 715                 720
Gln Ala Ser Val Asp Gly Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser
                725                 730                 735
Gly Val Ser Asn Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly
            740                 745                 750
Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe
        755                 760                 765
Gly Ser Ser Met Phe Gly Leu Ala Phe Thr Glu Val Phe Gly Arg Ser
    770                 775                 780
Lys Asp Tyr Val Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser
785                 790                 795                 800
Val Tyr Leu Ser Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly
                805                 810                 815
Asp Ala Phe Ile Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys
            820                 825                 830
Thr Ser Tyr Thr Phe Ala Glu Glu Ser Asp Val Arg Trp Asp Asn Asn
        835                 840                 845
Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro
    850                 855                 860
Ser Lys Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe
```

```
865                 870                 875                 880
Ser Tyr Ala Asp His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg
                885                 890                 895
Ala Phe Lys Ser Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val
            900                 905                 910
Lys Phe Asp Arg Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met
        915                 920                 925
Ala Ala Tyr Ile Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr
    930                 935                 940
Thr Leu Leu Ser His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu
945                 950                 955                 960
Ala Arg His Gly Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr
                965                 970                 975
Ser Asn Ile Glu Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala
            980                 985                 990
Ser Arg Gly Tyr Gly Leu Ser Ala Gly Ser Lys Val Arg Phe
        995                 1000                1005

<210> 191
<211> 977
<212> PRT
<213> Chlamydia

<400> 191
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
 1               5                  10                  15
Val Pro Ser Ser Asp Pro His His His His His His Gly Leu Ala Arg
            20                  25                  30
Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val Pro Asp Pro
        35                  40                  45
Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly Asp Thr His
    50                  55                  60
Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile Leu Ala Ile
65                  70                  75                  80
Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile Thr Asp Tyr
                85                  90                  95
Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe Ala Lys Asn
            100                 105                 110
Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser Pro Asn Ser
        115                 120                 125
Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile Phe Glu Asn
    130                 135                 140
Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr Ala Ala Asp
145                 150                 155                 160
Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu Tyr Ile Asn
                165                 170                 175
His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser Tyr Val Gln
            180                 185                 190
Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser Glu Asn Gln
        195                 200                 205
Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr Asn Thr Ala
    210                 215                 220
Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser Phe Glu Ser
225                 230                 235                 240
Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys Ala Gly Gly
                245                 250                 255
Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg Gly Asn Ile
            260                 265                 270
Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr Ala Ser Ser
        275                 280                 285
Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg Leu Asp Val
```

```
    290                 295                 300
Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr Lys Asn
305                 310                 315                 320
Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val Asp Asn Gly
                325                 330                 335
Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly Ala Ile
            340                 345                 350
Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg His Ala
        355                 360                 365
Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn Ala Asn Gly
    370                 375                 380
Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala
385                 390                 395                 400
Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu
                405                 410                 415
Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser
            420                 425                 430
Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala
        435                 440                 445
Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr
    450                 455                 460
Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His
465                 470                 475                 480
Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser
                485                 490                 495
Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly Thr Gly Asp
            500                 505                 510
Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly Leu Asn Leu
        515                 520                 525
Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu Trp Val Glu
    530                 535                 540
Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala Ala Thr Phe
545                 550                 555                 560
Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr Gly Asn Ser
                565                 570                 575
Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser Gln Pro Met
            580                 585                 590
Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser Glu Asn Ile
        595                 600                 605
Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln Gly Leu Trp
    610                 615                 620
Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala Ser Ser Ala
625                 630                 635                 640
Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg Thr Leu Leu
                645                 650                 655
Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys His Arg Ser
            660                 665                 670
Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu Ala Thr Glu
        675                 680                 685
Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His Pro Phe Trp
    690                 695                 700
Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln Asp Pro Arg
705                 710                 715                 720
Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr Ser Ala Gly
                725                 730                 735
Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe Ser Gln Thr
            740                 745                 750
Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val Ser Ser Lys
        755                 760                 765
Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln Glu Gly Phe
    770                 775                 780
```

```
Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp His Asn Cys
785                 790                 795                 800
His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln Gly Thr Phe
                805                 810                 815
Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu Pro Met Lys
            820                 825                 830
Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu Gly Ala Leu
        835                 840                 845
Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly Ala Tyr Pro
    850                 855                 860
Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu Val Pro Ile
865                 870                 875                 880
Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro Gln Ala Trp
                885                 890                 895
Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln Glu Pro Gly
            900                 905                 910
Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe Gly Ser Gly
        915                 920                 925
Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser Gln Gln Thr
    930                 935                 940
Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His Gly Phe Tyr
945                 950                 955                 960
Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile Ala Leu Arg
                965                 970                 975
Phe
```

<210> 192
<211> 848
<212> PRT
<213> Chlamydia

<400> 192

```
Met Ala Ser His His His His His His Gly Ala Ile Ser Cys Leu Arg
 1               5                  10                  15
Gly Asp Val Val Ile Ser Gly Asn Lys Gly Arg Val Glu Phe Lys Asp
            20                  25                  30
Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu Thr Val Glu Lys Val Glu
        35                  40                  45
Glu Val Glu Pro Ala Pro Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe
    50                  55                  60
Leu Gly Ser Val Glu Gln Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu
65                  70                  75                  80
Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser
                85                  90                  95
Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala
            100                 105                 110
Lys Arg Val Arg Ile Val Asp Asn Gln Glu Ala Val Val Phe Ser Asn
        115                 120                 125
Asn Phe Ser Asp Ile Tyr Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg
    130                 135                 140
Glu Glu Asp Lys Leu Asp Gly Gln Ile Pro Glu Val Leu Ile Ser Gly
145                 150                 155                 160
Asn Ala Gly Asp Val Val Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu
                165                 170                 175
His Leu Pro His Thr Gly Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr
            180                 185                 190
Ile Ser Gln Asn Thr Gly Asn Val Leu Phe Tyr Asn Asn Val Ala Cys
        195                 200                 205
Ser Gly Gly Ala Val Arg Ile Glu Asp His Gly Asn Val Leu Leu Glu
    210                 215                 220
```

```
Ala Phe Gly Gly Asp Ile Val Phe Lys Gly Asn Ser Ser Phe Arg Ala
225                 230                 235                 240
Gln Gly Ser Asp Ala Ile Tyr Phe Ala Gly Lys Glu Ser His Ile Thr
                245                 250                 255
Ala Leu Asn Ala Thr Glu Gly His Ala Ile Val Phe His Asp Ala Leu
            260                 265                 270
Val Phe Glu Asn Leu Lys Glu Arg Lys Ser Ala Glu Val Leu Leu Ile
        275                 280                 285
Asn Ser Arg Glu Asn Pro Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu
    290                 295                 300
Ala Glu Ser Lys Val Pro Gln Cys Ile His Val Gln Gln Gly Ser Leu
305                 310                 315                 320
Glu Leu Leu Asn Gly Ala Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp
                325                 330                 335
Ala Gly Ala Lys Leu Val Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu
            340                 345                 350
Asp Ser Gly Thr Pro Val Gln Gly His Ala Ile Ser Lys Pro Glu Ala
        355                 360                 365
Glu Ile Glu Ser Ser Ser Glu Pro Glu Gly Ala His Ser Leu Trp Ile
    370                 375                 380
Ala Lys Asn Ala Gln Thr Thr Val Pro Met Val Asp Ile His Thr Ile
385                 390                 395                 400
Ser Val Asp Leu Ala Ser Phe Ser Ser Ser Gln Gln Glu Gly Thr Val
                405                 410                 415
Glu Ala Pro Gln Val Ile Val Pro Gly Gly Ser Tyr Val Arg Ser Gly
            420                 425                 430
Glu Leu Asn Leu Glu Leu Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn
        435                 440                 445
His Ala Leu Leu Lys Asn Glu Ala Lys Val Pro Leu Met Ser Phe Val
    450                 455                 460
Ala Ser Ser Asp Glu Ala Ser Ala Glu Ile Ser Asn Leu Ser Val Ser
465                 470                 475                 480
Asp Leu Gln Ile His Val Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr
                485                 490                 495
Gly His Met Gly Asp Trp Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu
            500                 505                 510
Val Ile Asn Trp Asn Pro Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala
        515                 520                 525
Gly Ala Leu Val Phe Asn Ala Leu Trp Glu Glu Gly Ala Val Leu Ser
    530                 535                 540
Ala Leu Lys Asn Ala Arg Phe Ala His Asn Leu Thr Ala Gln Arg Met
545                 550                 555                 560
Glu Phe Asp Tyr Ser Thr Asn Val Trp Gly Phe Ala Phe Gly Gly Phe
                565                 570                 575
Arg Thr Leu Ser Ala Glu Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly
            580                 585                 590
Ala Tyr Gly Gly Ala Ser Ala Gly Val Asp Ile Gln Leu Met Glu Asp
        595                 600                 605
Phe Val Leu Gly Val Ser Gly Ala Ala Phe Leu Gly Lys Met Asp Ser
    610                 615                 620
Gln Lys Phe Asp Ala Glu Val Ser Arg Lys Gly Val Val Gly Ser Val
625                 630                 635                 640
Tyr Thr Gly Phe Leu Ala Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser
                645                 650                 655
Leu Gly Glu Thr Gln Asn Asp Met Lys Thr Arg Tyr Gly Val Leu Gly
            660                 665                 670
Glu Ser Ser Ala Ser Trp Thr Ser Arg Gly Val Leu Ala Asp Ala Leu
        675                 680                 685
Val Glu Tyr Arg Ser Leu Val Gly Pro Val Arg Pro Thr Phe Tyr Ala
    690                 695                 700
Leu His Phe Asn Pro Tyr Val Glu Val Ser Tyr Ala Ser Met Lys Phe
```

705 710 715 720
Pro Gly Phe Thr Glu Gln Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala
725 730 735
Ser Leu Thr Asn Ile Thr Ile Pro Leu Gly Met Lys Phe Glu Leu Ala
740 745 750
Phe Ile Lys Gly Gln Phe Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr
755 760 765
Ala Trp Glu Ala Tyr Arg Lys Val Glu Gly Gly Ala Val Gln Leu Leu
770 775 780
Glu Ala Gly Phe Asp Trp Glu Gly Ala Pro Met Asp Leu Pro Arg Gln
785 790 795 800
Glu Leu Arg Val Ala Leu Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe
805 810 815
Ser Thr Val Leu Gly Leu Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr
820 825 830
Asp Ser Lys Leu Gly Tyr Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
835 840 845

<210> 193
<211> 778
<212> PRT
<213> Chlamydia

<400> 193
Met His His His His His His Gly Leu Ala Ser Cys Val Asp Leu His
1 5 10 15
Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val Gly Pro Gln Ala
20 25 30
Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val Gly Ser Lys Asp
35 40 45
Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly Asp Pro Ser Ser
50 55 60
Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys Val Glu Gln Ser
65 70 75 80
Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln Gly Val Asp Gln
85 90 95
Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser Phe Thr Ser Ser
100 105 110
Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu Gly Ile Ala Phe
115 120 125
Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr Asp Val Lys Ala
130 135 140
Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp Leu Ile Phe Glu
145 150 155 160
Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser Ser Leu Glu Gln
165 170 175
Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His Asp Cys Gln Gly
180 185 190
Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala Glu Gly Ser Ser
195 200 205
Ala Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe Phe Val Thr Gly
210 215 220
Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala Gly Asp Met Val
225 230 235 240
Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly Asn Ser Ala Asn
245 250 255
Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys Val Leu Phe Val
260 265 270
Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg Ala Leu Ser Gly
275 280 285
Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln Asn Cys Ala Glu

```
    290                 295                 300
Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu Asp Lys Gly Ser
305                 310                 315                 320
Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val Leu Leu Gln Gly
                325                 330                 335
Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala Ser Gln Gly Gly
            340                 345                 350
Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn Glu Gly Pro Val
        355                 360                 365
Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly Ala Ile Ala Ala
    370                 375                 380
Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly Ile Ser Phe Glu
385                 390                 395                 400
Gly Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys Gly Ser Phe Ser
                405                 410                 415
Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp Ile Ser Lys Asn
            420                 425                 430
Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr Thr Ser Asp Leu
        435                 440                 445
Gly Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe Gly Glu Asn Ile
    450                 455                 460
Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys Asp Asn Ile Val
465                 470                 475                 480
Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly Gly Ala Ile Leu
                485                 490                 495
Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly Gly Ile Ser Phe
            500                 505                 510
Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr Gln Glu Glu Phe
        515                 520                 525
Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser Ser Gly Tyr Ser
    530                 535                 540
Gly Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile Leu His Asn Ala
545                 550                 555                 560
Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser Glu Glu Glu Ala
                565                 570                 575
Thr Leu Leu Gly Cys Cys Gly Gly Gly Ala Val His Gly Met Asp Ser
            580                 585                 590
Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly Asn Asn Tyr Ala
        595                 600                 605
Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser Lys Thr Val Gln
    610                 615                 620
Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn Ile Ala Ser Leu
625                 630                 635                 640
Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys Glu Leu Val Asp
                645                 650                 655
Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg Val Tyr Gly Gly
            660                 665                 670
Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser Gly Asn Lys Gly
        675                 680                 685
Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu
    690                 695                 700
Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro Glu Gln Lys Asp
705                 710                 715                 720
Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln Ser Phe Ile Thr
                725                 730                 735
Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro
            740                 745                 750
Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala
        755                 760                 765
Gly Gly Ala Asp Ser Ser Arg Ser Gly Cys
    770                 775
```

<210> 194
<211> 948
<212> PRT
<213> Chlamydia

<400> 194
Met Ala Ser Met His His His His His His Val Lys Ile Glu Asn Phe
1 5 10 15
Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr
20 25 30
Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala
35 40 45
Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr
50 55 60
Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala
65 70 75 80
Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val
85 90 95
Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr
100 105 110
Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val
115 120 125
Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly
130 135 140
Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys
145 150 155 160
Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg
165 170 175
Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr
180 185 190
Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr
195 200 205
Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn
210 215 220
Leu Val Thr Pro Thr Leu Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr
225 230 235 240
Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile
245 250 255
Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile
260 265 270
Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr
275 280 285
Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val
290 295 300
Lys Leu Thr Met Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp
305 310 315 320
Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr
325 330 335
Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser
340 345 350
Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys
355 360 365
Ser Tyr Ile Pro Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu
370 375 380
Lys Pro Asn Thr Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly
385 390 395 400
Ser Ser Leu Val Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val
405 410 415
Ala Asp Gly Ala Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser
420 425 430

```
Val Glu Lys Asn Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu
        435                 440                 445
Leu Arg Ile Ile Asp Thr Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser
    450                 455                 460
Thr Asp Ser Glu Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn
465                 470                 475                 480
Asn Asn Asp Ala Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser
                485                 490                 495
Pro Ala Val Ala Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala
            500                 505                 510
Ala Ala Thr Ala Thr Pro Thr Thr Thr Pro Thr Ala Thr Thr Thr Thr
        515                 520                 525
Ser Asn Gln Val Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn
    530                 535                 540
Gly Thr Phe Phe Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser
545                 550                 555                 560
Leu Leu Val Leu Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile
                565                 570                 575
Val Leu Thr Gly Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu
            580                 585                 590
Thr Leu Asp Pro Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp
        595                 600                 605
Lys Phe Asp Ser Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His
    610                 615                 620
Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val
625                 630                 635                 640
Lys Gln Gly Leu Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu
                645                 650                 655
Val Ser Tyr Asn Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser
            660                 665                 670
Gln Val Gly Thr Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly
        675                 680                 685
Ala Ser Val Ala Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly
    690                 695                 700
Ala Ala Phe Ser Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu
705                 710                 715                 720
Asn Asn Tyr Thr His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val
                725                 730                 735
Tyr Gly Gly Lys Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys
            740                 745                 750
Ser Leu Pro Leu Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys
        755                 760                 765
His Asp Thr Val Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly
    770                 775                 780
Glu Trp Glu Asp Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val
785                 790                 795                 800
Leu Arg Thr Pro Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly
                805                 810                 815
Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu
            820                 825                 830
Tyr Asp Pro Arg Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile
        835                 840                 845
Pro Met Gly Leu Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu
    850                 855                 860
Met Tyr Asn Arg Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn
865                 870                 875                 880
Ser Pro Thr Cys Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Gly Glu
                885                 890                 895
Ile Ile Cys Gly Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser
            900                 905                 910
Thr Gln Leu Tyr Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr
```

```
        915                 920                 925
Ile Glu Ala Asp Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala
    930                 935                 940
Arg Met Thr Phe
945

<210> 195
<211> 821
<212> PRT
<213> Chlamydia

<400> 195
Met His His His His His His Glu Ala Ser Ser Ile Gln Asp Gln Ile
 1               5                  10                  15
Lys Asn Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln
            20                  25                  30
Ala Phe Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala
        35                  40                  45
Asp Ser Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg
    50                  55                  60
Lys His Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val
65                  70                  75                  80
Ser Ser Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala
                85                  90                  95
Pro Ser Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn
            100                 105                 110
Gly Gly Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln
        115                 120                 125
Asp Ser Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe
    130                 135                 140
Phe Gly Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn
145                 150                 155                 160
Gly Gly Ala Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys
                165                 170                 175
Ser Leu Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val
            180                 185                 190
Tyr Ala Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe
        195                 200                 205
Ser Ser Asn Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln
    210                 215                 220
Asp Met Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala
225                 230                 235                 240
Ala Gly Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val
                245                 250                 255
Leu Leu Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser
            260                 265                 270
Thr Pro Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser
        275                 280                 285
Ser Glu Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro
    290                 295                 300
Ser Pro Asp Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys
305                 310                 315                 320
Ser Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn
                325                 330                 335
Ile Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser
            340                 345                 350
Cys Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln
        355                 360                 365
His Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr
    370                 375                 380
Thr Ser Glu Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe
```

```
385                 390                 395                 400
Ser Glu Asn Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys
                405                 410                 415
Leu Ser Leu Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala
            420                 425                 430
Lys Glu Ser Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr
        435                 440                 445
Thr Asp Thr Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser
    450                 455                 460
Thr Pro Glu Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser
465                 470                 475                 480
Thr Ala Glu Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln
                485                 490                 495
Thr Asp Gln Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser
            500                 505                 510
Ile Glu Asn Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys
        515                 520                 525
Lys Gly Gly Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn
    530                 535                 540
Asn Leu Glu Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu
545                 550                 555                 560
Cys Leu Thr Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser
                565                 570                 575
His Tyr Asn Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr
            580                 585                 590
Val Thr Leu Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr
        595                 600                 605
Val Lys Ala Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro
    610                 615                 620
Pro Val Glu Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn
625                 630                 635                 640
Thr Glu Gly Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp
                645                 650                 655
Thr Ala Asp Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr
            660                 665                 670
Ser Asp Thr Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr
        675                 680                 685
Gln Ser Asn Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser
    690                 695                 700
Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr
705                 710                 715                 720
Asp Glu Ser Val Ser Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln
                725                 730                 735
Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile
            740                 745                 750
Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser
        755                 760                 765
Ser Pro Val Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp
    770                 775                 780
Asn Pro Asp Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly
785                 790                 795                 800
Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile
                805                 810                 815
Gly Gly Gly Ala Ile
            820
```

<210> 196
<211> 525
<212> PRT
<213> Chlamydia

<400> 196

```
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1               5                   10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val Pro Arg Gly Ser
    130                 135                 140
Pro Leu Pro Val Gly Asn Pro Ala Glu Pro Ser Leu Leu Ile Asp Gly
145                 150                 155                 160
Thr Met Trp Glu Gly Ala Ser Gly Asp Pro Cys Asp Pro Cys Ala Thr
                165                 170                 175
Trp Cys Asp Ala Ile Ser Ile Arg Ala Gly Tyr Tyr Gly Asp Tyr Val
            180                 185                 190
Phe Asp Arg Val Leu Lys Val Asp Val Asn Lys Thr Phe Ser Gly Met
        195                 200                 205
Ala Ala Thr Pro Thr Gln Ala Ile Gly Asn Ala Ser Asn Thr Asn Gln
    210                 215                 220
Pro Glu Ala Asn Gly Arg Pro Asn Ile Ala Tyr Gly Arg His Met Gln
225                 230                 235                 240
Asp Ala Glu Trp Phe Ser Asn Ala Ala Phe Leu Ala Leu Asn Ile Trp
                245                 250                 255
Asp Arg Phe Asp Ile Phe Cys Thr Leu Gly Ala Ser Asn Gly Tyr Phe
            260                 265                 270
Lys Ala Ser Ser Ala Ala Phe Asn Leu Val Gly Leu Ile Gly Phe Ser
        275                 280                 285
Ala Ala Ser Ser Ile Ser Thr Asp Leu Pro Met Gln Leu Pro Asn Val
    290                 295                 300
Gly Ile Thr Gln Gly Val Val Glu Phe Tyr Thr Asp Thr Ser Phe Ser
305                 310                 315                 320
Trp Ser Val Gly Ala Arg Gly Ala Leu Trp Glu Cys Gly Cys Ala Thr
                325                 330                 335
Leu Gly Ala Glu Phe Gln Tyr Ala Gln Ser Asn Pro Lys Ile Glu Met
            340                 345                 350
Leu Asn Val Thr Ser Ser Pro Ala Gln Phe Val Ile His Lys Pro Arg
        355                 360                 365
Gly Tyr Lys Gly Ala Ser Ser Asn Phe Pro Leu Pro Ile Thr Ala Gly
    370                 375                 380
Thr Thr Glu Ala Thr Asp Thr Lys Ser Ala Thr Ile Lys Tyr His Glu
385                 390                 395                 400
Trp Gln Val Gly Leu Ala Leu Ser Tyr Arg Leu Asn Met Leu Val Pro
                405                 410                 415
Tyr Ile Gly Val Asn Trp Ser Arg Ala Thr Phe Asp Ala Asp Thr Ile
            420                 425                 430
Arg Ile Ala Gln Pro Lys Leu Lys Ser Glu Ile Leu Asn Ile Thr Thr
        435                 440                 445
Trp Asn Pro Ser Leu Ile Gly Ser Thr Thr Ala Leu Pro Asn Asn Ser
    450                 455                 460
Gly Lys Asp Val Leu Ser Asp Val Leu Gln Ile Ala Ser Ile Gln Ile
465                 470                 475                 480
```

```
Asn Lys Met Lys Ser Arg Lys Ala Cys Gly Val Ala Val Gly Ala Thr
                485                 490                 495
Leu Ile Asp Ala Asp Lys Trp Ser Ile Thr Gly Glu Ala Arg Leu Ile
            500                 505                 510
Asn Glu Arg Ala Ala His Met Asn Ala Gln Phe Arg Phe
        515                 520                 525
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<210> 197
<211> 43
<212> DNA
<213> Chlamydia

<400> 197
gataggcgcg ccgcaatcat gaaatttatg tcagctactg ctg 43

<210> 198
<211> 34
<212> DNA
<213> Chlamydia

<400> 198
cagaacgcgt ttagaatgtc atacgagcac cgca 34

<210> 199
<211> 6
<212> DNA
<213> Chlamydia

<400> 199
gcaatc 6

<210> 200
<211> 34
<212> DNA
<213> Chlamydia

<400> 200
tgcaatcatg agttcgcaga aagatataaa aagc 34

<210> 201
<211> 38
<212> DNA
<213> Chlamydia

<400> 201
cagagctagc ttaaaagatc aatcgcaatc cagtattc 38

<210> 202
<211> 5
<212> DNA
<213> Chlamydia

<400> 202
caatc 5

<210> 203
<211> 31
<212> DNA
<213> Chlamydia

<400> 203

tgcaatcatg aaaaaagcgt ttttcttttt c 31

<210> 204
<211> 31
<212> DNA
<213> Chlamydia

<400> 204
cagaacgcgt ctagaatcgc agagcaattt c 31

<210> 205
<211> 30
<212> DNA
<213> Chlamydia

<400> 205
gtgcaatcat gattcctcaa ggaatttacg 30

<210> 206
<211> 31
<212> DNA
<213> Chlamydia

<400> 206
cagaacgcgt ttagaaccgg actttacttc c 31

<210> 207
<211> 50
<212> DNA
<213> Chlamydia

<400> 207
cagacatatg catcaccatc accatcacga ggcgagctcg atccaagatc 50

<210> 208
<211> 40
<212> DNA
<213> Chlamydia

<400> 208
cagaggtacc tcagatagca ctctctccta ttaaagtagg 40

<210> 209
<211> 55
<212> DNA
<213> Chlamydia

<400> 209
cagagctagc atgcatcacc atcaccatca cgttaagatt gagaacttct ctggc 55

<210> 210
<211> 35
<212> DNA
<213> Chlamydia

<400> 210
cagaggtacc ttagaatgtc atacgagcac cgcag 35

<210> 211
<211> 36
<212> DNA

<213> Chlamydia

<400> 211
cagacatatg catcaccatc accatcacgg gttagc 36

<210> 212
<211> 35
<212> DNA
<213> Chlamydia

<400> 212
cagaggtacc tcagctcctc cagcacactc tcttc 35

<210> 213
<211> 51
<212> DNA
<213> Chlamydia

<400> 213
cagagctagc catcaccatc accatcacgg tgctatttct tgcttacgtg g 51

<210> 214
<211> 38
<212> DNA
<213> Chlamydia

<400> 214
cagaggtact taaaagatca atcgcaatcc agtattcg 38

<210> 215
<211> 48
<212> DNA
<213> Chlamydia

<400> 215
cagaggatcc acatcaccat caccatcacg gactagctag agaggttc 48

<210> 216
<211> 31
<212> DNA
<213> Chlamydia

<400> 216
cagagaattc ctagaatcgc agagcaattt c 31

<210> 217
<211> 7
<212> DNA
<213> Chlamydia

<400> 217
tgcaatc 7

<210> 218
<211> 22
<212> PRT
<213> Chlamydia

<400> 218
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
1 5 10 15

Val Pro Ser Ser Asp Pro
20

<210> 219
<211> 51
<212> DNA
<213> Chlamydia

<400> 219
cagaggtacc gcatcaccat caccatcaca tgattcctca aggaatttac g 51

<210> 220
<211> 33
<212> DNA
<213> Chlamydia

<400> 220
cagagcggcc gcttagaacc ggactttact tcc 33

<210> 221
<211> 24
<212> PRT
<213> Chlamydia

<400> 221
Met Ala Ser Met Thr Gly Gly Gln Gln Asn Gly Arg Asp Ser Ser Leu
1 5 10 15
Val Pro His His His His His His
20

<210> 222
<211> 46
<212> DNA
<213> Chlamydia

<400> 222
cagagctagc catcaccatc accatcacct ctttggccag gatccc 46

<210> 223
<211> 30
<212> DNA
<213> Chlamydia

<400> 223
cagaactagt ctagaacctg taagtggtcc 30

<210> 224
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 224
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile
1 5 10 15
Ser Thr Asp Leu
20

<210> 225

<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 225
Lys Asn Ser Ala Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala
1 5 10 15
Val Ile Val Gly
20

<210> 226
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 226
His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly
1 5 10 15
Pro Met Pro Arg
20

<210> 227
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 227
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
1 5 10 15
Glu Ile Val Lys
20

<210> 228
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 228
Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys
1 5 10 15
Val Trp Glu Tyr
20

<210> 229
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 229
Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile
1 5 10 15
Lys Lys His Asn
20

<210> 230
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 230
Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
1 5 10 15
Pro Asp Ala Asn
20

<210> 231
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 231
Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn
1 5 10 15
Leu Ala Lys Val
20

<210> 232
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 232
Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe
1 5 10 15
Gly Ser Ser Asp
20

<210> 233
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 233
Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro
1 5 10 15

Ile Asp Met Phe
20

<210> 234
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 234
Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln
1 5 10 15
Met Thr Lys Ala
20

<210> 235
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 235
Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala Leu
1 5 10 15
Ser Lys His Ile Val Lys
20

<210> 236
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 236
Val Glu Ile Thr Gln Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro
1 5 10 15
Tyr Pro Val Glu
20

<210> 237
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 237
Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile
1 5 10 15
Thr Ala Thr Gly
20

<210> 238
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 238
Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile Thr Ala Thr Gly Lys
1 5 10 15
Arg Asp Cys Val
20

<210> 239
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 239
Pro Tyr Pro Val Glu Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp
1 5 10 15
Val Ile Ile Thr
20

<210> 240
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 240
Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
1 5 10 15
Gln Leu Pro Cys Glu
20

<210> 241
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 241
Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu
1 5 10 15
Ala Glu Phe Val
20

<210> 242
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 242
Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg
1 5 10 15
Ser Asp Pro Ala
20

<210> 243
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 243
Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala
1 5 10 15
Thr Thr Pro Thr
20

<210> 244
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 244
Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala
1 5 10 15
Asp Gly Lys Leu
20

<210> 245
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 245
Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val
1 5 10 15
Trp Lys Ile Asp
20

<210> 246
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 246
Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg
1 5 10 15
Leu Gly Gln Gly

20

<210> 247
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 247
Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu
1 5 10 15
Lys Ser Lys Ile
20

<210> 248
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 248
Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr
1 5 10 15
Val Trp Val Lys
20

<210> 249
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 249
Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro
1 5 10 15
Leu Lys Glu Gly
20

<210> 250
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 250
Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15
Cys Cys Phe Thr
20

<210> 251
<211> 16
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 251
Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15

<210> 252
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 252
Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10

<210> 253
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 253
Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
1 5 10 15

<210> 254
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 254
Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala
1 5 10 15
Phe Gly Val Leu
20

<210> 255
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 255
Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn
1 5 10 15
Pro Glu Gly Ser
20

<210> 256
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 256
Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
1 5 10 15
Ala Leu Arg Ala
20

<210> 257
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 257
Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr
1 5 10 15
Phe Leu Ile Asp
20

<210> 258
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 258
Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys
1 5 10 15
His Gly Val Ile
20

<210> 259
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 259
Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg
1 5 10 15
His Ala Val Ile
20

<210> 260
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 260
Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn
1 5 10 15
Asp Leu Pro Leu
20

<210> 261
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 261
Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly
1 5 10 15
Arg Ser Ile Asp
20

<210> 262
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 262
Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu
1 5 10 15
Glu Leu Arg Ile
20

<210> 263
<211> 897
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 604
<223> n = A,T,C or G

<400> 263
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggagt ggataagact 120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg 360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc 420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt 600
gcgnaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc 660
gaagtgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc 780

gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct 840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa 897

<210> 264
<211> 298
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 202
<223> Xaa = Any Amino Acid

<400> 264
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Val Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100 105 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180 185 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Xaa Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
210 215 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275 280 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290 295

<210> 265
<211> 897
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature

<222> 604
<223> n = A,T,C or G

<400> 265
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atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcgnaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
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<210> 266
<211> 298
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 202
<223> Xaa = Any Amino Acid

<400> 266
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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1               5                   10                  15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                 185                 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Xaa Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
```

```
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                 280                 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295
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<210> 267
<211> 680
<212> DNA
<213> Chlamydia

<400> 267
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tctatatcca tattgatagg aaaaaacgtc gcagaaagat tttagctatg acgtttatcc     60
gagctttagg atattcaaca gatgcagata ttattgaaga gttcttttct gtagaggagc    120
gttccttacg ttcagagaag gattttgtcg cgttagttgg taaagtttta gctgataacg    180
tagttgatgc ggattcttca ttagtttacg ggaaagctgg agagaagcta agtactgcta    240
tgctaaaacg catcttagat acgggagtcc aatctttgaa gattgctgtt ggcgcagatg    300
aaaatcaccc aattattaag atgctcgcaa aagatcctac ggattcttac gaagctgctc    360
ttaaagattt ttatcgcaga ttacgaccag gagagcctgc aactttagct aatgctcgat    420
ccacaattat gcgtttattc ttcgatgcta aacgttataa tttaggccgc gttggacgtt    480
ataaattaaa taaaaaatta ggcttcccat tagacgacga aacattatct caagtgactt    540
tgagaaaaga agatgttatc ggcgcgttga aatatttgat tcgtttgcga atgggcgatg    600
agaagacatc tatcgatgat attgaccatt tggcaaaccg acgagttcgc tctgttggag    660
aactaattca gaatcactgt                                                680
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<210> 268
<211> 359
<212> DNA
<213> Chlamydia

<400> 268
```
cttatgttct ggagaatgtt gcaacaacat attaatcgaa ccagctcctc ctagtaacat     60
agaaaccaag cccttttgag aaaaaacctg tacttcgcat cctttagcca tttgttgaat    120
agctcctaac aaagagctaa ttttttcctc ttccttgttt ttctgaggcg ctgtggactc    180
taaatatagc aagtgctctt ggaacacctc atcaacaatc gcttgtccta gattaggtat    240
agagactgtc tctccatcaa ttaaatggag tttcaaagta atatcccctt ccgtccctcc    300
atcacaagac tctatgaaag ctatctgatt ccatcgagca gaaatgtatg gggaaatac     359
```

<210> 269
<211> 124
<212> DNA
<213> Chlamydia

<400> 269
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gatcgaatca attgagggag ctcattaaca agaatagctg cagtttcttt gcgttcttct     60
ggaataacaa gaaataggta atcggtacca ttgatagaac gaacacgaca aatcgcagaa    120
ggtt                                                                 124
```

<210> 270
<211> 219
<212> DNA
<213> Chlamydia

<400> 270
```
gatcctgttg ggcctagtaa taatacgttg gatttcccat aactcacttg tttatcctgc     60
ataagagcac ggatacgctt atagtggtta tagacggcaa ccgaaatcgt ttttttcgcg    120
cgctcttgtc caatgacata agagtcgatg tggcgtttga tttctttagg ggttaacact    180
ctcagacttg ttggagagct tgtggaagat gttgcgatc                           219
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<210> 271
<211> 511
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 447
<223> n = A,T,C or G

<400> 271
ggatccgaat tcggcacgag gagaaaatat aggaggttcc akcatcggaa gatctaatag 60
acaaagaggt tttggcatag atggctcctc cttgtacgtt caacgatgat tgggagggat 120
tgttatcgat agcttggttc ccagagaact gacaagtccc gctacattga gagaatgtaa 180
cctgttctcc atagatagct cctcctacta cacctgaata agttggtgtt gctggagatg 240
atggtgcggc tgctgcggct gcttgtaggg aagcagcagc tgcagcaggt gctgaagctg 300
ttgttgcgac tcctgtggat gaggagtttg ctttgttgtt cgagaaagag aagcctgatt 360
tcagattaga aatatttaca gttttagcat gtaagcctcc accttctttc ccaacaaggt 420
tctctgttac agataaggag actagangca tctagtttta aagatttttt acagcagata 480
cctccaccta tctctgtagc ggagttctca g 511

<210> 272
<211> 598
<212> DNA
<213> Chlamydia

<400> 272
ctcttcctct cctcaatcta gttctggagc aactacagtc tccgactcag gagactctag 60
ctctggctca aactcggata cctcaaaaac agttccagtc acagctaaag gcggtgggct 120
ttatactgat aagaatcttt cgattactaa catcacagga attatcgaaa ttgcaaataa 180
caaagcgaca gatgttggag gtggtgctta cgtaaaagga acccttactt gtaaaaactc 240
tcaccgtcta caatttttga aaaactcttc cgataaacaa ggtggaggaa tctacggaga 300
agacaacatc accctatcta atttgacagg gaagactcta ttccaagaga atactgccaa 360
aaaagagggc ggtggactct tcataaaagg tacagataaa gctcttacaa tgacaggact 420
ggatagtttc tgtttaatta ataacacatc agaaaaacat ggtggtggga gcctttgtta 480
ccaaagaaat ctctcagact tacacctctt gatgtggaaa caattccagg aatcacgcct 540
gtacatggtg aaacagtcat tactggcaat aaatctacag gaggtaatgg tggagggc 598

<210> 273
<211> 126
<212> DNA
<213> Chlamydia

<400> 273
ggatccgaat tcggcacgag atgagcctta tagtttaaca aaagcttctc acattccttc 60
gatagctttt tattagccgt ttttagcatc ctaatgagat ctcctcgttc gtaacaaata 120
cgagag 126

<210> 274
<211> 264
<212> DNA
<213> Chlamydia

<400> 274
ggatccgaat tcggcacgag ctcttttaaa tcttaattac aaaaagacaa attaattcaa 60
tttttcaaaa aagaatttaa acattaattg ttgtaaaaaa acaatattta ttctaaaata 120
ataaccatag ttacgggga atctctttca tggtttattt tagagctcat caacctaggc 180
atacgcctaa aacatttcct ttgaaagttc accattcgtt ctccgataag catcctcaaa 240
ttgctaaagc tatgtggatt acgg 264

<210> 275
<211> 359
<212> DNA
<213> Chlamydia

<400> 275
ggatccgaat tcggcacgag ataaaacctg aaccacaaca aagatctaaa acttcttgat 60
tttcagctgc aaattctttt agataaatat caaccatttc ttcagtttca tatcttggaa 120
ttaaaacttg ttctcttaaa ttaattctag tatttaagta ttcaacatag cccattatta 180
attgaattgg ataattttgc cttaataatt cacattcttt ttcagtaatt ttaggttcta 240
aaccgtaccg cttttttttct aaaattaatg tttcttcatt attcatttta taagccactt 300
tcctttattt tttgattttg ttcttctgtt agtaatgctt caataatagt taataatttt 359

<210> 276
<211> 357
<212> DNA
<213> Chlamydia

<400> 276
aaaacaattg atataatttt ttttttcata acttccagac tcctttctag aaaagtcttt 60
atgggtagta gtgactctaa cgtttttttat tattaagacg atccccggag atccttttaa 120
tgatgaaaac ggaaacatcc tttcgccaga aactttagca ctattaaaga atcgttacgg 180
gttagataag cctttattca cccagtatct tatctatttg aaatgtctgc taacactaga 240
tttcggggaa tctcttatct acaaagatcg aaatctcagc attattgctg ccgctcttcc 300
atcttccgct attcttggac ttgaaagctt gtgtttactc gtgccgaatt cggatcc 357

<210> 277
<211> 505
<212> DNA
<213> Chlamydia

<400> 277
ggatccgaat tcggcacgag ctcgtgccga ttgcttgctt cagtcacccc atcggtatag 60
agcactaaaa gagactcctc ttcaagaacg agagtgtaag cagggtgagg aggaacttca 120
ggtaaaaatc ctaaggccat accaggatgc gacaggaaag agatatctcc attaggagct 180
cggagacacg ctgggttgtg gccacaagaa tagtattcta gttctcgtgt tgcgtaatga 240
taacaataaa tgcatagtgt tacaaacatc ccagattcag ctgtctgttg atagaagaga 300
gcagctgttt gttgaacggc ttcttgaata gaggagagct cactcaaaaa ggtatgtaac 360
atgtttttca ggaataagga gtaggcgcac gcattgactc ctttcccgga agcatcagca 420
acgattagaa agagtttagc ttggggacct tcgcctataa caaagatatc aaagaaatct 480
cctcctaccg taactgcagg aatat 505

<210> 278
<211> 407
<212> DNA
<213> Chlamydia

<400> 278
ggatccgaat tcggcacgag aactactgag caaattgggt atccaacttc ctctttacga 60
aagaaaaaca gaaggcattc tccataccaa gatttgttgc atcgacaata aaactccaat 120
ctttggctct gctaactgga gcggtgctgg tatgattaaa aactttgaag acctattcat 180
ccttcgccca attacagaga cacagcttca ggcctttatg gacgtctggt ctcttctaga 240
aacaaatagc tcctatctgt ccccagagag cgtgcttacg gcccctactc cttcaagtag 300
acctactcaa caagatacag attctgatga cgaacaaccg agtaccagcc agcaagctat 360
ccgtatgaga aaataggatt agggaaacaa aacgacagca aaccaca 407

<210> 279
<211> 351
<212> DNA
<213> Chlamydia

<400> 279
ctcgtgccgc ttacaggagg cttgtatcct ttaaaataga gtttttctta tgaccccatg 60
tggcgatagg ccgggtctag cgccgatagt agaaatatcg gttggttttt gtccttgagg 120
ggatcgtata ctttttcaaa gtatggtccc cgtatcgatt atctggaggc tcttatgtct 180
tttttcata ctagaaaata taagcttatc ctcagaggac tcttgtgttt agcaggctgt 240
ttcttaatga acagctgttc ctctagtcga ggaaatcaac ccgctgatga gagcatctat 300
gtcttgtcta tgaatcgcat gatttgtgat tctcgtgccg aattcggatc c 351

<210> 280
<211> 522
<212> DNA
<213> Chlamydia

<400> 280
ggatccgaat tcggcacgag cagaggaaaa aggcgatact cctcttgaag atcgtttcac 60
agaagatctt tccgaagtct ctggagaaga ttttcgagga ttgaaaaatt cgttcgatga 120
tgattcttct tctgacgaaa ttctcgatgc gctcacaagt aaattttctg atcccacaat 180
aaaggatcta gctcttgatt atctaattca aatagctccc tctgatggga aacttaagtc 240
cgctctcatt caggcaaagc atcaactgat gagccagaat cctcaggcga ttgttggagg 300
acgcaatgtt ctgttagctt cagaaacctt tgcttccaga gcaaatacat ctccttcatc 360
gcttcgctcc ttatatttcc aagtaacctc atccccctct aattgcgcta atttacatca 420
aatgcttgct tcttactcgc catcagagaa aaccgctgtt atggagtttc tagtgaatgg 480
catggtagca gatttaaaat cggagggccc ttccattcct cc 522

<210> 281
<211> 577
<212> DNA
<213> Chlamydia

<400> 281
ggatccgaat tcggcacgag atgcttctat tacaattggt ttggatgcgg aaaaagctta 60
ccagcttatt ctagaaaagt tgggagatca aattcttggt ggaattgctg atactattgt 120
tgatagtaca gtccaagata ttttagacaa aatcacaaca gacccttctc taggtttgtt 180
gaaagctttt aacaactttc caatcactaa taaaattcaa tgcaacgggt tattcactcc 240
caggaacatt gaaactttat taggaggaac tgaaatagga aaattcacag tcacacccaa 300
aagctctggg agcatgttct tagtctcagc agatattatt gcatcaagaa tggaaggcgg 360
cgttgttcta gctttggtac gagaaggtga ttctaagccc tacgcgatta gttatggata 420
ctcatcaggc gttcctaatt tatgtagtct aagaaccaga attattaata caggattgac 480
tccgacaacg tattcattac gtgtaggcgg tttagaaagc ggtgtggtat gggttaatgc 540
cctttctaat ggcaatgata ttttaggaat aacaaat 577

<210> 282
<211> 607
<212> DNA
<213> Chlamydia

<400> 282
actmatcttc cccgggctcg agtgcggccg caagcttgtc gacggagctc gatacaaaaa 60
tgtgtgcgtg tgaaccgctt cttcaaaagc ttgtcttaaa agatattgtc tcgcttccgg 120
attagttaca tgtttaaaaa ttgctagaac aatattattc ccaaccaagc tctctgcggt 180
gctgaaaaaa cctaaattca aaagaatgac tcgccgctca tcttcagaaa gacgatccga 240
cttccataat tcgatgtctt tccccatggg gatctctgta gggagccagt tatttgcgca 300
gccattcaaa taatgttccc aagcccattt gtacttaata ggaacaagtt ggttgacatc 360
gacctggttg cagttcacta gacgcttgct atttagatta acgcgtttct gttttccatc 420
taaaatatct gcttgcataa gaaccgttaa ttttattgtt aatttatatg attaattact 480
gacatgcttc acacccttct tccaaagaac agacaggtgc tttcttcgct ctttcaacaa 540
taattcctgc cgaagcagac ttattcttca tccaacgagg ctgaattcct ctcttattaa 600
tatctac 607

<210> 283
<211> 1077

<212> DNA
<213> Chlamydia

<400> 283
ggatccgaat tcggcacgag aagttaacga tgacgatttg ttcctttggt agagaaggag 60
caatcgaaac taaatgtgcg agagcatgtg aagactccaa tgcaggaata atcccctcat 120
ttctagtaag caggaaaaaa gctcgtaacg cctcttcatc ggtggctaat gtataaaagg 180
ctcgtcctga ctcatgcatt tcggcatgat ctggcccaac tgaaggataa tctaatccag 240
cggaaatgga gtgagtttgt aatacttgtc catcgtcatc ttgaagaaga tacgaataaa 300
atccgtggaa tactccaggt cgccctgttg caaaacgtgc tgcatgtttt cctgaagaaa 360
tgcccagtcc tccccccttcc actccaatta attggacttt tggattcggg ataaaatgat 420
ggaaaaatcc aatagcgttg gagccacctc cgatacatgc aatcagaata tcaggatctc 480
ttcctgcaac tgcatggatt tgctctttca cttcagcgct tataacagac tgaaaaaatc 540
gaacgatatc gggataaggt aaaggtccta aggccgatcc taagcaatag tgagtaaatg 600
agtgtgttgt tgcccaatct tgtagagctt gattaactgc atctttgagt ccacaagatc 660
cttttgttac agaaacgact tcagcaccta aaaagcgcat tttctctaca tttggtttct 720
gtcgttccac atcttttgct cccatgtata ctacacaatc taatcctaga taagcacacg 780
ctgttgctgt tgctactcca tgttgtcccg cacctgtttc agctacaaca cgtgttttcc 840
caagatattt agcaagcaaa cactgaccaa gagcattatt cagtttatgt gctcctgtat 900
gcaaaagatc ttcgcgttta agaaatactc tagggccatc aatagctcga gcaaaattct 960
taacttcagt cagaggagtt tgtctccccg catagttttt caaaatacaa tctagttcag 1020
ataaaaaact ttgctgagtt ttgagaatct cccattccgc ttttagattc tgtatag 1077

<210> 284
<211> 407
<212> DNA
<213> Chlamydia

<400> 284
ggatccgaat tcggcacgag aactactgag caaattgggt atccaacttc ctctttacga 60
aagaaaaaca gaaggcattc tccataccaa gatttgttgc atcgacaata aaactccaat 120
ctttggctct gctaactgga gcggtgctgg tatgattaaa aactttgaag acctattcat 180
ccttcgccca attacagaga cacagcttca ggcctttatg gacgtctggt ctcttctaga 240
aacaaatagc tcctatctgt ccccagagag cgtgcttacg gcccctactc cttcaagtag 300
acctactcaa caagatacag attctgatga cgaacaaccg agtaccagcc agcaagctat 360
ccgtatgaga aaataggatt agggaaacaa aacgacagca aaccaca 407

<210> 285
<211> 802
<212> DNA
<213> Chlamydia

<400> 285
ggatccgaat tcggcacgag ttagcttaat gtctttgtca tctctaccta catttgcagc 60
taattctaca ggcacaattg gaatcgttaa tttacgtcgc tgcctagaag agtctgctct 120
tgggaaaaaa gaatctgctg aattcgaaaa gatgaaaaac caattctcta acagcatggg 180
gaagatggag gaagaactgt cttctatcta ttccaagctc caagacgacg attacatgga 240
aggtctatcc gagaccgcag ctgccgaatt aagaaaaaaa ttcgaagatc tatctgcaga 300
atacaacaca gctcaagggc agtattacca aatattaaac caaagtaatc tcaagcgcat 360
gcaaaagatt atggaagaag tgaaaaaagc ttctgaaact gtgcgtattc aagaaggctt 420
gtcagtcctt cttaacgaag atattgtctt atctatcgat agttcggcag ataaaaccga 480
tgctgttatt aaagttcttg atgattcttt tcaaaataat taacatgcga agctagccga 540
ggagtgccgt atgtctcaat ccacttattc tcttgaacaa ttagctgatt ttttgaaagt 600
cgagtttcaa ggaaatggag ctactcttct ttccggagtt gaagagatcg aggaagcaaa 660
aacggcacac atcacattct tagataatga aaaatatgct aaacatttaa aatcatcgga 720
agctggcgct atcatcatat ctcgaacaca gtttcaaaaa tatcgagact tgaataaaaa 780
ctttcttatc acttctgagt ct 802

<210> 286
<211> 588
<212> DNA

<213> Chlamydia

<400> 286
ggatccgaat tcggcacgag gcaatattta ctcccaacat tacggttcca aataagcgat 60
aaggtcttct aataaggaag ttaatgtaag aggcttttt attgcttttc gtaaggtagt 120
attgcaaccg cacgcgattg aatgatacgc aagccatttc catcatggaa aagaaccctt 180
ggacaaaaat acaaaggagg ttcactccta accagaaaaa gggagagtta gtttccatgg 240
gttttcctta tatacacccg tttcacacaa ttaggagccg cgtctagtat ttggaataca 300
aattgtcccc aagcgaattt tgttcctgtt tcagggattt ctcctaattg ttctgtcagc 360
catccgccta tggtaacgca attagctgta gtaggaagat caactccaaa caggtcatag 420
aaatcagaaa gctcataggt gcctgcagca ataacaacat tcttgtctga gtgagcgaat 480
tgtttaaaag atgggcgatt atgagctacc tcatcagaga ctattttaaa tagatcattt 540
tgggtaatca atccttctat agacccatat tcatcaatga taatctcg 588

<210> 287
<211> 489
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 488
<223> n = A,T,C or G

<400> 287
agtgcctatt gttttgcagg ctttgtctga tgatagcgat accgtacgtg agattgctgt 60
acaagtagct gttatgtatg gttctagttg cttactgcgc gccgtgggcg atttagcgaa 120
aaatgattct tctattcaag tacgcatcac tgcttatcgt gctgcagccg tgttggagat 180
acaagatctt gtgcctcatt tacgagttgt agtccaaaat acacaattag atggaacgga 240
aagaagagaa gcttggagat ctttatgtgt tcttactcgg cctcatagtg gtgtattaac 300
tggcatagat caagctttaa tgacctgtga gatgttaaag gaatatcctg aaaagtgtac 360
ggaagaacag attcgtacat tattggctgc agatcatcca gaagtgcagg tagctacttt 420
acagatcatt ctgagaggag gtagagtatt ccggtcatct tctataatgg aatcggttct 480
cgtgccgnt 489

<210> 288
<211> 191
<212> DNA
<213> Chlamydia

<400> 288
ggatccgaat tcaggatatg ctgttgggtt atcaataaaa agggttttgc catttttaa 60
gacgactttg tagataacgc taggagctgt agcaataata tcgagatcaa attctctaga 120
gattctctca aagatgattt ctaagtgcag cagtcctaaa aatccacagc ggaacccaaa 180
tccgagagag t 191

<210> 289
<211> 515
<212> DNA
<213> Chlamydia

<400> 289
ggatccgaat tcggcacgag gagcgacgtg aaatagtgga atcttcccgt attcttatta 60
cttctgcgtt gccttacgca aatggtcctt tgcattttgg acatattacc ggtgcttatt 120
tgcctgcaga tgtttatgcg cgttttcaga gactacaagg caaagaggtt ttgtatattt 180
gtggttctga tgaatacgga atcgcaatta cccttaatgc agagttggca ggcatggggt 240
atcaagaata tgtcgacatg tatcataagc ttcataaaga taccttcaag aaattgggaa 300
tttctgtaga tttcttttcc agaactacga acgcttatca tcctgctatt gtgcaagatt 360
tctatcgaaa cttgcaggaa cgcggactgg tagagaatca ggtgaccgaa cagctgtatt 420
ctgaggaaga agggaagttt ttagcggacc gttatgttgt aggtacttgt cccaagtgtg 480
ggtttgatcg agctcgagga gatgagtgtc agcag 515

<210> 290
<211> 522
<212> DNA
<213> Chlamydia

<400> 290
ggatccgaat tcggcacgag ggaggaatgg aagggccctc cgattktama tctgctacca 60
tgccattcac tagaaactcc ataacagcgg ttttctctga tggcgagtaa gaagcaagca 120
tttgatgtaa attagcgcaa ttagaggggg atgaggttac ttggaaatat aaggagcgaa 180
gcgatgaagg agatgtattt gctctggaag caaaggtttc tgaagctaac agaacattgc 240
gtcctccaac aatcgcctga ggattctggc tcatcagttg atgctttgcc tgaatgagag 300
cggacttaag tttcccatca gagggagcta tttgaattag ataatcaaga gctagatcct 360
ttattgtggg atcagaaaat ttacttgtga gcgcatcgag aatttcgtca gaagaagaat 420
catcatcgaa cgaatttttc aatcctcgaa aatcttctcc agagacttcg gaaagatctt 480
ctgtgaaacg atcttcaaga ggagtatcgc ctttttccyc tg 522

<210> 291
<211> 1002
<212> DNA
<213> Chlamydia

<400> 291
atggcgacta acgcaattag atcggcagga agtgcagcaa gtaagatgct gctgccagtt 60
gccaaagaac cagcggctgt cagctccttt gctcagaaag ggatttattg tattcaacaa 120
ttttttacaa accctgggaa taagttagca aagtttgtag ggcaacaaa aagtttagat 180
aaatgcttta agctaagtaa ggcggtttct gactgtgtcg taggatcgct ggaagaggcg 240
ggatgcacag ggacgcatt gacctccgcg agaaacgccc agggtatgtt aaaaacaact 300
cgagaagttg ttgccttagc taatgtgctc aatggagctg ttccatctat cgttaactcg 360
actcagaggt gttaccaata cacacgtcaa gccttcgagt taggaagcaa gacaaaagaa 420
agaaaaacgc ctggggagta tagtaaaatg ctattaactc gaggtgatta cctattggca 480
gcttccaggg aagcttgtac ggcagtcggt gcaacgactt actcagcgac attcggtgtt 540
ttacgtccgt taatgttaat caataaactc acagcaaaac cattcttaga caaagcgact 600
gtaggcaatt ttggcacggc tgttgctgga attatgacca ttaatcatat ggcaggagtt 660
gctggtgctg ttggcggaat cgcattagaa caaaagctgt tcaaacgtgc gaaggaatcc 720
ctatacaatg agagatgtgc cttagaaaac caacaatctc agttgagtgg ggacgtgatt 780
ctaagcgcgg aaagggcatt acgtaaagaa cacgttgcta ctctaaaaag aaatgtttta 840
actcttcttg aaaaagcttt agagttggta gtggatggag tcaaactcat tcctttaccg 900
attacagtgg cttgctccgc tgcaatttct ggagccttga cggcagcatc cgcaggaatt 960
ggcttatata gcatatggca gaaaacaaag tctggcaaat aa 1002

<210> 292
<211> 333
<212> PRT
<213> Chlamydia

<400> 292
Met Ala Thr Asn Ala Ile Arg Ser Ala Gly Ser Ala Ala Ser Lys Met
1 5 10 15
Leu Leu Pro Val Ala Lys Glu Pro Ala Ala Val Ser Ser Phe Ala Gln
20 25 30
Lys Gly Ile Tyr Cys Ile Gln Gln Phe Phe Thr Asn Pro Gly Asn Lys
35 40 45
Leu Ala Lys Phe Val Gly Ala Thr Lys Ser Leu Asp Lys Cys Phe Lys
50 55 60
Leu Ser Lys Ala Val Ser Asp Cys Val Val Gly Ser Leu Glu Glu Ala
65 70 75 80
Gly Cys Thr Gly Asp Ala Leu Thr Ser Ala Arg Asn Ala Gln Gly Met
85 90 95
Leu Lys Thr Thr Arg Glu Val Val Ala Leu Ala Asn Val Leu Asn Gly
100 105 110

```
Ala Val Pro Ser Ile Val Asn Ser Thr Gln Arg Cys Tyr Gln Tyr Thr
        115                 120                 125
Arg Gln Ala Phe Glu Leu Gly Ser Lys Thr Lys Glu Arg Lys Thr Pro
    130                 135                 140
Gly Glu Tyr Ser Lys Met Leu Leu Thr Arg Gly Asp Tyr Leu Leu Ala
145                 150                 155                 160
Ala Ser Arg Glu Ala Cys Thr Ala Val Gly Ala Thr Thr Tyr Ser Ala
                165                 170                 175
Thr Phe Gly Val Leu Arg Pro Leu Met Leu Ile Asn Lys Leu Thr Ala
            180                 185                 190
Lys Pro Phe Leu Asp Lys Ala Thr Val Gly Asn Phe Gly Thr Ala Val
        195                 200                 205
Ala Gly Ile Met Thr Ile Asn His Met Ala Gly Val Ala Gly Ala Val
    210                 215                 220
Gly Gly Ile Ala Leu Glu Gln Lys Leu Phe Lys Arg Ala Lys Glu Ser
225                 230                 235                 240
Leu Tyr Asn Glu Arg Cys Ala Leu Glu Asn Gln Gln Ser Gln Leu Ser
                245                 250                 255
Gly Asp Val Ile Leu Ser Ala Glu Arg Ala Leu Arg Lys Glu His Val
            260                 265                 270
Ala Thr Leu Lys Arg Asn Val Leu Thr Leu Leu Glu Lys Ala Leu Glu
        275                 280                 285
Leu Val Val Asp Gly Val Lys Leu Ile Pro Leu Pro Ile Thr Val Ala
    290                 295                 300
Cys Ser Ala Ala Ile Ser Gly Ala Leu Thr Ala Ala Ser Ala Gly Ile
305                 310                 315                 320
Gly Leu Tyr Ser Ile Trp Gln Lys Thr Lys Ser Gly Lys
                325                 330
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<210> 293
<211> 7
<212> DNA
<213> Chlamydia

<400> 293
tgcaatc

<210> 294
<211> 196
<212> PRT
<213> Chlamydia

<400> 294

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Thr Met Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys
                5                   10                  15

Ala Val Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg
            20                  25                  30

Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val
        35                  40                  45

Cys Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu
    50                  55                  60

Glu His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr
65                  70                  75                  80

His Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly
                85                  90                  95
```

```
Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala
            100                 105                 110

Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe
        115                 120                 125

Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu
    130                 135                 140

Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu
145                 150                 155                 160

Ile Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser
                165                 170                 175

Gly Glu Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe
            180                 185                 190

Gln Thr Met Asp
        195


<210> 295
<211> 181
<212> PRT
<213> Chlamydia

<400> 295
Lys Gly Gly Lys Met Ser Thr Thr Ile Ser Gly Asp Ala Ser Ser Leu
                  5                  10                  15

Pro Leu Pro Thr Ala Ser Cys Val Glu Thr Lys Ser Thr Ser Ser Ser
             20                  25                  30

Thr Lys Gly Asn Thr Cys Ser Lys Ile Leu Asp Ile Ala Leu Ala Ile
         35                  40                  45

Val Gly Ala Leu Val Val Val Ala Gly Val Leu Ala Leu Val Leu Cys
     50                  55                  60

Ala Ser Asn Val Ile Phe Thr Val Ile Gly Ile Pro Ala Leu Ile Ile
 65                  70                  75                  80

Gly Ser Ala Cys Val Gly Ala Gly Ile Ser Arg Leu Met Tyr Arg Ser
                 85                  90                  95

Ser Tyr Ala Ser Leu Glu Ala Lys Asn Val Leu Ala Glu Gln Arg Leu
            100                 105                 110

Arg Asn Leu Ser Glu Glu Lys Asp Ala Leu Ala Ser Val Ser Phe Ile
        115                 120                 125

Asn Lys Met Phe Leu Arg Gly Leu Thr Asp Asp Leu Gln Ala Leu Glu
    130                 135                 140

Ala Lys Val Met Glu Phe Glu Ile Asp Cys Leu Asp Arg Leu Glu Lys
145                 150                 155                 160

Asn Glu Gln Ala Leu Leu Ser Asp Val Arg Leu Val Leu Ser Ser Tyr
                165                 170                 175
```

Thr Arg Trp Leu Asp
180

<210> 296
<211> 124
<212> PRT
<213> Chlamydia

<400> 296
Ile Tyr Glu Val Met Asn Met Asp Leu Glu Thr Arg Arg Ser Phe Ala
5 10 15

Val Gln Gln Gly His Tyr Gln Asp Pro Arg Ala Ser Asp Tyr Asp Leu
20 25 30

Pro Arg Ala Ser Asp Tyr Asp Leu Pro Arg Ser Pro Tyr Pro Thr Pro
35 40 45

Pro Leu Pro Ser Arg Tyr Gln Leu Gln Asn Met Asp Val Glu Ala Gly
50 55 60

Phe Arg Glu Ala Val Tyr Ala Ser Phe Val Ala Gly Met Tyr Asn Tyr
65 70 75 80

Val Val Thr Gln Pro Gln Glu Arg Ile Pro Asn Ser Gln Gln Val Glu
85 90 95

Gly Ile Leu Arg Asp Met Leu Thr Asn Gly Ser Gln Thr Phe Ser Asn
100 105 110

Leu Met Gln Arg Trp Asp Arg Glu Val Asp Arg Glu
115 120

<210> 297
<211> 488
<212> PRT
<213> Chlamydia

<400> 297
Lys Gly Ser Leu Pro Ile Leu Gly Pro Phe Leu Asn Gly Lys Met Gly
5 10 15

Phe Trp Arg Thr Ser Ile Met Lys Met Asn Arg Ile Trp Leu Leu Leu
20 25 30

Leu Thr Phe Ser Ser Ala Ile His Ser Pro Val Arg Gly Glu Ser Leu
35 40 45

Val Cys Lys Asn Ala Leu Gln Asp Leu Ser Phe Leu Glu His Leu Leu
50 55 60

Gln Val Lys Tyr Ala Pro Lys Thr Trp Lys Glu Gln Tyr Leu Gly Trp
65 70 75 80

Asp Leu Val Gln Ser Ser Val Ser Ala Gln Gln Lys Leu Arg Thr Gln
85 90 95

Glu Asn Pro Ser Thr Ser Phe Cys Gln Gln Val Leu Ala Asp Phe Ile
100 105 110

Gly Gly Leu Asn Asp Phe His Ala Gly Val Thr Phe Phe Ala Ile Glu
115 120 125

Ser Ala Tyr Leu Pro Tyr Thr Val Gln Lys Ser Ser Asp Gly Arg Phe
130 135 140

Tyr Phe Val Asp Ile Met Thr Phe Ser Ser Glu Ile Arg Val Gly Asp
145 150 155 160

Glu Leu Leu Glu Val Asp Gly Ala Pro Val Gln Asp Val Leu Ala Thr
165 170 175

Leu Tyr Gly Ser Asn His Lys Gly Thr Ala Ala Glu Glu Ser Ala Ala
180 185 190

Leu Arg Thr Leu Phe Ser Arg Met Ala Ser Leu Gly His Lys Val Pro
195 200 205

Ser Gly Arg Thr Thr Leu Lys Ile Arg Arg Pro Phe Gly Thr Thr Arg
210 215 220

Glu Val Arg Val Lys Trp Arg Tyr Val Pro Glu Gly Val Gly Asp Leu
225 230 235 240

Ala Thr Ile Ala Pro Ser Ile Arg Ala Pro Gln Leu Gln Lys Ser Met
245 250 255

Arg Ser Phe Phe Pro Lys Lys Asp Asp Ala Phe His Arg Ser Ser Ser
260 265 270

Leu Phe Tyr Ser Pro Met Val Pro His Phe Trp Ala Glu Leu Arg Asn
275 280 285

His Tyr Ala Thr Ser Gly Leu Lys Ser Gly Tyr Asn Ile Gly Ser Thr
290 295 300

Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser Glu Gly
305 310 315 320

Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly Lys Ser
325 330 335

His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln Asp Met
340 345 350

Glu Asp Phe Asp Pro Ser Gly Pro Pro Pro Trp Glu Glu Phe Ala Lys
355 360 365

Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile Asp Gln
370 375 380

Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu Leu Ser
385 390 395 400

Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met Ile Leu
405 410 415

Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu Leu Glu
420 425 430

Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp Asn Met
435 440 445

Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys Ser Phe
450 455 460

Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu Leu Ser
465 470 475 480

Thr Pro Ile Pro Leu Phe Gly Phe
485

<210> 298
<211> 140
<212> PRT
<213> Chlamydia

<400> 298
Arg Ile Asp Ile Ser Ser Val Thr Phe Phe Ile Gly Ile Leu Leu Ala
5 10 15

Val Asn Ala Leu Thr Tyr Ser His Val Leu Arg Asp Leu Ser Val Ser
20 25 30

Met Asp Ala Leu Phe Ser Arg Asn Thr Leu Ala Val Leu Leu Gly Leu
35 40 45

Val Ser Ser Val Leu Asp Asn Val Pro Leu Val Ala Ala Thr Ile Gly
50 55 60

Met Tyr Asp Leu Pro Met Asn Asp Pro Leu Trp Lys Leu Ile Ala Tyr
65 70 75 80

Thr Ala Gly Thr Gly Gly Ser Ile Leu Ile Ile Gly Ser Ala Ala Gly
85 90 95

Val Ala Tyr Met Gly Met Glu Lys Val Ser Phe Gly Trp Tyr Val Lys
100 105 110

His Ala Ser Trp Ile Ala Leu Ala Ser Tyr Phe Gly Gly Leu Ala Val
115 120 125

Tyr Phe Leu Met Glu Asn Cys Val Asn Leu Phe Val
130 135 140

<210> 299
<211> 361
<212> PRT
<213> Chlamydia

<400> 299
His Gln Glu Ile Ala Asp Ser Pro Leu Val Lys Lys Ala Glu Glu Gln
5 10 15

Ile Asn Gln Ala Gln Gln Asp Ile Gln Thr Ile Thr Pro Ser Gly Leu
20 25 30

Asp Ile Pro Ile Val Gly Pro Ser Gly Ser Ala Ala Ser Ala Gly Ser
35 40 45

```
Ala Ala Gly Ala Leu Lys Ser Ser Asn Asn Ser Gly Arg Ile Ser Leu
    50                  55                  60

Leu Leu Asp Asp Val Asp Asn Glu Met Ala Ala Ile Ala Met Gln Gly
65                  70                  75                  80

Phe Arg Ser Met Ile Glu Gln Phe Asn Val Asn Asn Pro Ala Thr Ala
                85                  90                  95

Lys Glu Leu Gln Ala Met Glu Ala Gln Leu Thr Ala Met Ser Asp Gln
            100                 105                 110

Leu Val Gly Ala Asp Gly Glu Leu Pro Ala Glu Ile Gln Ala Ile Lys
        115                 120                 125

Asp Ala Leu Ala Gln Ala Leu Lys Gln Pro Ser Ala Asp Gly Leu Ala
    130                 135                 140

Thr Ala Met Gly Gln Val Ala Phe Ala Ala Ala Lys Val Gly Gly Gly
145                 150                 155                 160

Ser Ala Gly Thr Ala Gly Thr Val Gln Met Asn Val Lys Gln Leu Tyr
                165                 170                 175

Lys Thr Ala Phe Ser Ser Thr Ser Ser Ser Ser Tyr Ala Ala Ala Leu
            180                 185                 190

Ser Asp Gly Tyr Ser Ala Tyr Lys Thr Leu Asn Ser Leu Tyr Ser Glu
        195                 200                 205

Ser Arg Ser Gly Val Gln Ser Ala Ile Ser Gln Thr Ala Asn Pro Ala
    210                 215                 220

Leu Ser Arg Ser Val Ser Arg Ser Gly Ile Glu Ser Gln Gly Arg Ser
225                 230                 235                 240

Ala Asp Ala Ser Gln Arg Ala Ala Glu Thr Ile Val Arg Asp Ser Gln
                245                 250                 255

Thr Leu Gly Asp Val Tyr Ser Arg Leu Gln Val Leu Asp Ser Leu Met
            260                 265                 270

Ser Thr Ile Val Ser Asn Pro Gln Ala Asn Gln Glu Glu Ile Met Gln
        275                 280                 285

Lys Leu Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr Pro Ala
    290                 295                 300

Val Gln Asn Ser Val Asp Ser Leu Gln Lys Phe Ala Ala Gln Leu Glu
305                 310                 315                 320

Arg Glu Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Gln Glu Asn
                325                 330                 335

Ala Phe Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val Asn Ile
            340                 345                 350

Ala Ser Leu Phe Ser Gly Tyr Leu Ser
        355                 360
```

<210> 300
<211> 207
<212> PRT
<213> Chlamydia

<400> 300
Ser Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val Ala Asp Ala Arg
5 10 15

Met Cys Lys Ala Glu Leu Ile Lys Lys Glu Ala Asp Ala Tyr Leu Phe
20 25 30

Cys Glu Lys Ser Gly Ile Tyr Leu Thr Lys Lys Glu Gly Ile Leu Ile
35 40 45

Pro Ser Ala Gly Ile Asp Glu Ser Asn Thr Asp Gln Pro Phe Val Leu
50 55 60

Tyr Pro Lys Asp Ile Leu Gly Ser Cys Asn Arg Ile Gly Glu Trp Leu
65 70 75 80

Arg Asn Tyr Phe Arg Val Lys Glu Leu Gly Val Ile Ile Thr Asp Ser
85 90 95

His Thr Thr Pro Met Arg Arg Gly Val Leu Gly Ile Gly Leu Cys Trp
100 105 110

Tyr Gly Phe Ser Pro Leu His Asn Tyr Ile Gly Ser Leu Asp Cys Phe
115 120 125

Gly Arg Pro Leu Gln Met Thr Gln Ser Asn Leu Val Asp Ala Leu Ala
130 135 140

Val Ala Ala Val Val Cys Met Gly Glu Gly Asn Glu Gln Thr Pro Leu
145 150 155 160

Ala Val Ile Glu Gln Ala Pro Asn Met Val Tyr His Ser Tyr Pro Thr
165 170 175

Ser Arg Glu Glu Tyr Cys Ser Leu Arg Ile Asp Glu Thr Glu Asp Leu
180 185 190

Tyr Gly Pro Phe Leu Gln Ala Val Thr Trp Ser Gln Glu Lys Lys
195 200 205

<210> 301
<211> 183
<212> PRT
<213> Chlamydia

<400> 301
Ile Pro Pro Ala Pro Arg Gly His Pro Gln Ile Glu Val Thr Phe Asp
5 10 15

Ile Asp Ala Asn Gly Ile Leu His Val Ser Ala Lys Asp Ala Ala Ser
20 25 30

Gly Arg Glu Gln Lys Ile Arg Ile Glu Ala Ser Ser Gly Leu Lys Glu
35 40 45

Asp Glu Ile Gln Gln Met Ile Arg Asp Ala Glu Leu His Lys Glu Glu
50 55 60

Asp Lys Gln Arg Lys Glu Ala Ser Asp Val Lys Asn Glu Ala Asp Gly
65 70 75 80

Met Ile Phe Arg Ala Glu Lys Ala Val Lys Asp Tyr His Asp Lys Ile
85 90 95

Pro Ala Glu Leu Val Lys Glu Ile Glu Glu His Ile Glu Lys Val Arg
100 105 110

Gln Ala Ile Lys Glu Asp Ala Ser Thr Thr Ala Ile Lys Ala Ala Ser
115 120 125

Asp Glu Leu Ser Thr Arg Met Gln Lys Ile Gly Glu Ala Met Gln Ala
130 135 140

Gln Ser Ala Ser Ala Ala Ala Ser Ser Ala Ala Asn Ala Gln Gly Gly
145 150 155 160

Pro Asn Ile Asn Ser Glu Asp Leu Lys Lys His Ser Phe Ser Thr Arg
165 170 175

Pro Pro Ala Gly Gly Ser Ala
180

<210> 302
<211> 232
<212> PRT
<213> Chlamydia

<400> 302
Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp
5 10 15

Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln
20 25 30

Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu
35 40 45

Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser
50 55 60

Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala
65 70 75 80

Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly
85 90 95

Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp
100 105 110

Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
115 120 125

Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr
130 135 140

Val Thr Thr Asp Val Val Lys Thr Ile Ala Glu Leu Arg Lys Gly Lys
145 150 155 160

Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala
165 170 175

Lys Leu Ser Phe Asp Ser Ala Gln Ile Lys Glu Asn Val Glu Ala Leu
180 185 190

Cys Ala Ala Leu Val Lys Ala Lys Pro Ala Thr Ala Lys Gly Gln Tyr
195 200 205

Leu Val Asn Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Val Thr Val
210 215 220

Asp Thr Arg Glu Leu Ile Ala Leu
225 230

<210> 303
<211> 238
<212> PRT
<213> chlamydia

<400> 303
Ile Asn Ser Lys Leu Glu Thr Lys Asn Leu Ile Tyr Leu Lys Leu Lys
5 10 15

Ile Lys Lys Ser Phe Lys Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn
20 25 30

Thr Gln Asn Cys Val Phe Ala Asp Asn Ile Lys Val Gly Gln Met Thr
35 40 45

Glu Pro Leu Lys Asp Gln Gln Ile Ile Leu Gly Thr Thr Ser Thr Pro
50 55 60

Val Ala Ala Lys Met Thr Ala Ser Asp Gly Ile Ser Leu Thr Val Ser
65 70 75 80

Asn Asn Pro Ser Thr Asn Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu
85 90 95

Lys Ala Tyr Gln Leu Ile Leu Glu Lys Leu Gly Asp Gln Ile Leu Gly
100 105 110

Gly Ile Ala Asp Thr Ile Val Asp Ser Thr Val Gln Asp Ile Leu Asp
115 120 125

Lys Ile Thr Thr Asp Pro Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn
130 135 140

Phe Pro Ile Thr Asn Lys Ile Gln Cys Asn Gly Leu Phe Thr Pro Arg
145 150 155 160

Asn Ile Glu Thr Leu Leu Gly Gly Thr Glu Ile Gly Lys Phe Thr Val
165 170 175

Thr Pro Lys Ser Ser Gly Ser Met Phe Leu Val Ser Ala Asp Ile Ile
180 185 190

Ala Ser Arg Met Glu Gly Gly Val Val Leu Ala Leu Val Arg Glu Gly
195 200 205

Asp Ser Lys Pro Tyr Ala Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro
210 215 220

Asn Leu Cys Ser Leu Arg Thr Arg Ile Ile Asn Thr Gly Leu
225 230 235

<210> 304
<211> 133
<212> PRT
<213> Chlamydia

<400> 304
His Met His His His His His His Met Ala Ser Ile Cys Gly Arg Leu
5 10 15

Gly Ser Gly Thr Gly Asn Ala Leu Lys Ala Phe Phe Thr Gln Pro Ser
20 25 30

Asn Lys Met Ala Arg Val Val Asn Lys Thr Lys Gly Met Asp Lys Thr
35 40 45

Val Lys Val Ala Lys Ser Ala Ala Glu Leu Thr Ala Asn Ile Leu Glu
50 55 60

Gln Ala Gly Gly Ala Gly Ser Ser Ala His Ile Thr Ala Ser Gln Val
65 70 75 80

Ser Lys Gly Leu Gly Asp Thr Arg Thr Val Val Ala Leu Gly Asn Ala
85 90 95

Phe Asn Gly Ala Leu Pro Gly Thr Val Gln Ser Ala Gln Ser Phe Phe
100 105 110

Ser His Met Lys Ala Ala Ser Gln Lys Thr Gln Glu Gly Asp Glu Gly
115 120 125

Leu Thr Ala Asp Leu
130

<210> 305
<211> 125
<212> PRT
<213> Chlamydia

<400> 305
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
5 10 15

Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30

Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45

Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60

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Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
65                  70                  75                  80

Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95

Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110

Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu
        115                 120                 125


<210> 306
<211> 38
<212> DNA
<213> Chlamydia trachomatis

<400> 306
gagagcggcc gctcatgttt ataacaaagg aacttatg                              38

<210> 307
<211> 39
<212> DNA
<213> Chlamydia trachomatis

<400> 307
gagagcggcc gcttacttag gtgagaagaa gggagtttc                             39

<210> 308
<211> 1860
<212> DNA
<213> Chlamydia trachomatis

<400> 308
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg      60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc     120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac     180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc     240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac     300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc     360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat     420
ccatcacact ggcggccgct catgtttata acaaaggaac ttatgaatcg agttatagaa     480
atccatgctc actacgatca aagacaactt tctcaatctc caaatacaaa cttcttagta     540
catcatcctt atcttactct tattcccaag tttctactag gagctctaat cgtctatgct     600
ccttattcgt ttgcagaaat ggaattagct atttctggac ataaacaagg taaagatcga     660
gataccttta ccatgatctc ttcctgtcct gaaggcacta attacatcat caatcgcaaa     720
ctcatactca gtgatttctc gttactaaat aaagtttcat caggggggagc ctttcggaat     780
ctagcaggga aaatttcctt cttaggaaaa aattcttctg cgtccattca ttttaaacac     840
attaatatca atggttttgg agccggagtc ttttctgaat cctctattga atttactgat     900
ttacgaaaac ttgttgcttt tggatctgaa agcacaggag gaatttttac tgcgaaagag     960
gacatctctt ttaaaaacaa ccaccacatt gccttccgca ataatatcac caaagggaat    1020
ggtggcgtta tccagctcca aggagatatg aaaggaagcg tatcctttgt agatcaacgt    1080
ggagctatca tctttaccaa taaccaagct gtaacttctt catcaatgaa acatagtggt    1140
cgtggaggag caattagcgg tgacttcgca ggatccagaa ttctttttct taataaccaa    1200
caaattactt tcgaaggcaa tagcgctgtg catggaggtg ctatctacaa taagaatggc    1260
cttgtcgagt tcttaggaaa tgcaggacct cttgccttta aagagaacac aacaatagct    1320
aacgggggag ctatatacac aagtaatttc aaagcgaatc aacaaacatc cccattcta     1380
ttctctcaaa atcatgcgaa taagaaaggc ggagcgattt acgcgcaata tgtgaactta    1440
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gaacagaatc aagatactat tcgctttgaa aaaaataccg ctaaagaagg cggtggagcc 1500
atcacctctt ctcaatgctc aattactgct cataatacca tcacttttc cgataatgct 1560
gccggagatc ttggaggagg agcaattctt ctagaaggga aaaaaccttc tctaaccttg 1620
attgctcata gtggtaatat tgcatttagc ggcaatacca tgcttcatat caccaaaaaa 1680
gcttccctag atcgacacaa ttctatctta atcaaagaag ctccctataa aatccaactt 1740
gcagcgaaca aaaaccattc tattcatttc tttgatcctg tcatggcatt gtcagcatca 1800
tcttccccta tacaaatcaa tgctcctgag tatgaaactc ccttcttctc acctaagtaa 1860

<210> 309
<211> 619
<212> PRT
<213> Chlamydia trachomatis

<400> 309
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Met Phe Ile Thr Lys Glu Leu Met Asn Arg Val Ile Glu
145 150 155 160
Ile His Ala His Tyr Asp Gln Arg Gln Leu Ser Gln Ser Pro Asn Thr
165 170 175
Asn Phe Leu Val His His Pro Tyr Leu Thr Leu Ile Pro Lys Phe Leu
180 185 190
Leu Gly Ala Leu Ile Val Tyr Ala Pro Tyr Ser Phe Ala Glu Met Glu
195 200 205
Leu Ala Ile Ser Gly His Lys Gln Gly Lys Asp Arg Asp Thr Phe Thr
210 215 220
Met Ile Ser Ser Cys Pro Glu Gly Thr Asn Tyr Ile Ile Asn Arg Lys
225 230 235 240
Leu Ile Leu Ser Asp Phe Ser Leu Leu Asn Lys Val Ser Ser Gly Gly
245 250 255
Ala Phe Arg Asn Leu Ala Gly Lys Ile Ser Phe Leu Gly Lys Asn Ser
260 265 270
Ser Ala Ser Ile His Phe Lys His Ile Asn Ile Asn Gly Phe Gly Ala
275 280 285
Gly Val Phe Ser Glu Ser Ser Ile Glu Phe Thr Asp Leu Arg Lys Leu
290 295 300
Val Ala Phe Gly Ser Glu Ser Thr Gly Gly Ile Phe Thr Ala Lys Glu
305 310 315 320
Asp Ile Ser Phe Lys Asn Asn His His Ile Ala Phe Arg Asn Asn Ile
325 330 335
Thr Lys Gly Asn Gly Gly Val Ile Gln Leu Gln Gly Asp Met Lys Gly
340 345 350
Ser Val Ser Phe Val Asp Gln Arg Gly Ala Ile Ile Phe Thr Asn Asn
355 360 365
Gln Ala Val Thr Ser Ser Ser Met Lys His Ser Gly Arg Gly Gly Ala

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    370                 375                 380
Ile Ser Gly Asp Phe Ala Gly Ser Arg Ile Leu Phe Leu Asn Asn Gln
385                 390                 395                 400
Gln Ile Thr Phe Glu Gly Asn Ser Ala Val His Gly Gly Ala Ile Tyr
                405                 410                 415
Asn Lys Asn Gly Leu Val Glu Phe Leu Gly Asn Ala Gly Pro Leu Ala
            420                 425                 430
Phe Lys Glu Asn Thr Thr Ile Ala Asn Gly Gly Ala Ile Tyr Thr Ser
        435                 440                 445
Asn Phe Lys Ala Asn Gln Gln Thr Ser Pro Ile Leu Phe Ser Gln Asn
    450                 455                 460
His Ala Asn Lys Lys Gly Gly Ala Ile Tyr Ala Gln Tyr Val Asn Leu
465                 470                 475                 480
Glu Gln Asn Gln Asp Thr Ile Arg Phe Glu Lys Asn Thr Ala Lys Glu
                485                 490                 495
Gly Gly Gly Ala Ile Thr Ser Ser Gln Cys Ser Ile Thr Ala His Asn
            500                 505                 510
Thr Ile Thr Phe Ser Asp Asn Ala Ala Gly Asp Leu Gly Gly Gly Ala
        515                 520                 525
Ile Leu Leu Glu Gly Lys Lys Pro Ser Leu Thr Leu Ile Ala His Ser
    530                 535                 540
Gly Asn Ile Ala Phe Ser Gly Asn Thr Met Leu His Ile Thr Lys Lys
545                 550                 555                 560
Ala Ser Leu Asp Arg His Asn Ser Ile Leu Ile Lys Glu Ala Pro Tyr
                565                 570                 575
Lys Ile Gln Leu Ala Ala Asn Lys Asn His Ser Ile His Phe Phe Asp
            580                 585                 590
Pro Val Met Ala Leu Ser Ala Ser Ser Ser Pro Ile Gln Ile Asn Ala
        595                 600                 605
Pro Glu Tyr Glu Thr Pro Phe Phe Ser Pro Lys
    610                 615

<210> 310
<211> 39
<212> DNA
<213> Chlamydia trachomatis

<400> 310
gagagcggcc gctccattct attcatttct ttgatcctg                            39

<210> 311
<211> 33
<212> DNA
<213> Chlamydia trachomatis

<400> 311
gagagcggcc gcttagaagc caacatagcc tcc                                  33

<210> 312
<211> 2076
<212> DNA
<213> Chlamydia trachomatis

<400> 312
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg      60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc     120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac     180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc     240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac     300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc     360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat     420
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ccatcacact ggcggccgct ccattctatt catttctttg atcctgtcat ggcattgtca     480
gcatcatctt cccctataca aatcaatgct cctgagtatg aaactccctt cttctcacct     540
aagggtatga tcgttttctc gggtgcgaat cttttagatg atgctaggga agatgttgca     600
aatagaacat cgatttttaa ccaacccgtt catctatata atggcaccct atctatcgaa     660
aatggagccc atctgattgt ccaaagcttc aaacagaccg gaggacgtat cagtttatct     720
ccaggatcct ccttggctct atacacgatg aactcgttct tccatggcaa catatccagc     780
aaagaacccc tagaaattaa tggtttaagc tttggagtag atatctctcc ttctaatctt     840
caagcagaga tccgtgccgg caacgctcct ttacgattat ccggatcccc atctatccat     900
gatcctgaag gattattcta cgaaaatcgc gatactgcag catcaccata ccaaatggaa     960
atcttgctca cctctgataa aactgtagat atctccaaat ttactactga ttctctagtt    1020
acgaacaaac aatcaggatt ccaaggagcc tggcatttta gctggcagcc aaatactata    1080
aacaatacta aacaaaaaat attaagagct tcttggctcc caacaggaga atatgtcctt    1140
gaatccaatc gagtggggcg tgccgttcct aattccttat ggagcacatt tttactttta    1200
cagacagcct ctcataactt aggcgatcat ctatgtaata atcgatctct tattcctact    1260
tcatacttcg gagttttaat tggaggaact ggagcagaaa tgtctaccca ctcctcagaa    1320
gaagaaagct ttatatctcg tttaggagct acaggaacct ctatcatacg cttaactccc    1380
tccctgacac tctctggagg aggctcacat atgttcggag attcgttcgt tgcagactta    1440
ccagaacaca tcacttcaga aggaattgtt cagaatgtcg gtttaaccca tgtctgggga    1500
ccccttactg tcaattctac attatgtgca gccttagatc acaacgcgat ggtccgcata    1560
tgctccaaaa aagatcacac ctatgggaaa tgggatacat tcggtatgcg aggaacatta    1620
ggagcctctt atacattcct agaatatgat caaactatgc gcgtattctc attcgccaac    1680
atcgaagcca caaatatctt gcaaagagct tttactgaaa caggctataa cccaagaagt    1740
ttttccaaga caaaacttct aaacatcgcc atccccatag ggattggtta tgaattctgc    1800
ttagggaata gctcttttgc tctactaggt aagggatcca tcggttactc tcgagatatt    1860
aaacgagaaa acccatccac tcttgctcac ctggctatga atgattttgc ttggactacc    1920
aatggctgtt cagttccaac ctccgcacac acattggcaa atcaattgat tcttcgctat    1980
aaagcatgtt ccttatacat cacggcatat actatcaacc gtgaagggaa gaacctctcc    2040
aatagcttat cctgcggagg ctatgttggc ttctaa                              2076
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<210> 313
<211> 691
<212> PRT
<213> Chlamydia trachomatis

<400> 313

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Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1               5                   10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu His Ser Ile His Phe Phe Asp Pro Val Met Ala Leu Ser
145                 150                 155                 160
Ala Ser Ser Ser Pro Ile Gln Ile Asn Ala Pro Glu Tyr Glu Thr Pro
                165                 170                 175
Phe Phe Ser Pro Lys Gly Met Ile Val Phe Ser Gly Ala Asn Leu Leu
            180                 185                 190
Asp Asp Ala Arg Glu Asp Val Ala Asn Arg Thr Ser Ile Phe Asn Gln
        195                 200                 205
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Pro Val His Leu Tyr Asn Gly Thr Leu Ser Ile Glu Asn Gly Ala His
    210                 215                 220
Leu Ile Val Gln Ser Phe Lys Gln Thr Gly Gly Arg Ile Ser Leu Ser
225                 230                 235                 240
Pro Gly Ser Ser Leu Ala Leu Tyr Thr Met Asn Ser Phe Phe His Gly
                245                 250                 255
Asn Ile Ser Ser Lys Glu Pro Leu Glu Ile Asn Gly Leu Ser Phe Gly
            260                 265                 270
Val Asp Ile Ser Pro Ser Asn Leu Gln Ala Glu Ile Arg Ala Gly Asn
        275                 280                 285
Ala Pro Leu Arg Leu Ser Gly Ser Pro Ser Ile His Asp Pro Glu Gly
    290                 295                 300
Leu Phe Tyr Glu Asn Arg Asp Thr Ala Ala Ser Pro Tyr Gln Met Glu
305                 310                 315                 320
Ile Leu Leu Thr Ser Asp Lys Thr Val Asp Ile Ser Lys Phe Thr Thr
                325                 330                 335
Asp Ser Leu Val Thr Asn Lys Gln Ser Gly Phe Gln Gly Ala Trp His
            340                 345                 350
Phe Ser Trp Gln Pro Asn Thr Ile Asn Asn Thr Lys Gln Lys Ile Leu
        355                 360                 365
Arg Ala Ser Trp Leu Pro Thr Gly Glu Tyr Val Leu Glu Ser Asn Arg
    370                 375                 380
Val Gly Arg Ala Val Pro Asn Ser Leu Trp Ser Thr Phe Leu Leu Leu
385                 390                 395                 400
Gln Thr Ala Ser His Asn Leu Gly Asp His Leu Cys Asn Asn Arg Ser
                405                 410                 415
Leu Ile Pro Thr Ser Tyr Phe Gly Val Leu Ile Gly Gly Thr Gly Ala
            420                 425                 430
Glu Met Ser Thr His Ser Ser Glu Glu Glu Ser Phe Ile Ser Arg Leu
        435                 440                 445
Gly Ala Thr Gly Thr Ser Ile Ile Arg Leu Thr Pro Ser Leu Thr Leu
    450                 455                 460
Ser Gly Gly Gly Ser His Met Phe Gly Asp Ser Phe Val Ala Asp Leu
465                 470                 475                 480
Pro Glu His Ile Thr Ser Glu Gly Ile Val Gln Asn Val Gly Leu Thr
                485                 490                 495
His Val Trp Gly Pro Leu Thr Val Asn Ser Thr Leu Cys Ala Ala Leu
            500                 505                 510
Asp His Asn Ala Met Val Arg Ile Cys Ser Lys Lys Asp His Thr Tyr
        515                 520                 525
Gly Lys Trp Asp Thr Phe Gly Met Arg Gly Thr Leu Gly Ala Ser Tyr
    530                 535                 540
Thr Phe Leu Glu Tyr Asp Gln Thr Met Arg Val Phe Ser Phe Ala Asn
545                 550                 555                 560
Ile Glu Ala Thr Asn Ile Leu Gln Arg Ala Phe Thr Glu Thr Gly Tyr
                565                 570                 575
Asn Pro Arg Ser Phe Ser Lys Thr Lys Leu Leu Asn Ile Ala Ile Pro
            580                 585                 590
Ile Gly Ile Gly Tyr Glu Phe Cys Leu Gly Asn Ser Ser Phe Ala Leu
        595                 600                 605
Leu Gly Lys Gly Ser Ile Gly Tyr Ser Arg Asp Ile Lys Arg Glu Asn
    610                 615                 620
Pro Ser Thr Leu Ala His Leu Ala Met Asn Asp Phe Ala Trp Thr Thr
625                 630                 635                 640
Asn Gly Cys Ser Val Pro Thr Ser Ala His Thr Leu Ala Asn Gln Leu
                645                 650                 655
Ile Leu Arg Tyr Lys Ala Cys Ser Leu Tyr Ile Thr Ala Tyr Thr Ile
            660                 665                 670
Asn Arg Glu Gly Lys Asn Leu Ser Asn Ser Leu Ser Cys Gly Gly Tyr
        675                 680                 685
Val Gly Phe
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690

<210> 314
<211> 38
<212> DNA
<213> Chlamydia trachomatis

<400> 314
gagagcggcc gctcatgatt aaaagaactt ctctatcc 38

<210> 315
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 315
agcggccgct tataattctg catcatcttc tatggc 36

<210> 316
<211> 1941
<212> DNA
<213> Chlamydia trachomatis

<400> 316
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct catgattaaa agaacttctc tatcctttgc ttgcctcagt 480
tttttttatc tttcaactat atccattttg caagctaatg aaacggatac gctacagttc 540
cggcgattta ctttttcgga tagagagatt cagttcgtcc tagatcccgc ctctttaatt 600
accgcccaaa acatcgtttt atctaattta cagtcaaacg gaaccggagc ctgtaccatt 660
tcaggcaata cgcaaactca aatcttttct aattccgtta acaccaccgc agattctggt 720
ggagcctttg atatggttac tacctcattc acggcctctg ataatgctaa tctactcttc 780
tgcaacaact actgcacaca taataaaggc ggaggagcta ttcgttccgg aggacctatt 840
cgattcttaa ataatcaaga cgtgcttttt tataataaca tatcggcagg ggctaaatat 900
gttggaacag gagatcacaa cgaaaaaaat aggggcggtg cgctttatgc aactactatc 960
actttgacag ggaatcgaac tcttgccttt attaacaata tgtctggaga ctgcggtgga 1020
gccatctctg ctgacactca aatatcaata actgataccg ttaaaggaat tttatttgaa 1080
aacaatcaca cgctcaatca tataccgtac acgcaagctg aaaatatggc acgaggagga 1140
gcaatctgta gtagaagaga cttgtgctca atcagcaata attctggtcc catagttttt 1200
aactataacc aaggcgggaa aggtggagct attagcgcta cccgatgtgt tattgacaat 1260
aacaaagaaa gaatcatctt ttcaaacaat agttccctgg gatggagcca atcttcttct 1320
gcaagtaacg gaggagccat tcaaacgaca caaggattta ctttacgaaa taataaaggc 1380
tctatctact tcgacagcaa cactgctaca cacgccgggg gagccattaa ctgtggttac 1440
attgacatcc gagataacgg acccgtctat tttctaaata actctgctgc ctggggagcg 1500
gcctttaatt tatcgaaacc acgttcagcg acaaattata tccatacagg gacaggcgat 1560
attgttttta ataataacgt tgtctttact cttgacggta atttattagg gaaacggaaa 1620
ctttttcata ttaataataa tgagataaca ccatatacat tgtctctcgg cgctaaaaaa 1680
gatactcgta tctattttta tgatcttttc caatgggagc gtgttaaaga aaatactagc 1740
aataacccac catctcctac cagtagaaac accattaccg ttaacccgga aacagagttt 1800
tctggagctg ttgtgttctc ctacaatcaa atgtctagtg acatacgaac tctgatgggt 1860
aaagaacaca attacattaa agaagcccca actactttaa aattcggaac gctagccata 1920
gaagatgatg cagaattata a 1941

<210> 317
<211> 646
<212> PRT

<213> Chlamydia trachomatis

<400> 317
```
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1               5                  10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Met Ile Lys Arg Thr Ser Leu Ser Phe Ala Cys Leu Ser
145                 150                 155                 160
Phe Phe Tyr Leu Ser Thr Ile Ser Ile Leu Gln Ala Asn Glu Thr Asp
                165                 170                 175
Thr Leu Gln Phe Arg Arg Phe Thr Phe Ser Asp Arg Glu Ile Gln Phe
            180                 185                 190
Val Leu Asp Pro Ala Ser Leu Ile Thr Ala Gln Asn Ile Val Leu Ser
        195                 200                 205
Asn Leu Gln Ser Asn Gly Thr Gly Ala Cys Thr Ile Ser Gly Asn Thr
    210                 215                 220
Gln Thr Gln Ile Phe Ser Asn Ser Val Asn Thr Thr Ala Asp Ser Gly
225                 230                 235                 240
Gly Ala Phe Asp Met Val Thr Thr Ser Phe Thr Ala Ser Asp Asn Ala
                245                 250                 255
Asn Leu Leu Phe Cys Asn Asn Tyr Cys Thr His Asn Lys Gly Gly Gly
            260                 265                 270
Ala Ile Arg Ser Gly Gly Pro Ile Arg Phe Leu Asn Asn Gln Asp Val
        275                 280                 285
Leu Phe Tyr Asn Asn Ile Ser Ala Gly Ala Lys Tyr Val Gly Thr Gly
    290                 295                 300
Asp His Asn Glu Lys Asn Arg Gly Gly Ala Leu Tyr Ala Thr Thr Ile
305                 310                 315                 320
Thr Leu Thr Gly Asn Arg Thr Leu Ala Phe Ile Asn Asn Met Ser Gly
                325                 330                 335
Asp Cys Gly Gly Ala Ile Ser Ala Asp Thr Gln Ile Ser Ile Thr Asp
            340                 345                 350
Thr Val Lys Gly Ile Leu Phe Glu Asn Asn His Thr Leu Asn His Ile
        355                 360                 365
Pro Tyr Thr Gln Ala Glu Asn Met Ala Arg Gly Gly Ala Ile Cys Ser
    370                 375                 380
Arg Arg Asp Leu Cys Ser Ile Ser Asn Asn Ser Gly Pro Ile Val Phe
385                 390                 395                 400
Asn Tyr Asn Gln Gly Gly Lys Gly Gly Ala Ile Ser Ala Thr Arg Cys
                405                 410                 415
Val Ile Asp Asn Asn Lys Glu Arg Ile Ile Phe Ser Asn Asn Ser Ser
            420                 425                 430
Leu Gly Trp Ser Gln Ser Ser Ser Ala Ser Asn Gly Gly Ala Ile Gln
        435                 440                 445
Thr Thr Gln Gly Phe Thr Leu Arg Asn Asn Lys Gly Ser Ile Tyr Phe
    450                 455                 460
```

```
Asp Ser Asn Thr Ala Thr His Ala Gly Gly Ala Ile Asn Cys Gly Tyr
465                 470                 475                 480
Ile Asp Ile Arg Asp Asn Gly Pro Val Tyr Phe Leu Asn Asn Ser Ala
                485                 490                 495
Ala Trp Gly Ala Ala Phe Asn Leu Ser Lys Pro Arg Ser Ala Thr Asn
            500                 505                 510
Tyr Ile His Thr Gly Thr Gly Asp Ile Val Phe Asn Asn Asn Val Val
        515                 520                 525
Phe Thr Leu Asp Gly Asn Leu Leu Gly Lys Arg Lys Leu Phe His Ile
    530                 535                 540
Asn Asn Asn Glu Ile Thr Pro Tyr Thr Leu Ser Leu Gly Ala Lys Lys
545                 550                 555                 560
Asp Thr Arg Ile Tyr Phe Tyr Asp Leu Phe Gln Trp Glu Arg Val Lys
                565                 570                 575
Glu Asn Thr Ser Asn Asn Pro Pro Ser Pro Thr Ser Arg Asn Thr Ile
            580                 585                 590
Thr Val Asn Pro Glu Thr Glu Phe Ser Gly Ala Val Val Phe Ser Tyr
        595                 600                 605
Asn Gln Met Ser Ser Asp Ile Arg Thr Leu Met Gly Lys Glu His Asn
    610                 615                 620
Tyr Ile Lys Glu Ala Pro Thr Thr Leu Lys Phe Gly Thr Leu Ala Ile
625                 630                 635                 640
Glu Asp Asp Ala Glu Leu
                645
```

<210> 318
<211> 34
<212> DNA
<213> Chlamydia trachomatis

<400> 318
gagagcggcc gctcgacata cgaactctga tggg 34

<210> 319
<211> 33
<212> DNA
<213> Chlamydia trachomatis

<400> 319
gagagcggcc gcttaaaaga ccagagctcc tcc 33

<210> 320
<211> 2148
<212> DNA
<213> Chlamydia trachomatis

<400> 320
```
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg     60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc    120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac    180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc    240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac    300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc    360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat    420
ccatcacact ggcggccgct cgacatacga actctgatgg gtaaagaaca caattacatt    480
aaagaagccc caactacttt aaaattcgga acgctagcca tagaagatga tgcagaatta    540
gaaatcttca atatcccgtt tacccaaaat ccgactagcc ttcttgcttt aggaagcggc    600
gctacgctga ctgttggaaa gcacggtaag ctcaatatta caaatcttgg tgttatttta    660
cccattattc tcaaagaggg gaagagtccg ccttgtattc gcgtcaaccc acaagatatg    720
acccaaaata ctggtaccgg ccaaactcca tcaagcacaa gtagtataag cactccaatg    780
attatcttta atgggcgcct ctcaattgta gacgaaaatt atgaatcagt ctacgacagt    840
```

```
atggacctct ccagagggaa agcagaacaa ctaattctat ccatagaaac cactaatgat     900
gggcaattag actccaattg gcaaagttct ctgaatactt ctctactctc tcctccacac     960
tatggctatc aaggtctatg gactcctaat tggataacaa caacctatac catcacgctt    1020
aataataatt cttcagctcc aacatctgct acctccatcg ctgagcagaa aaaaactagt    1080
gaaactttta ctcctagtaa cacaactaca gctagtatcc ctaatattaa agcttccgca    1140
ggatcaggct ctggatcggc ttccaattca ggagaagtta cgattaccaa acatacccct    1200
gttgtaaact gggcaccagt cggctacata gtagatccta ttcgtagagg agatctgata    1260
gccaatagct tagtacattc aggaagaaac atgaccatgg gcttacgatc attactcccg    1320
gataactctt ggtttgcttt gcaaggagct gcaacaacat tatttacaaa acaacaaaaa    1380
cgtttgagtt atcatggcta ctcttctgca tcaaaggggt ataccgtctc ttctcaagca    1440
tcaggagctc atggtcataa gtttcttctt tccttctccc agtcatctga taagatgaaa    1500
gaaaaagaaa caaataaccg cctttcttct cgttactatc tttctgcttt atgtttcgaa    1560
catcctatgt ttgatcgcat tgctcttatc ggagcagcag cttgcaatta tggaacacat    1620
aacatgcgga gtttctatgg aactaaaaaa tcttctaaag ggaaatttca ctctacaacc    1680
ttaggagctt ctcttcgctg tgaactacgc gatagtatgc ctttacgatc aataatgctc    1740
accccatttg ctcaggcttt attctctcga acagaaccag cttctatccg agaaagcggt    1800
gatctagcta gattatttac attagagcaa gcccatactg ccgttgtctc tccaatagga    1860
atcaaaggag cttattcttc tgatacatgg ccaacactct cttgggaaat ggaactagct    1920
taccaaccca ccctctactg gaaacgtcct ctactcaaca cactattaat ccaaaataac    1980
ggttcttggg tcaccacaaa taccccatta gctaaacatt ccttttatgg gagaggttct    2040
cactccctca aatttctca tctgaaacta tttgctaact atcaagcaga agtggctact     2100
tccactgtct cacactacat caatgcagga ggagctctgg tcttttaa                 2148
```

<210> 321
<211> 715
<212> PRT
<213> Chlamydia trachomatis

<400> 321

```
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1               5                  10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Asp Ile Arg Thr Leu Met Gly Lys Glu His Asn Tyr Ile
145                 150                 155                 160
Lys Glu Ala Pro Thr Thr Leu Lys Phe Gly Thr Leu Ala Ile Glu Asp
                165                 170                 175
Asp Ala Glu Leu Glu Ile Phe Asn Ile Pro Phe Thr Gln Asn Pro Thr
            180                 185                 190
Ser Leu Leu Ala Leu Gly Ser Gly Ala Thr Leu Thr Val Gly Lys His
        195                 200                 205
Gly Lys Leu Asn Ile Thr Asn Leu Gly Val Ile Leu Pro Ile Ile Leu
    210                 215                 220
Lys Glu Gly Lys Ser Pro Pro Cys Ile Arg Val Asn Pro Gln Asp Met
225                 230                 235                 240
Thr Gln Asn Thr Gly Thr Gly Gln Thr Pro Ser Ser Thr Ser Ser Ile
                245                 250                 255
```

```
Ser Thr Pro Met Ile Ile Phe Asn Gly Arg Leu Ser Ile Val Asp Glu
            260                 265                 270
Asn Tyr Glu Ser Val Tyr Asp Ser Met Asp Leu Ser Arg Gly Lys Ala
        275                 280                 285
Glu Gln Leu Ile Leu Ser Ile Glu Thr Thr Asn Asp Gly Gln Leu Asp
    290                 295                 300
Ser Asn Trp Gln Ser Ser Leu Asn Thr Ser Leu Leu Ser Pro Pro His
305                 310                 315                 320
Tyr Gly Tyr Gln Gly Leu Trp Thr Pro Asn Trp Ile Thr Thr Thr Tyr
                325                 330                 335
Thr Ile Thr Leu Asn Asn Asn Ser Ser Ala Pro Thr Ser Ala Thr Ser
            340                 345                 350
Ile Ala Glu Gln Lys Lys Thr Ser Glu Thr Phe Thr Pro Ser Asn Thr
        355                 360                 365
Thr Thr Ala Ser Ile Pro Asn Ile Lys Ala Ser Ala Gly Ser Gly Ser
    370                 375                 380
Gly Ser Ala Ser Asn Ser Gly Glu Val Thr Ile Thr Lys His Thr Leu
385                 390                 395                 400
Val Val Asn Trp Ala Pro Val Gly Tyr Ile Val Asp Pro Ile Arg Arg
                405                 410                 415
Gly Asp Leu Ile Ala Asn Ser Leu Val His Ser Gly Arg Asn Met Thr
            420                 425                 430
Met Gly Leu Arg Ser Leu Leu Pro Asp Asn Ser Trp Phe Ala Leu Gln
        435                 440                 445
Gly Ala Ala Thr Thr Leu Phe Thr Lys Gln Gln Lys Arg Leu Ser Tyr
    450                 455                 460
His Gly Tyr Ser Ser Ala Ser Lys Gly Tyr Thr Val Ser Ser Gln Ala
465                 470                 475                 480
Ser Gly Ala His Gly His Lys Phe Leu Leu Ser Phe Ser Gln Ser Ser
                485                 490                 495
Asp Lys Met Lys Glu Lys Glu Thr Asn Asn Arg Leu Ser Ser Arg Tyr
            500                 505                 510
Tyr Leu Ser Ala Leu Cys Phe Glu His Pro Met Phe Asp Arg Ile Ala
        515                 520                 525
Leu Ile Gly Ala Ala Ala Cys Asn Tyr Gly Thr His Asn Met Arg Ser
    530                 535                 540
Phe Tyr Gly Thr Lys Lys Ser Ser Lys Gly Lys Phe His Ser Thr Thr
545                 550                 555                 560
Leu Gly Ala Ser Leu Arg Cys Glu Leu Arg Asp Ser Met Pro Leu Arg
                565                 570                 575
Ser Ile Met Leu Thr Pro Phe Ala Gln Ala Leu Phe Ser Arg Thr Glu
            580                 585                 590
Pro Ala Ser Ile Arg Glu Ser Gly Asp Leu Ala Arg Leu Phe Thr Leu
        595                 600                 605
Glu Gln Ala His Thr Ala Val Val Ser Pro Ile Gly Ile Lys Gly Ala
    610                 615                 620
Tyr Ser Ser Asp Thr Trp Pro Thr Leu Ser Trp Glu Met Glu Leu Ala
625                 630                 635                 640
Tyr Gln Pro Thr Leu Tyr Trp Lys Arg Pro Leu Leu Asn Thr Leu Leu
                645                 650                 655
Ile Gln Asn Asn Gly Ser Trp Val Thr Thr Asn Thr Pro Leu Ala Lys
            660                 665                 670
His Ser Phe Tyr Gly Arg Gly Ser His Ser Leu Lys Phe Ser His Leu
        675                 680                 685
Lys Leu Phe Ala Asn Tyr Gln Ala Glu Val Ala Thr Ser Thr Val Ser
    690                 695                 700
His Tyr Ile Asn Ala Gly Gly Ala Leu Val Phe
705                 710                 715
```

<210> 322
<211> 37

<212> DNA
<213> Chlamydia trachomatis

<400> 322
gagagcggcc gctcatgcct ttttctttga gatctac 37

<210> 323
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 323
gagagcggcc gcttacacag atccattacc ggactg 36

<210> 324
<211> 1896
<212> DNA
<213> Chlamydia trachomatis

<400> 324
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct catgcctttt tctttgagat ctacatcatt ttgtttttta 480
gcttgtttgt gttcctattc gtatggattc gcgagctctc ctcaagtgtt aacacctaat 540
gtaaccactc cttttaaggg ggacgatgtt tacttgaatg gagactgcgc ttttgtcaat 600
gtctatgcag gggcagagaa cggctcaatt atctcagcta atggcgacaa tttaacgatt 660
accggacaaa accatacatt atcatttaca gattctcaag ggccagttct tcaaaattat 720
gccttcattt cagcaggaga gacacttact ctgaaagatt tttcgagttt gatgttctcg 780
aaaaatgttt cttgcggaga aaagggaatg atctcaggga aaaccgtgag tatttccgga 840
gcaggcgaag tgattttttg ggataactct gtggggtatt ctcctttgtc tattgtgcca 900
gcatcgactc caactcctcc agcaccagca ccagctcctg ctgcttcaag ctctttatct 960
ccaacagtta gtgatgctcg gaaagggtct atttttctg tagagactag tttggagatc 1020
tcaggcgtca aaaaaggggt catgttcgat aataatgccg ggaattttgg aacagttttt 1080
cgaggtaata gtaataataa tgctggtagt ggggggtagtg ggtctgctac aacaccaagt 1140
tttacagtta aaaactgtaa agggaaagtt tctttcacag ataacgtagc ctcctgtgga 1200
ggcggagtag tctacaaagg aactgtgctt ttcaaagaca atgaaggagg catattcttc 1260
cgagggaaca cagcatacga tgatttaggg attcttgctg ctactagtcg ggatcagaat 1320
acggagacag gaggcggtgg aggagttatt tgctctccag atgattctgt aaagtttgaa 1380
ggcaataaag gttctattgt ttttgattac aactttgcaa aaggcagagg cggaagcatc 1440
ctaacgaaag aattctctct tgtagcagat gattcggttg tctttagtaa caatacagca 1500
gaaaaaggcg gtggagctat ttatgctcct actatcgata taagcacgaa tggaggatcg 1560
attctgtttg aaagaaaccg agctgcagaa ggaggcgcca tctgcgtgag tgaagcaagc 1620
tctggttcaa ctggaaatct tactttaagc gcttctgatg gggatattgt tttttctggg 1680
aatatgacga gtgatcgtcc tggagagcgc agcgcagcaa gaatcttaag tgatggaacg 1740
actgtttctt taaatgcttc cggactatcg aagctgatct tttatgatcc tgtagtacaa 1800
aataattcag cagcgggtgc atcgacacca tcaccatctt cttcttctat gcctggtgct 1860
gtcacgatta atcagtccgg taatggatct gtgtaa 1896

<210> 325
<211> 631
<212> PRT
<213> Chlamydia trachomatis

<400> 325
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15

```
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Met Pro Phe Ser Leu Arg Ser Thr Ser Phe Cys Phe Leu
145                 150                 155                 160
Ala Cys Leu Cys Ser Tyr Ser Tyr Gly Phe Ala Ser Ser Pro Gln Val
                165                 170                 175
Leu Thr Pro Asn Val Thr Thr Pro Phe Lys Gly Asp Asp Val Tyr Leu
            180                 185                 190
Asn Gly Asp Cys Ala Phe Val Asn Val Tyr Ala Gly Ala Glu Asn Gly
        195                 200                 205
Ser Ile Ile Ser Ala Asn Gly Asp Asn Leu Thr Ile Thr Gly Gln Asn
    210                 215                 220
His Thr Leu Ser Phe Thr Asp Ser Gln Gly Pro Val Leu Gln Asn Tyr
225                 230                 235                 240
Ala Phe Ile Ser Ala Gly Glu Thr Leu Thr Leu Lys Asp Phe Ser Ser
                245                 250                 255
Leu Met Phe Ser Lys Asn Val Ser Cys Gly Glu Lys Gly Met Ile Ser
            260                 265                 270
Gly Lys Thr Val Ser Ile Ser Gly Ala Gly Glu Val Ile Phe Trp Asp
        275                 280                 285
Asn Ser Val Gly Tyr Ser Pro Leu Ser Ile Val Pro Ala Ser Thr Pro
    290                 295                 300
Thr Pro Pro Ala Pro Ala Pro Ala Pro Ala Ala Ser Ser Ser Leu Ser
305                 310                 315                 320
Pro Thr Val Ser Asp Ala Arg Lys Gly Ser Ile Phe Ser Val Glu Thr
                325                 330                 335
Ser Leu Glu Ile Ser Gly Val Lys Lys Gly Val Met Phe Asp Asn Asn
            340                 345                 350
Ala Gly Asn Phe Gly Thr Val Phe Arg Gly Asn Ser Asn Asn Asn Ala
        355                 360                 365
Gly Ser Gly Gly Ser Gly Ser Ala Thr Thr Pro Ser Phe Thr Val Lys
    370                 375                 380
Asn Cys Lys Gly Lys Val Ser Phe Thr Asp Asn Val Ala Ser Cys Gly
385                 390                 395                 400
Gly Gly Val Val Tyr Lys Gly Thr Val Leu Phe Lys Asp Asn Glu Gly
                405                 410                 415
Gly Ile Phe Phe Arg Gly Asn Thr Ala Tyr Asp Asp Leu Gly Ile Leu
            420                 425                 430
Ala Ala Thr Ser Arg Asp Gln Asn Thr Glu Thr Gly Gly Gly Gly Gly
        435                 440                 445
Val Ile Cys Ser Pro Asp Asp Ser Val Lys Phe Glu Gly Asn Lys Gly
    450                 455                 460
Ser Ile Val Phe Asp Tyr Asn Phe Ala Lys Gly Arg Gly Gly Ser Ile
465                 470                 475                 480
Leu Thr Lys Glu Phe Ser Leu Val Ala Asp Asp Ser Val Val Phe Ser
                485                 490                 495
Asn Asn Thr Ala Glu Lys Gly Gly Gly Ala Ile Tyr Ala Pro Thr Ile
```

```
            500                 505                 510
Asp Ile Ser Thr Asn Gly Gly Ser Ile Leu Phe Glu Arg Asn Arg Ala
        515                 520                 525
Ala Glu Gly Gly Ala Ile Cys Val Ser Glu Ala Ser Ser Gly Ser Thr
    530                 535                 540
Gly Asn Leu Thr Leu Ser Ala Ser Asp Gly Asp Ile Val Phe Ser Gly
545                 550                 555                 560
Asn Met Thr Ser Asp Arg Pro Gly Glu Arg Ser Ala Ala Arg Ile Leu
                565                 570                 575
Ser Asp Gly Thr Thr Val Ser Leu Asn Ala Ser Gly Leu Ser Lys Leu
            580                 585                 590
Ile Phe Tyr Asp Pro Val Val Gln Asn Asn Ser Ala Ala Gly Ala Ser
        595                 600                 605
Thr Pro Ser Pro Ser Ser Ser Ser Met Pro Gly Ala Val Thr Ile Asn
    610                 615                 620
Gln Ser Gly Asn Gly Ser Val
625                 630
```

<210> 326
<211> 40
<212> DNA
<213> Chlamydia trachomatis

<400> 326
gagagcggcc gctcgatcct gtagtacaaa ataattcagc 40

<210> 327
<211> 33
<212> DNA
<213> Chlamydia trachomatis

<400> 327
gagagcggcc gcttaaaaga ttctattcaa gcc 33

<210> 328
<211> 2148
<212> DNA
<213> Chlymadia trachomatis

<400> 328
```
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg      60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc     120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac     180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc     240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac     300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc     360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat     420
ccatcacact ggcggccgct cgatcctgta gtacaaaata attcagcagc gggtgcatcg     480
acaccatcac catcttcttc ttctatgcct ggtgctgtca cgattaatca gtccggtaat     540
ggatctgtga tttttaccgc cgagtcattg actccttcag aaaaacttca agttcttaac     600
tctacttcta acttcccagg agctctgact gtgtcaggag gggagttggt tgtgacggaa     660
ggagctacct taactactgg gaccattaca gccacctctg gacgagtgac tttaggatcc     720
ggagcttcgt tgtctgccgt tgcaggtgct gcaaataata attatacttg tacagtatct     780
aagttgggga ttgatttaga atcctttta actcctaact ataagacggc catactgggt      840
gcggatggaa cagttactgt taacagcggc tctactttag acctagtgat ggagaatgag     900
gcagaggtct atgataatcc gctttttgtg ggatcgctga caattccttt tgttactcta     960
tcttctagta gtgctagtaa cggagttaca aaaaattctg tcactattaa tgatgcagac    1020
gctgcgcact atgggtatca aggctcttgg tctgcagatt ggacgaaacc gcctctggct    1080
cctgatgcta aggggatggt acctcctaat accaataaca ctctgtatct gacatggaga    1140
cctgcttcga attacggtga atatcgactg gatcctcaga gaaagggaga actagtaccc    1200
aactctcttt gggtagcggg atctgcatta agaaccttta ctaatggttt gaaagaacac    1260
```

```
tatgtttcta gagatgttgg atttgtagca tctctgcatg ctctcgggga ttatattctg    1320
aattatacgc aagatgatcg ggatggcttt ttagctagat atgggggatt ccaggcgacc    1380
gcagcctccc attatgaaaa tgggtcaata tttggagtgg cttttggaca actctatggt    1440
cagacaaaga gcagaatgta ttactctaaa gatgctggga acatgacgat gttgtcctgt    1500
ttcggaagaa gttacgtaga tattaaagga acagaaactg ttatgtattg ggagacggct    1560
tatggctatt ctgtgcacag aatgcatacg cagtatttta atgacaaaac gcagaagttc    1620
gatcattcga aatgtcattg gcacaacaat aactattatg cgtttgtagg tgccgagcat    1680
aatttcttag agtactgcat tcctactcgt cagttagcta gagattatga gcttacaggg    1740
tttatgcgtt ttgaaatggc cggaggatgg tccagttcta cacgagaaac tggctcccta    1800
actagatatt tcgctcgcgg gtcagggcat aatatgtcgc ttccaatagg aattgtagct    1860
catgcagttt ctcatgtgcg aagatctcct ccttctaaac tgacactaaa tatgggatat    1920
agaccagaca tttggcgtgt cactccacat tgcaatatgg aaattattgc taacggagtg    1980
aagacaccta tacaaggatc cccgctggca cggcatgcct tcttcttaga agtgcatgat    2040
actttgtata ttcatcattt tggaagagcc tatatgaact attcattaga tgctcgtcgt    2100
cgacaaaccg cacattttgt atctatgggc ttgaatagaa tcttttaa                 2148

<210> 329
<211> 715
<212> PRT
<213> Chlamydia trachomatis

<400> 329
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1               5                  10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Asp Pro Val Val Gln Asn Asn Ser Ala Ala Gly Ala Ser
145                 150                 155                 160
Thr Pro Ser Pro Ser Ser Ser Ser Met Pro Gly Ala Val Thr Ile Asn
                165                 170                 175
Gln Ser Gly Asn Gly Ser Val Ile Phe Thr Ala Glu Ser Leu Thr Pro
            180                 185                 190
Ser Glu Lys Leu Gln Val Leu Asn Ser Thr Ser Asn Phe Pro Gly Ala
        195                 200                 205
Leu Thr Val Ser Gly Gly Glu Leu Val Val Thr Glu Gly Ala Thr Leu
    210                 215                 220
Thr Thr Gly Thr Ile Thr Ala Thr Ser Gly Arg Val Thr Leu Gly Ser
225                 230                 235                 240
Gly Ala Ser Leu Ser Ala Val Ala Gly Ala Ala Asn Asn Asn Tyr Thr
                245                 250                 255
Cys Thr Val Ser Lys Leu Gly Ile Asp Leu Glu Ser Phe Leu Thr Pro
            260                 265                 270
Asn Tyr Lys Thr Ala Ile Leu Gly Ala Asp Gly Thr Val Thr Val Asn
        275                 280                 285
Ser Gly Ser Thr Leu Asp Leu Val Met Glu Asn Glu Ala Glu Val Tyr
    290                 295                 300
Asp Asn Pro Leu Phe Val Gly Ser Leu Thr Ile Pro Phe Val Thr Leu
```

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305                 310                 315                 320
Ser Ser Ser Ser Ala Ser Asn Gly Val Thr Lys Asn Ser Val Thr Ile
                325                 330                 335
Asn Asp Ala Asp Ala Ala His Tyr Gly Tyr Gln Gly Ser Trp Ser Ala
            340                 345                 350
Asp Trp Thr Lys Pro Pro Leu Ala Pro Asp Ala Lys Gly Met Val Pro
        355                 360                 365
Pro Asn Thr Asn Asn Thr Leu Tyr Leu Thr Trp Arg Pro Ala Ser Asn
    370                 375                 380
Tyr Gly Glu Tyr Arg Leu Asp Pro Gln Arg Lys Gly Glu Leu Val Pro
385                 390                 395                 400
Asn Ser Leu Trp Val Ala Gly Ser Ala Leu Arg Thr Phe Thr Asn Gly
                405                 410                 415
Leu Lys Glu His Tyr Val Ser Arg Asp Val Gly Phe Val Ala Ser Leu
            420                 425                 430
His Ala Leu Gly Asp Tyr Ile Leu Asn Tyr Thr Gln Asp Asp Arg Asp
        435                 440                 445
Gly Phe Leu Ala Arg Tyr Gly Gly Phe Gln Ala Thr Ala Ala Ser His
    450                 455                 460
Tyr Glu Asn Gly Ser Ile Phe Gly Val Ala Phe Gly Gln Leu Tyr Gly
465                 470                 475                 480
Gln Thr Lys Ser Arg Met Tyr Tyr Ser Lys Asp Ala Gly Asn Met Thr
                485                 490                 495
Met Leu Ser Cys Phe Gly Arg Ser Tyr Val Asp Ile Lys Gly Thr Glu
            500                 505                 510
Thr Val Met Tyr Trp Glu Thr Ala Tyr Gly Tyr Ser Val His Arg Met
        515                 520                 525
His Thr Gln Tyr Phe Asn Asp Lys Thr Gln Lys Phe Asp His Ser Lys
    530                 535                 540
Cys His Trp His Asn Asn Asn Tyr Tyr Ala Phe Val Gly Ala Glu His
545                 550                 555                 560
Asn Phe Leu Glu Tyr Cys Ile Pro Thr Arg Gln Leu Ala Arg Asp Tyr
                565                 570                 575
Glu Leu Thr Gly Phe Met Arg Phe Glu Met Ala Gly Gly Trp Ser Ser
            580                 585                 590
Ser Thr Arg Glu Thr Gly Ser Leu Thr Arg Tyr Phe Ala Arg Gly Ser
        595                 600                 605
Gly His Asn Met Ser Leu Pro Ile Gly Ile Val Ala His Ala Val Ser
    610                 615                 620
His Val Arg Arg Ser Pro Pro Ser Lys Leu Thr Leu Asn Met Gly Tyr
625                 630                 635                 640
Arg Pro Asp Ile Trp Arg Val Thr Pro His Cys Asn Met Glu Ile Ile
                645                 650                 655
Ala Asn Gly Val Lys Thr Pro Ile Gln Gly Ser Pro Leu Ala Arg His
            660                 665                 670
Ala Phe Phe Leu Glu Val His Asp Thr Leu Tyr Ile His His Phe Gly
        675                 680                 685
Arg Ala Tyr Met Asn Tyr Ser Leu Asp Ala Arg Arg Arg Gln Thr Ala
    690                 695                 700
His Phe Val Ser Met Gly Leu Asn Arg Ile Phe
705                 710                 715
```

<210> 330
<211> 38
<212> DNA
<213> Chlymadia trachomatis

<400> 330
gagagcggcc gctcatgaaa tggctgtcag ctactgcg 38

<210> 331

<211> 34
<212> DNA
<213> Chlymadia trachomatis

<400> 331
gagcggccgc ttacttaatg cgaatttctt caag 34

<210> 332
<211> 1557
<212> DNA
<213> Chlymadia trachomatis

<400> 332
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct catgaaatgg ctgtcagcta ctgcggtgtt tgctgctgtt 480
ctcccctcag tttcagggtt ttgcttccca gaacctaaag aattaaattt ctctcgcgta 540
gaaacttctt cctctaccac ttttactgaa acaattggag aagctggggc agaatatatc 600
gtctctggta acgcatcttt cacaaaattt accaacattc ctactaccga tacaacaact 660
cccacgaact caaactcctc tagctctagc ggagaaactg cttccgtttc tgaggatagt 720
gactctacaa caacgactcc tgatcctaaa ggtggcggcg ccttttataa cgcgcactcc 780
ggagttttgt cctttatgac acgatcagga acagaaggtt ccttaactct gtctgagata 840
aaaatgactg gtgaaggcgg tgctatcttc tctcaaggag agctgctatt tacagatctg 900
acaagtctaa ccatccaaaa taacttatcc cagctatccg gaggagcgat tttggagga 960
tctacaatct ccctatcagg gattactaaa gcgactttct cctgcaactc tgcagaagtt 1020
cctgctcctg ttaagaaacc tacagaacct aaagctcaaa cagcaagcga aacgtcgggt 1080
tctagtagtt ctagcggaaa tgattcggtg tcttccccca gttccagtag agctgaaccc 1140
gcagcagcta atcttcaaag tcactttatt tgtgctacag ctactcctgc tgctcaaacc 1200
gatacagaaa catcaactcc ctctcataag ccaggatctg gggagctat ctatgctaaa 1260
ggcgacctta ctatcgcaga ctctcaagag gtactattct caataaataa agctactaaa 1320
gatggaggag cgatctttgc tgagaaagat gtttctttcg agaatattac atcattaaaa 1380
gtacaaacta acggtgctga agaaaaggga ggagctatct atgctaaagg tgacctctca 1440
attcaatctt ctaaacagag tctttttaat tctaactaca gtaaacaagg tggggggct 1500
ctatatgttg aaggaggtat aaacttccaa gatcttgaag aaattcgcat taagtaa 1557

<210> 333
<211> 518
<212> PRT
<213> Chlymadia trachomatis

<400> 333
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr

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        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val
145                 150                 155                 160
Leu Pro Ser Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn
                165                 170                 175
Phe Ser Arg Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile
            180                 185                 190
Gly Glu Ala Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr
        195                 200                 205
Lys Phe Thr Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser
    210                 215                 220
Asn Ser Ser Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser
225                 230                 235                 240
Asp Ser Thr Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr
                245                 250                 255
Asn Ala His Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu
            260                 265                 270
Gly Ser Leu Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Gly Ala
        275                 280                 285
Ile Phe Ser Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr
    290                 295                 300
Ile Gln Asn Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Gly
305                 310                 315                 320
Ser Thr Ile Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn
                325                 330                 335
Ser Ala Glu Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala
            340                 345                 350
Gln Thr Ala Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp
        355                 360                 365
Ser Val Ser Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn
    370                 375                 380
Leu Gln Ser His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr
385                 390                 395                 400
Asp Thr Glu Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala
                405                 410                 415
Ile Tyr Ala Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu
            420                 425                 430
Phe Ser Ile Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu
        435                 440                 445
Lys Asp Val Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn
    450                 455                 460
Gly Ala Glu Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser
465                 470                 475                 480
Ile Gln Ser Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln
                485                 490                 495
Gly Gly Gly Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu
            500                 505                 510
Glu Glu Ile Arg Ile Lys
        515
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<210> 334
<211> 37
<212> DNA
<213> Chlymadia trachomatis

<400> 334
gagagcggcc gctcggtgac ctctcaattc aatcttc 37

<210> 335

<211> 39
<212> DNA
<213> Chlamydia trachomatis

<400> 335
gagagcggcc gcttagttct ctgttacaga taaggagac 39

<210> 336
<211> 1758
<212> DNA
<213> Chlymadia trachomatis

<400> 336
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct cggtgacctc tcaattcaat cttctaaaca gagtcttttt 480
aattctaact acagtaaaca aggtgggggg gctctatatg ttgaaggagg tataaacttc 540
caagatcttg aagaaattcg cattaagtac aataaagctg gaacgttcga aacaaaaaaa 600
atcactttac cttctttaaa agctcaagca tctgcaggaa atgcagatgc ttgggcctct 660
tcctctcctc aatctggttc tggagcaact acagtctccg actcaggaga ctctagctct 720
ggctcagact cggatacctc agaaacagtt ccagtcacag ctaaaggcgg tgggctttat 780
actgataaga atctttcgat tactaacatc acaggaatta tcgaaattgc aaataacaaa 840
gcgacagatg ttggaggtgg tgcttacgta aaaggaaccc ttacttgtga aaactctcac 900
cgtctacaat ttttgaaaaa ctcttccgat aaacaaggtg gaggaatcta cggagaagac 960
aacatcaccc tatctaattt gacagggaag actctattcc aagagaatac tgccaaagaa 1020
gagggcggtg gactcttcat aaaaggtaca gataaagctc ttacaatgac aggactggat 1080
agtttctgtt taattaataa cacatcagaa aaacatggtg gtggagcctt tgttaccaaa 1140
gaaatctctc agacttacac ctctgatgtg gaaacaattc caggaatcac gcctgtacat 1200
ggtgaaacag tcattactgg caataaatct acaggaggta atggtggagg cgtgtgtaca 1260
aaacgtcttg ccttatctaa ccttcaaagc atttctatat ccgggaattc tgcagcagaa 1320
aatggtggtg gagcccacac atgcccagat agcttcccaa cggcggatac tgcagaacag 1380
cccgcagcag cttctgccgc gacgtctact cccaaatctg ccccggtctc aactgctcta 1440
agcacacctt catcttctac cgtctcttca ttaaccttac tagcagcctc ttcacaagcc 1500
tctcctgcaa cctctaataa ggaaactcaa gatcctaatg ctgatacaga cttattgatc 1560
gattatgtag ttgatacgac tatcagcaaa aacactgcta agaaaggcgg tggaatctat 1620
gctaaaaaag ccaagatgtc ccgcatagac caactgaata tctctgagaa ctccgctaca 1680
gagataggtg gaggtatctg ctgtaaagaa tctttagaac tagatgctct agtctcctta 1740
tctgtaacag agaactaa 1758

<210> 337
<211> 585
<212> PRT
<213> Chlamydia trachomatis

<400> 337
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1   5   10   15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20   25   30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35   40   45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50   55   60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65   70   75   80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr

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                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Gly Asp Leu Ser Ile Gln Ser Ser Lys Gln Ser Leu Phe
145                 150                 155                 160
Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly Ala Leu Tyr Val Glu Gly
                165                 170                 175
Gly Ile Asn Phe Gln Asp Leu Glu Glu Ile Arg Ile Lys Tyr Asn Lys
            180                 185                 190
Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr Leu Pro Ser Leu Lys Ala
        195                 200                 205
Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp Ala Ser Ser Ser Pro Gln
    210                 215                 220
Ser Gly Ser Gly Ala Thr Thr Val Ser Asp Ser Gly Asp Ser Ser Ser
225                 230                 235                 240
Gly Ser Asp Ser Asp Thr Ser Glu Thr Val Pro Val Thr Ala Lys Gly
                245                 250                 255
Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser Ile Thr Asn Ile Thr Gly
            260                 265                 270
Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr Asp Val Gly Gly Gly Ala
        275                 280                 285
Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn Ser His Arg Leu Gln Phe
    290                 295                 300
Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly Gly Ile Tyr Gly Glu Asp
305                 310                 315                 320
Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys Thr Leu Phe Gln Glu Asn
                325                 330                 335
Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe Ile Lys Gly Thr Asp Lys
            340                 345                 350
Ala Leu Thr Met Thr Gly Leu Asp Ser Phe Cys Leu Ile Asn Asn Thr
        355                 360                 365
Ser Glu Lys His Gly Gly Gly Ala Phe Val Thr Lys Glu Ile Ser Gln
    370                 375                 380
Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile Thr Pro Val His
385                 390                 395                 400
Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly Gly Asn Gly Gly
                405                 410                 415
Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu Gln Ser Ile Ser
            420                 425                 430
Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly Ala His Thr Cys
        435                 440                 445
Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln Pro Ala Ala Ala
    450                 455                 460
Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala Pro Val Ser Thr Ala Leu
465                 470                 475                 480
Ser Thr Pro Ser Ser Ser Thr Val Ser Ser Leu Thr Leu Leu Ala Ala
                485                 490                 495
Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Lys Glu Thr Gln Asp Pro
            500                 505                 510
Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val Val Asp Thr Thr Ile
        515                 520                 525
Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile Tyr Ala Lys Lys Ala
    530                 535                 540
Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser Glu Asn Ser Ala Thr
545                 550                 555                 560
Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu Ser Leu Glu Leu Asp Ala
                565                 570                 575
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Leu Val Ser Leu Ser Val Thr Glu Asn
580 585

<210> 338
<211> 38
<212> DNA
<213> Chlamydai trachomatis

<400> 338
gagagcggcc gctcgaccaa ctgaatatct ctgagaac 38

<210> 339
<211> 35
<212> DNA
<213> Chlamydia trachomatis

<400> 339
gagagcggcc gcttaagaga ctacgtggag ttctg 35

<210> 340
<211> 1965
<212> DNA
<213> Chlamydia trachomatis

<400> 340
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct cgaccaactg aatatctctg agaactccgc tacagagata 480
ggtggaggta tctgctgtaa agaatcttta gaactagatg ctctagtctc cttatctgta 540
acagagaacc ttgttgggaa agaaggtgga ggcttacatg ctaaaactgt aaatatttct 600
aatctgaaat caggcttctc tttctcgaac aacaaagcaa actcctcatc cacaggagtc 660
gcaacaacag cttcagcacc tgctgcagct gctgcttccc tacaagcagc cgcagcagcc 720
gcaccatcat ctccagcaac accaacttat tcaggtgtag taggaggagc tatctatgga 780
gaaaaggtta cattctctca atgtagcggg acttgtcagt tctctgggaa ccaagctatc 840
gataacaatc cctcccaatc atcgttgaac gtacaaggag gagccatcta tgccaaaacc 900
tctttgtcta ttggatcttc cgatgctgga acctcctata ttttctcggg gaacagtgtc 960
tccactggga aatctcaaac aacagggcaa atagcgggag gagcgatcta ctcccctact 1020
gttacattga attgtcctgc gacattctct aacaatacag cctctatagc tacaccgaag 1080
acttcttctg aagatggatc ctcaggaaat tctattaaag ataccattgg aggagccatt 1140
gcagggacag ccattaccct atctggagtc tctcgatttt cagggaatac ggctgattta 1200
ggagctgcaa taggaactct agctaatgca aatacaccca gtgcaactag cggatctcaa 1260
aatagcatta cagaaaaaat tactttagaa aacggttctt ttatttttga aagaaaccaa 1320
gctaataaac gtggagcgat ttactctcct agcgtttcca ttaaagggaa taatattacc 1380
ttcaatcaaa atacatccac tcatgatgga agcgctatct actttacaaa agatgctacg 1440
attgagtctt taggatctgt tctttttaca ggaaataacg ttacagctac acaagctagt 1500
tctgcaacat ctggacaaaa tacaaatact gccaactatg ggcagccat ctttggagat 1560
ccaggaacca ctcaatcgtc tcaaacagat gccattttaa cccttcttgc ttcttctgga 1620
aacattactt ttagcaacaa cagtttacag aataaccaag gtgatactcc cgctagcaag 1680
ttttgtagta ttgcaggata cgtcaaactc tctctacaag ccgctaaagg gaagactatt 1740
agctttttcg attgtgtgca cacctctacc aaaaaaacag gttcaacaca aaacgtttat 1800
gaaactttag atattaataa agaagagaac agtaatccat atacaggaac tattgtgttc 1860
tcttctgaat tacatgaaaa caaatcttac atcccacaga atgcaatcct tcacaacgga 1920
actttagttc ttaaagagaa aacagaactc cacgtagtct cttaa 1965

<210> 341
<211> 654

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<212> PRT
<213> Chlamydia trachomatis

<400> 341
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1               5                   10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Asp Gln Leu Asn Ile Ser Glu Asn Ser Ala Thr Glu Ile
145                 150                 155                 160
Gly Gly Gly Ile Cys Cys Lys Glu Ser Leu Glu Leu Asp Ala Leu Val
                165                 170                 175
Ser Leu Ser Val Thr Glu Asn Leu Val Gly Lys Glu Gly Gly Gly Leu
            180                 185                 190
His Ala Lys Thr Val Asn Ile Ser Asn Leu Lys Ser Gly Phe Ser Phe
        195                 200                 205
Ser Asn Asn Lys Ala Asn Ser Ser Ser Thr Gly Val Ala Thr Thr Ala
    210                 215                 220
Ser Ala Pro Ala Ala Ala Ala Ala Ser Leu Gln Ala Ala Ala Ala Ala
225                 230                 235                 240
Ala Pro Ser Ser Pro Ala Thr Pro Thr Tyr Ser Gly Val Val Gly Gly
                245                 250                 255
Ala Ile Tyr Gly Glu Lys Val Thr Phe Ser Gln Cys Ser Gly Thr Cys
            260                 265                 270
Gln Phe Ser Gly Asn Gln Ala Ile Asp Asn Asn Pro Ser Gln Ser Ser
        275                 280                 285
Leu Asn Val Gln Gly Gly Ala Ile Tyr Ala Lys Thr Ser Leu Ser Ile
    290                 295                 300
Gly Ser Ser Asp Ala Gly Thr Ser Tyr Ile Phe Ser Gly Asn Ser Val
305                 310                 315                 320
Ser Thr Gly Lys Ser Gln Thr Thr Gly Gln Ile Ala Gly Gly Ala Ile
                325                 330                 335
Tyr Ser Pro Thr Val Thr Leu Asn Cys Pro Ala Thr Phe Ser Asn Asn
            340                 345                 350
Thr Ala Ser Ile Ala Thr Pro Lys Thr Ser Ser Glu Asp Gly Ser Ser
        355                 360                 365
Gly Asn Ser Ile Lys Asp Thr Ile Gly Gly Ala Ile Ala Gly Thr Ala
    370                 375                 380
Ile Thr Leu Ser Gly Val Ser Arg Phe Ser Gly Asn Thr Ala Asp Leu
385                 390                 395                 400
Gly Ala Ala Ile Gly Thr Leu Ala Asn Ala Asn Thr Pro Ser Ala Thr
                405                 410                 415
Ser Gly Ser Gln Asn Ser Ile Thr Glu Lys Ile Thr Leu Glu Asn Gly
            420                 425                 430
Ser Phe Ile Phe Glu Arg Asn Gln Ala Asn Lys Arg Gly Ala Ile Tyr
        435                 440                 445
Ser Pro Ser Val Ser Ile Lys Gly Asn Asn Ile Thr Phe Asn Gln Asn
```

```
    450                 455                 460
Thr Ser Thr His Asp Gly Ser Ala Ile Tyr Phe Thr Lys Asp Ala Thr
465                 470                 475                 480
Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Asn Val Thr Ala
                485                 490                 495
Thr Gln Ala Ser Ser Ala Thr Ser Gly Gln Asn Thr Asn Thr Ala Asn
            500                 505                 510
Tyr Gly Ala Ala Ile Phe Gly Asp Pro Gly Thr Thr Gln Ser Ser Gln
        515                 520                 525
Thr Asp Ala Ile Leu Thr Leu Leu Ala Ser Ser Gly Asn Ile Thr Phe
    530                 535                 540
Ser Asn Asn Ser Leu Gln Asn Asn Gln Gly Asp Thr Pro Ala Ser Lys
545                 550                 555                 560
Phe Cys Ser Ile Ala Gly Tyr Val Lys Leu Ser Leu Gln Ala Ala Lys
                565                 570                 575
Gly Lys Thr Ile Ser Phe Phe Asp Cys Val His Thr Ser Thr Lys Lys
            580                 585                 590
Thr Gly Ser Thr Gln Asn Val Tyr Glu Thr Leu Asp Ile Asn Lys Glu
        595                 600                 605
Glu Asn Ser Asn Pro Tyr Thr Gly Thr Ile Val Phe Ser Ser Glu Leu
    610                 615                 620
His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Ala Ile Leu His Asn Gly
625                 630                 635                 640
Thr Leu Val Leu Lys Glu Lys Thr Glu Leu His Val Val Ser
                645                 650
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<210> 342
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 342
gagagcggcc gctcggaact attgtgttct cttctg 36

<210> 343
<211> 35
<212> DNA
<213> Chlamydia trachomatis

<400> 343
gagagcggcc gcttagaaga tcatgcgagc accgc 35

<210> 344
<211> 2103
<212> DNA
<213> Chlamydia trachomatis

<400> 344
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atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg     60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc    120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac    180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc    240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac    300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc    360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat    420
ccatcacact ggcggccgct cggaactatt gtgttctctt ctgaattaca tgaaaacaaa    480
tcttacatcc cacagaatgc aatccttcac aacggaactt tagttcttaa agagaaaaca    540
gaactccacg tagtctcttt tgagcagaaa gaagggtcta aattaattat ggaacccgga    600
gctgtgttat ctaaccaaaa catagctaac ggagctctag ctatcaatgg gttaacgatt    660
gatctttcca gtatggggac tcctcaagca ggggaaatct tctctcctcc agaattacgt    720
atcgttgcca cgacctctag tgcatccgga ggaagcgggg tcagcagtag tataccaaca    780
```

aatcctaaaa ggatttctgc agcagtgcct tcaggttctg ccgcaactac tccaactatg 840
agcgagaaca aagttttcct aacaggagac cttactttaa tagatcctaa tggaaacttt 900
taccaaaacc ctatgttagg aagcgatcta gatgtaccac taattaagct tccgactaac 960
acaagtgacg tccaagtcta tgatttaact ttatctgggg atcttttccc tcagaaaggg 1020
tacatgggaa cctggacatt agattctaat ccacaaacag ggaaacttca agccagatgg 1080
acattcgata cctatcgtcg ctgggtatac atacctaggg ataatcattt ttatgcgaac 1140
tctatcttag gctcccaaaa ctcaatgatt gttgtgaagc aagggcttat caacaacatg 1200
ttgaataatg cccgcttcga tgatatcgct tacaataact tctgggtttc aggagtagga 1260
actttcttag ctcaacaagg aactcctctt tccgaagaat tcagttacta cagccgcgga 1320
acttcagttg ccatcgatgc caaacctaga caagatttta tcctaggagc tgcatttagt 1380
aagatagtgg ggaaaaccaa agccatcaaa aaaatgcata attacttcca taagggctct 1440
gagtactctt accaagcttc tgtctatgga ggtaaattcc tgtatttctt gctcaataag 1500
caacatggtt gggcacttcc tttcctaata caaggagtcg tgtcctatgg acatattaaa 1560
catgatacaa caacacttta cccttctatc catgaaagaa ataaaggaga ttgggaagat 1620
ttaggatggt tagcggatct tcgtatctct atggatctta aagaaccttc taaagattct 1680
tctaaacgga tcactgtcta tggggaactc gagtattcca gcattcgcca gaaacagttc 1740
acagaaatcg attacgatcc aagacacttc gatgattgtg cttacagaaa tctgtcgctt 1800
cctgtgggat gcgctgtcga aggagctatc atgaactgta atattcttat gtataataag 1860
cttgcattag cctacatgcc ttctatctac agaaataatc ctgtctgtaa atatcgggta 1920
ttgtcttcga atgaagctgg tcaagttatc tgcggagtgc caactagaac ctctgctaga 1980
gcagaataca gtactcaact atatcttggt cccttctgga ctctctacgg aaactatact 2040
atcgatgtag gcatgtatac gctatcgcaa atgactagct gcggtgctcg catgatcttc 2100
taa 2103

<210> 345
<211> 700
<212> PRT
<213> Chlamydia trachomatis

<400> 345
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
100 105 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
115 120 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
130 135 140
Arg Pro Leu Gly Thr Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys
145 150 155 160
Ser Tyr Ile Pro Gln Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu
165 170 175
Lys Glu Lys Thr Glu Leu His Val Val Ser Phe Glu Gln Lys Glu Gly
180 185 190
Ser Lys Leu Ile Met Glu Pro Gly Ala Val Leu Ser Asn Gln Asn Ile
195 200 205
Ala Asn Gly Ala Leu Ala Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser
210 215 220
Met Gly Thr Pro Gln Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg
225 230 235 240
Ile Val Ala Thr Thr Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser

```
                    245                     250                     255
Ser Ile Pro Thr Asn Pro Lys Arg Ile Ser Ala Ala Val Pro Ser Gly
                260                 265                 270
Ser Ala Ala Thr Thr Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr
            275                 280                 285
Gly Asp Leu Thr Leu Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro
    290                 295                 300
Met Leu Gly Ser Asp Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn
305                 310                 315                 320
Thr Ser Asp Val Gln Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe
                325                 330                 335
Pro Gln Lys Gly Tyr Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln
            340                 345                 350
Thr Gly Lys Leu Gln Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp
        355                 360                 365
Val Tyr Ile Pro Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly
    370                 375                 380
Ser Gln Asn Ser Met Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met
385                 390                 395                 400
Leu Asn Asn Ala Arg Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val
                405                 410                 415
Ser Gly Val Gly Thr Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu
            420                 425                 430
Glu Phe Ser Tyr Tyr Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys
        435                 440                 445
Pro Arg Gln Asp Phe Ile Leu Gly Ala Ala Phe Ser Lys Ile Val Gly
    450                 455                 460
Lys Thr Lys Ala Ile Lys Lys Met His Asn Tyr Phe His Lys Gly Ser
465                 470                 475                 480
Glu Tyr Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe
                485                 490                 495
Leu Leu Asn Lys Gln His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly
            500                 505                 510
Val Val Ser Tyr Gly His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro
        515                 520                 525
Ser Ile His Glu Arg Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu
    530                 535                 540
Ala Asp Leu Arg Ile Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser
545                 550                 555                 560
Ser Lys Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg
                565                 570                 575
Gln Lys Gln Phe Thr Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp
            580                 585                 590
Cys Ala Tyr Arg Asn Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly
        595                 600                 605
Ala Ile Met Asn Cys Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala
    610                 615                 620
Tyr Met Pro Ser Ile Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val
625                 630                 635                 640
Leu Ser Ser Asn Glu Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg
                645                 650                 655
Thr Ser Ala Arg Ala Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe
            660                 665                 670
Trp Thr Leu Tyr Gly Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu
        675                 680                 685
Ser Gln Met Thr Ser Cys Gly Ala Arg Met Ile Phe
    690                 695                 700
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<210> 346
<211> 37
<212> DNA

<213> Chlamydia trachomatis

<400> 346
gagagcggcc gctcatgaaa tttatgtcag ctactgc 37

<210> 347
<211> 37
<212> DNA
<213> Chlamydia trachomatis

<400> 347
gagagcggcc gcttaccctg taattccagt gatggtc 37

<210> 348
<211> 1464
<212> DNA
<213> Chlamydia trachomatis

<400> 348
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct catgaaattt atgtcagcta ctgctgtatt tgctgcagta 480
ctctcctccg ttactgaggc gagctcgatc caagatcaaa taaagaatac cgactgcaat 540
gttagcaaag taggatattc aacttctcaa gcatttactg atatgatgct agcagacaac 600
acagagtatc gagctgctga tagtgtttca ttctatgact tttcgacatc ttccggatta 660
cctagaaaac atcttagtag tagtagtgaa gcttctccaa cgacagaagg agtgtcttca 720
tcttcatctg gagaaaatac tgagaattca caagattcag ctccctcttc tggagaaact 780
gataagaaaa cagaagaaga actagacaat ggcggaatca tttatgctag agagaaacta 840
actatctcag aatctcagga ctctctctct aatccaagca tagaactcca tgacaatagt 900
tttttcttcg gagaaggtga agttatcttt gatcacagag ttgccctcaa aaacggagga 960
gctatttatg gagagaaaga ggtagtcttt gaaaacataa aatctctact agtagaagta 1020
aatatctcgg tcgagaaagg gggtagcgtc tatgcaaaag aacgagtatc tttagaaaat 1080
gttaccgaag caaccttctc ctccaatggt ggggaacaag gtggtggtgg aatctattca 1140
gaacaagata tgttaatcag tgattgcaac aatgtacatt tccaagggaa tgctgcagga 1200
gcaacagcag taaaacaatg tctggatgaa gaaatgatcg tattgctcac agaatgcgtt 1260
gatagcttat ccgaagatac actggatagc actccagaaa cggaacagac taagtcaaat 1320
ggaaatcaag atggttcgtc tgaaacaaaa gatacacaag tatcagaatc accagaatca 1380
actcctagcc ccgacgatgt tttaggtaaa ggtggtggta tctatacaga aaaatctttg 1440
accatcactg gaattacagg gtaa 1464

<210> 349
<211> 487
<212> PRT
<213> Chlamydia trachomatis

<400> 349
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80

```
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val
145                 150                 155                 160
Leu Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn
                165                 170                 175
Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe
            180                 185                 190
Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser
        195                 200                 205
Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His
    210                 215                 220
Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser
225                 230                 235                 240
Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser
                245                 250                 255
Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly
            260                 265                 270
Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser
        275                 280                 285
Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Phe Gly
    290                 295                 300
Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly
305                 310                 315                 320
Ala Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu
                325                 330                 335
Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala
            340                 345                 350
Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser
        355                 360                 365
Asn Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met
    370                 375                 380
Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly
385                 390                 395                 400
Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu
                405                 410                 415
Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro
            420                 425                 430
Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu
        435                 440                 445
Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro
    450                 455                 460
Asp Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser Leu
465                 470                 475                 480
Thr Ile Thr Gly Ile Thr Gly
                485
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<210> 350
<211> 37
<212> DNA
<213> Chlamydia trachomatis

<400> 350
gagagcggcc gctcgataca caagtatcag aatcacc 37

<210> 351
<211> 37
<212> DNA
<213> Chlamydia trachomatis

<400> 351
gagagcggcc gcttaagagg acgatgagac actctcg 37

<210> 352
<211> 1752
<212> DNA
<213> Chlamydia trachomatis

<400> 352
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct cgatacacaa gtatcagaat caccagaatc aactcctagc 480
cccgacgatg ttttaggtaa aggtggtggt atctatacag aaaaatcttt gaccatcact 540
ggaattacag ggactataga ttttgtcagt aacatagcta ccgattctgg agcaggtgta 600
ttcactaaag aaaacttgtc ttgcaccaac acgaatagcc tacagttttt gaaaaactcg 660
gcaggtcaac atggaggagg agcctacgtt actcaaacca tgtctgttac taatacaact 720
agtgaaagta taactactcc ccctctcgta ggagaagtga ttttctctga aaatacagct 780
aaagggcacg gtggtggtat ctgcactaac aaactttctt tatctaattt aaaaacggtg 840
actctcacta aaaactctgc aaaggagtct ggaggagcta tttttacaga tctagcgtct 900
ataccaacaa cagatacccc agagtcttct accccctctt cctcctcgcc tgcaagcact 960
cccgaagtag ttgcttctgc taaaataaat cgattctttg cctctacggc agaaccggca 1020
gccccttctc taacagaggc tgagtctgat caaacggatc aaacagaaac ttctgatact 1080
aatagcgata tagacgtgtc gattgagaac attttgaatg tcgctatcaa tcaaaacact 1140
tctgcgaaaa aaggaggggc tatttacggg aaaaaagcta aactttcccg tattaacaat 1200
cttgaacttt cagggaattc atcccaggat gtaggaggag gtctctgttt aactgaaagc 1260
gtagaatttg atgcaattgg atcgctctta tcccactata actctgctgc taaagaaggt 1320
ggggttattc attctaaaac ggttactcta tctaacctca agtctacctt cacttttgca 1380
gataacactg ttaaagcaat agtagaaagc actcctgaag ctccagaaga gattcctcca 1440
gtagaaggag aagagtctac agcaacagaa aatccgaatt ctaatacaga aggaagttcg 1500
gctaacacta accttgaagg atctcaaggg gatactgctg atacagggac tggtgttgtt 1560
aacaatgagt ctcaagacac atcagatact ggaaacgctg aatctggaga acaactacaa 1620
gattctacac aatctaatga agaaaatacc cttcccaata gtagtattga tcaatctaac 1680
gaaaacacag acgaatcatc tgatagccac actgaggaaa taactgacga gagtgtctca 1740
tcgtcctctt aa 1752

<210> 353
<211> 583
<212> PRT
<213> Chlamydia trachomatis

<400> 353
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80

```
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130                 135                 140
Arg Pro Leu Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser
145                 150                 155                 160
Pro Asp Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser
                165                 170                 175
Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile
            180                 185                 190
Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys
        195                 200                 205
Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His
    210                 215                 220
Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr
225                 230                 235                 240
Ser Glu Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser
                245                 250                 255
Glu Asn Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys Leu
            260                 265                 270
Ser Leu Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys
        275                 280                 285
Glu Ser Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr
    290                 295                 300
Asp Thr Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser Thr
305                 310                 315                 320
Pro Glu Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr
                325                 330                 335
Ala Glu Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr
            340                 345                 350
Asp Gln Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile
        355                 360                 365
Glu Asn Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys
    370                 375                 380
Gly Gly Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn
385                 390                 395                 400
Leu Glu Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys
                405                 410                 415
Leu Thr Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His
            420                 425                 430
Tyr Asn Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val
        435                 440                 445
Thr Leu Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val
    450                 455                 460
Lys Ala Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro
465                 470                 475                 480
Val Glu Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr
                485                 490                 495
Glu Gly Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr
            500                 505                 510
Ala Asp Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser
        515                 520                 525
Asp Thr Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln
    530                 535                 540
Ser Asn Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn
545                 550                 555                 560
Glu Asn Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp
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565 570 575
Glu Ser Val Ser Ser Ser Ser
580

<210> 354
<211> 39
<212> DNA
<213> Chlamydia trachomatis

<400> 354
gagagcggcc gctcgatcaa tctaacgaaa acacagacg 39

<210> 355
<211> 36
<212> DNA
<213> Chlamydia trachomatis

<400> 355
gagagcggcc gcttagacca aagctccatc agcaac 36

<210> 356
<211> 2052
<212> DNA
<213> Chlamydia trachomatis

<400> 356
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt ctgcagatat 420
ccatcacact ggcggccgct cgatcaatct aacgaaaaca cagacgaatc atctgatagc 480
cacactgagg aaataactga cgagagtgtc tcatcgtcct ctaaaagtgg atcatctact 540
cctcaagatg gaggagcagc ttcttcaggg gctccctcag gagatcaatc tatctctgca 600
aacgcttgtt tagctaaaag ctatgctgcg agtactgata gctcccctgt atctaattct 660
tcaggttcag acgttactgc atcttctgat aatccagact cttcctcatc tggagatagc 720
gctggagact ctgaaggacc gactgagcca gaagctggtt ctacaacaga aactcctact 780
ttaataggag gaggwgctat ctatggagaa actgttaaga ttgagaactt ctctggccaa 840
ggaatatttt ctggaaacaa agctatcgat aacaccacag aaggctcctc ttccaaatct 900
aacgtcctcg gaggtgcggt ctatgctaaa acattgttta atctcgatag cgggagctct 960
agacgaactg tcaccttctc cgggaatact gtctcttctc aatctacaac aggtcaggtt 1020
gctggaggag ctatctactc tcctactgta accattgcta ctcctgtagt attttctaaa 1080
aactctgcaa caaacaatgc taataacgct acagatactc agagaaaaga cacctttgga 1140
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acaacctcag gagatgtaac aaaatatggt gctgctatct ttggacaaat agcaagctca 1560
aacggatctc agacggataa ccttcccctg aaactcattg cttcaggagg aaatatttgt 1620
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attgcgggag atgttaaatt aaccatgcaa gctgcaaaag ggaaaacgat cagtttcttt 1740
gatgcaatcc ggacctctac taagaaaaca ggtacacagg caactgccta cgatactctc 1800
gatattaata aatctgagga ttcagaaact gtaaactctg cgtttacagg aacgattctg 1860
ttctcctctg aattacatga aaataaatcc tatattccac aaaacgtagt tctacacagt 1920
ggatctcttg tattgaagcc aaataccgag cttcatgtca tttcttttga gcagaaagaa 1980
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gctttggtct aa 2052

<210> 357
<211> 683
<212> PRT
<213> Chlamydia trachomatis

<400> 357
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1   5   10   15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20   25   30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
        35   40   45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50   55   60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65   70   75   80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85   90   95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100   105   110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115   120   125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Cys Arg Tyr Pro Ser His Trp
    130   135   140
Arg Pro Leu Asp Gln Ser Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser
145   150   155   160
His Thr Glu Glu Ile Thr Asp Glu Ser Val Ser Ser Ser Ser Lys Ser
                165   170   175
Gly Ser Ser Thr Pro Gln Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro
            180   185   190
Ser Gly Asp Gln Ser Ile Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr
        195   200   205
Ala Ala Ser Thr Asp Ser Ser Pro Val Ser Asn Ser Ser Gly Ser Asp
    210   215   220
Val Thr Ala Ser Ser Asp Asn Pro Asp Ser Ser Ser Ser Gly Asp Ser
225   230   235   240
Ala Gly Asp Ser Glu Gly Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr
                245   250   255
Glu Thr Pro Thr Leu Ile Gly Gly Gly Ala Ile Tyr Gly Glu Thr Val
            260   265   270
Lys Ile Glu Asn Phe Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala
        275   280   285
Ile Asp Asn Thr Thr Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly
    290   295   300
Gly Ala Val Tyr Ala Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser
305   310   315   320
Arg Arg Thr Val Thr Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr
                325   330   335
Thr Gly Gln Val Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile
            340   345   350
Ala Thr Pro Val Val Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn
        355   360   365
Asn Ala Thr Asp Thr Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile Gly
    370   375   380
Ala Thr Ser Ala Val Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn
385   390   395   400
Val Ala Asp Leu Gly Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn
                405   410   415
Thr Glu Thr Val Lys Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn
            420   425   430

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Lys Ala Leu Lys Arg Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys
        435                 440                 445
Ala Tyr Thr Ala Thr Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser
    450                 455                 460
Ala Ile Tyr Phe Thr Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val
465                 470                 475                 480
Leu Phe Thr Gly Asn Leu Val Thr Pro Thr Leu Ser Thr Thr Thr Glu
                485                 490                 495
Gly Thr Pro Ala Thr Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala
            500                 505                 510
Ile Phe Gly Gln Ile Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu
        515                 520                 525
Pro Leu Lys Leu Ile Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn Asn
    530                 535                 540
Glu Tyr Arg Pro Thr Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys Ser
545                 550                 555                 560
Ile Ala Gly Asp Val Lys Leu Thr Met Gln Ala Ala Lys Gly Lys Thr
                565                 570                 575
Ile Ser Phe Phe Asp Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly Thr
            580                 585                 590
Gln Ala Thr Ala Tyr Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp Ser
        595                 600                 605
Glu Thr Val Asn Ser Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser Glu
    610                 615                 620
Leu His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Val Val Leu His Ser
625                 630                 635                 640
Gly Ser Leu Val Leu Lys Pro Asn Thr Glu Leu His Val Ile Ser Phe
                645                 650                 655
Glu Gln Lys Glu Gly Ser Ser Leu Val Met Thr Pro Gly Ser Val Leu
            660                 665                 670
Ser Asn Gln Thr Val Ala Asp Gly Ala Leu Val
        675                 680
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<210> 358
<211> 1248
<212> DNA
<213> Chlamydia

<400> 358

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catatgcatc accatcacca tcaccctcca gaatcgggct taatcatagc cattcacgat 60
gatcctcgct ctctttctcc agaaaaagga gaaaatgctt tccatttttc tttgtccaag 120
gctttatttg ctactctctt cagagaagag ctctctggat taacccctgc tctggtctcc 180
tcctatcaag tttcggaaga cgggcggttt tatcgttttt gtattcgtaa agatgctaag 240
tggagtgacg gctctctttt acttgcagaa gatgtaatag ctgcttggga acacactaaa 300
caagctgggc gatattccct actttttgaa aagctatctt ttcgagcctc ttcttcttcg 360
gaaatcctta ttgaactcaa agaacccgag cctcaactat tggcgatatt agcctctccg 420
tttttgctg tgtatcgtcc agaaaatcct tttctttctt ctggaccttt tatgccaaaa 480
acctatgtgc aagggcaaac gctcgttcta caaaaaaacc cttattacta tgaccatgcg 540
catgtggaat tacattccat agactttcgc atcattccca acatttacac agctctacac 600
ctcttaagaa gaggtgacgt ggattgggtg gggcagcctt ggcaccaagg gattcctttt 660
gagcttcgga ctacctctgc tctctacacc cattaccctg tagatggcac attctggctt 720
attcttaatc ccaaagatcc tgtactttcc tctctatcta atcgtcagcg attgattgct 780
gccatccaaa aggaaaaact ggtgaagcaa gctttaggaa cacaatatcg agtagctgaa 840
agctctccat ctccagaggg aatcatagct catcaagaag cttctactcc ttttcctggg 900
aaaattactt tgatatatcc caataatatt acgcgctgtc agcgtttggc cgaggtattg 960
caagaacaat gccgagacgc aggtatccag ctgactcttg aaggactcga ataccatgta 1020
tttgttcaaa aacgagccac tcaagatttc tctgtctcca cagcaacttc tatagctttc 1080
catcccttg ctaaatctaa gttcgatcaa acggctctag acaatttcac ttgtctgccc 1140
ttgtaccaca tagaatatga ttatattttg agcagaccgc tagatcaaat tgttcactat 1200
ccttcaggta gtgttgattt gacctatgca cactttcact aggaattc             1248
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<210> 359
<211> 1311
<212> DNA
<213> Chlamydia

<400> 359
catatgcatc accatcacca tcacatgtat gttcgctcta tcttttttag tattatcgcc 60
ttcctaacgg tcggatgctc cttttctcct ccagaatcgg gcttaatcat agccattcac 120
gatgatcctc gctctctttc tccagaaaaa ggagaaaatg ctttccattt ttctttgtcc 180
aaggctttat ttgctactct cttcagagaa gagctctctg gattaacccc tgctctggtc 240
tcctcctatc aagtttcgga agacgggcgg ttttatcgtt tttgtattcg taaagatgct 300
aagtggagtg acggctctct tttacttgca gaagatgtaa tagctgcttg ggaacacact 360
aaacaagctg ggcgatattc cctacttttt gaaaagctat cttttcgagc ctcttcttct 420
tcggaaatcc ttattgaact caaagaaccc gagcctcaac tattggcgat attagcctct 480
ccgtttttttg ctgtgtatcg tccagaaaat ccttttcttt cttctggacc ttttatgcca 540
aaaacctatg tgcaagggca aacgctcgtt ctacaaaaaa acccttatta ctatgaccat 600
gcgcatgtgg aattacattc catagacttt cgcatcattc ccaacattta cacagctcta 660
cacctcttaa gaagaggtga cgtggattgg gtggggcagc cttggcacca agggattcct 720
tttgagcttc ggactacctc tgctctctac acccattacc ctgtagatgg cacattctgg 780
cttattctta atcccaaaga tcctgtactt tcctctctat ctaatcgtca gcgattgatt 840
gctgccatcc aaaaggaaaa actggtgaag caagctttag gaacacaata tcgagtagct 900
gaaagctctc catctccaga gggaatcata gctcatcaag aagcttctac tccttttcct 960
gggaaaatta ctttgatata tcccaataat attacgcgct gtcagcgttt ggccgaggta 1020
ttgcaagaac aatgccgaga cgcaggtatc cagctgactc ttgaaggact cgaataccat 1080
gtatttgttc aaaaacgagc cactcaagat ttctctgtct ccacagcaac ttctatagct 1140
ttccatcccc ttgctaaatc taagttcgat caaacggctc tagacaattt cacttgtctg 1200
cccttgtacc acatagaata tgattatatt ttgagcagac cgctagatca aattgttcac 1260
tatccttcag gtagtgttga tttgacctat gcacactttc actaggaatt c 1311

<210> 360
<211> 813
<212> DNA
<213> Chlamydia

<400> 360
atgcatcacc atcaccatca cggaaattct ggtttttatt tgtataacac tcaaaactgc 60
gtctttgctg ataatatcaa agttgggcaa atgacagagc cgctcaagga ccagcaaata 120
atccttggga caacatcaac acctgtcgca gccaaaatga cagcttctga tggaatatct 180
ttaacagtct ccaataatcc atcaaccaat gcttctatta caattggttt ggatgcggaa 240
aaagcttacc agcttattct agaaaagttg ggagatcaaa ttcttggtgg aattgctgat 300
actattgttg atagtacagt ccaagatatt ttagacaaaa tcacaacaga cccttctcta 360
ggtttgttga aagcttttaa caactttcca atcactaata aaattcaatg caacgggtta 420
ttcactccca ggaacattga aactttatta ggaggaactg aaataggaaa attcacagtc 480
acacccaaaa gctctgggag catgttctta gtctcagcag atattattgc atcaagaatg 540
gaaggcggcg ttgttctagc tttggtacga gaaggtgatt ctaagcccta cgcgattagt 600
tatggatact catcaggcgt tcctaattta tgtagtctaa gaaccagaat tattaataca 660
ggattgactc cgacaacgta ttcattacgt gtaggcggtt tagaaagcgg tgtggtatgg 720
gttaatgccc tttctaatgg caatgatatt ttaggaataa caaatacttc taatgtatct 780
tttttggagg taatacctca aacaaacgct taa 813

<210> 361
<211> 750
<212> DNA
<213> Chlamydia

<400> 361
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gattcgcttc aagagatctt gcaagaggct ttgccgcctc tgcaagaacg gagtgtggta 120
gttgtctctt caaagattgt gagtttatgt gaaggcgctg tcgctgatgc aagaatgtgc 180
aaagcagagt tgataaaaaa agaagcggat gcttatttgt tttgtgagaa aagcgggata 240

tatctaacga aaaaagaagg tattttgatt ccttctgcag ggattgatga atcgaatacg 300
gaccagcctt ttgttttata tcctaaagat attttgggat cgtgtaatcg catcggagaa 360
tggttaagaa attattttcg agtgaaagag ctaggcgtaa tcattacaga tagccatact 420
actccaatgc ggcgtggagt actgggtatc gggctgtgtt ggtatggatt ttctccatta 480
cacaactata taggatcgct agattgtttc ggtcgtccct tacagatgac gcaaagtaat 540
cttgtagatg ccttagcagt tgcggctgtt gtttgtatgg gagaggggaa tgagcaaaca 600
ccgttagcgg tgatagagca ggcacctaat atggtctacc attcatatcc tacttctcga 660
gaagagtatt gttctttgcg catagatgaa acagaggact tatacggacc tttttgcaa 720
gcggttacgt ggagtcaaga aaagaaatag 750

<210> 362
<211> 412
<212> PRT
<213> Chlamydia

<400> 362
Met His His His His His His Pro Pro Glu Ser Gly Leu Ile Ile Ala
1 5 10 15
Ile His Asp Asp Pro Arg Ser Leu Ser Pro Glu Lys Gly Glu Asn Ala
20 25 30
Phe His Phe Ser Leu Ser Lys Ala Leu Phe Ala Thr Leu Phe Arg Glu
35 40 45
Glu Leu Ser Gly Leu Thr Pro Ala Leu Val Ser Ser Tyr Gln Val Ser
50 55 60
Glu Asp Gly Arg Phe Tyr Arg Phe Cys Ile Arg Lys Asp Ala Lys Trp
65 70 75 80
Ser Asp Gly Ser Leu Leu Leu Ala Glu Asp Val Ile Ala Ala Trp Glu
85 90 95
His Thr Lys Gln Ala Gly Arg Tyr Ser Leu Leu Phe Glu Lys Leu Ser
100 105 110
Phe Arg Ala Ser Ser Ser Ser Glu Ile Leu Ile Glu Leu Lys Glu Pro
115 120 125
Glu Pro Gln Leu Leu Ala Ile Leu Ala Ser Pro Phe Phe Ala Val Tyr
130 135 140
Arg Pro Glu Asn Pro Phe Leu Ser Ser Gly Pro Phe Met Pro Lys Thr
145 150 155 160
Tyr Val Gln Gly Gln Thr Leu Val Leu Gln Lys Asn Pro Tyr Tyr Tyr
165 170 175
Asp His Ala His Val Glu Leu His Ser Ile Asp Phe Arg Ile Ile Pro
180 185 190
Asn Ile Tyr Thr Ala Leu His Leu Leu Arg Arg Gly Asp Val Asp Trp
195 200 205
Val Gly Gln Pro Trp His Gln Gly Ile Pro Phe Glu Leu Arg Thr Thr
210 215 220
Ser Ala Leu Tyr Thr His Tyr Pro Val Asp Gly Thr Phe Trp Leu Ile
225 230 235 240
Leu Asn Pro Lys Asp Pro Val Leu Ser Ser Leu Ser Asn Arg Gln Arg
245 250 255
Leu Ile Ala Ala Ile Gln Lys Glu Lys Leu Val Lys Gln Ala Leu Gly
260 265 270
Thr Gln Tyr Arg Val Ala Glu Ser Ser Pro Ser Pro Glu Gly Ile Ile
275 280 285
Ala His Gln Glu Ala Ser Thr Pro Phe Pro Gly Lys Ile Thr Leu Ile
290 295 300
Tyr Pro Asn Asn Ile Thr Arg Cys Gln Arg Leu Ala Glu Val Leu Gln
305 310 315 320
Glu Gln Cys Arg Asp Ala Gly Ile Gln Leu Thr Leu Glu Gly Leu Glu
325 330 335
Tyr His Val Phe Val Gln Lys Arg Ala Thr Gln Asp Phe Ser Val Ser
340 345 350
Thr Ala Thr Ser Ile Ala Phe His Pro Leu Ala Lys Ser Lys Phe Asp

```
    355                 360                 365
Gln Thr Ala Leu Asp Asn Phe Thr Cys Leu Pro Leu Tyr His Ile Glu
    370                 375                 380
Tyr Asp Tyr Ile Leu Ser Arg Pro Leu Asp Gln Ile Val His Tyr Pro
385                 390                 395                 400
Ser Gly Ser Val Asp Leu Thr Tyr Ala His Phe His
                405                 410


<210> 363
<211> 433
<212> PRT
<213> Chlamydia

<400> 363
Met His His His His His His Met Tyr Val Arg Ser Ile Phe Phe Ser
                5                   10                  15
Ile Ile Ala Phe Leu Thr Val Gly Cys Ser Phe Ser Pro Pro Glu Ser
            20                  25                  30
Gly Leu Ile Ile Ala Ile His Asp Asp Pro Arg Ser Leu Ser Pro Glu
        35                  40                  45
Lys Gly Glu Asn Ala Phe His Phe Ser Leu Ser Lys Ala Leu Phe Ala
    50                  55                  60
Thr Leu Phe Arg Glu Glu Leu Ser Gly Leu Thr Pro Ala Leu Val Ser
65                  70                  75                  80
Ser Tyr Gln Val Ser Glu Asp Gly Arg Phe Tyr Arg Phe Cys Ile Arg
                85                  90                  95
Lys Asp Ala Lys Trp Ser Asp Gly Ser Leu Leu Leu Ala Glu Asp Val
            100                 105                 110
Ile Ala Ala Trp Glu His Thr Lys Gln Ala Gly Arg Tyr Ser Leu Leu
        115                 120                 125
Phe Glu Lys Leu Ser Phe Arg Ala Ser Ser Ser Ser Glu Ile Leu Ile
    130                 135                 140
Glu Leu Lys Glu Pro Glu Pro Gln Leu Leu Ala Ile Leu Ala Ser Pro
145                 150                 155                 160
Phe Phe Ala Val Tyr Arg Pro Glu Asn Pro Phe Leu Ser Ser Gly Pro
                165                 170                 175
Phe Met Pro Lys Thr Tyr Val Gln Gly Gln Thr Leu Val Leu Gln Lys
            180                 185                 190
Asn Pro Tyr Tyr Tyr Asp His Ala His Val Glu Leu His Ser Ile Asp
        195                 200                 205
Phe Arg Ile Ile Pro Asn Ile Tyr Thr Ala Leu His Leu Leu Arg Arg
    210                 215                 220
Gly Asp Val Asp Trp Val Gly Gln Pro Trp His Gln Gly Ile Pro Phe
225                 230                 235                 240
Glu Leu Arg Thr Thr Ser Ala Leu Tyr Thr His Tyr Pro Val Asp Gly
                245                 250                 255
Thr Phe Trp Leu Ile Leu Asn Pro Lys Asp Pro Val Leu Ser Ser Leu
            260                 265                 270
Ser Asn Arg Gln Arg Leu Ile Ala Ala Ile Gln Lys Glu Lys Leu Val
        275                 280                 285
Lys Gln Ala Leu Gly Thr Gln Tyr Arg Val Ala Glu Ser Ser Pro Ser
    290                 295                 300
Pro Glu Gly Ile Ile Ala His Gln Glu Ala Ser Thr Pro Phe Pro Gly
305                 310                 315                 320
Lys Ile Thr Leu Ile Tyr Pro Asn Asn Ile Thr Arg Cys Gln Arg Leu
                325                 330                 335
Ala Glu Val Leu Gln Glu Gln Cys Arg Asp Ala Gly Ile Gln Leu Thr
            340                 345                 350
Leu Glu Gly Leu Glu Tyr His Val Phe Val Gln Lys Arg Ala Thr Gln
        355                 360                 365
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Asp Phe Ser Val Ser Thr Ala Thr Ser Ile Ala Phe His Pro Leu Ala
370 375 380
Lys Ser Lys Phe Asp Gln Thr Ala Leu Asp Asn Phe Thr Cys Leu Pro
385 390 395 400
Leu Tyr His Ile Glu Tyr Asp Tyr Ile Leu Ser Arg Pro Leu Asp Gln
405 410 415
Ile Val His Tyr Pro Ser Gly Ser Val Asp Leu Thr Tyr Ala His Phe
420 425 430
His

<210> 364
<211> 264
<212> PRT
<213> Chlamydia

<400> 364
Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn Thr Gln Asn Cys Val Phe
5 10 15
Ala Asp Asn Ile Lys Val Gly Gln Met Thr Glu Pro Leu Lys Asp Gln
20 25 30
Gln Ile Ile Leu Gly Thr Thr Ser Thr Pro Val Ala Ala Lys Met Thr
35 40 45
Ala Ser Asp Gly Ile Ser Leu Thr Val Ser Asn Asn Pro Ser Thr Asn
50 55 60
Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu Lys Ala Tyr Gln Leu Ile
65 70 75 80
Leu Glu Lys Leu Gly Asp Gln Ile Leu Gly Gly Ile Ala Asp Thr Ile
85 90 95
Val Asp Ser Thr Val Gln Asp Ile Leu Asp Lys Ile Thr Thr Asp Pro
100 105 110
Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn Phe Pro Ile Thr Asn Lys
115 120 125
Ile Gln Cys Asn Gly Leu Phe Thr Pro Arg Asn Ile Glu Thr Leu Leu
130 135 140
Gly Gly Thr Glu Ile Gly Lys Phe Thr Val Thr Pro Lys Ser Ser Gly
145 150 155 160
Ser Met Phe Leu Val Ser Ala Asp Ile Ile Ala Ser Arg Met Glu Gly
165 170 175
Gly Val Val Leu Ala Leu Val Arg Glu Gly Asp Ser Lys Pro Tyr Ala
180 185 190
Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro Asn Leu Cys Ser Leu Arg
195 200 205
Thr Arg Ile Ile Asn Thr Gly Leu Thr Pro Thr Thr Tyr Ser Leu Arg
210 215 220
Val Gly Gly Leu Glu Ser Gly Val Val Trp Val Asn Ala Leu Ser Asn
225 230 235 240
Gly Asn Asp Ile Leu Gly Ile Thr Asn Thr Ser Asn Val Ser Phe Leu
245 250 255
Glu Val Ile Pro Gln Thr Asn Ala
260

<210> 365
<211> 249
<212> PRT
<213> Chlamydia

<400> 365
Met His His His His His His Lys Ile Thr Pro Ile Lys Thr Arg Lys
5 10 15

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Val Phe Ala His Asp Ser Leu Gln Glu Ile Leu Gln Glu Ala Leu Pro
            20                  25                  30
Pro Leu Gln Glu Arg Ser Val Val Val Val Ser Ser Lys Ile Val Ser
        35                  40                  45
Leu Cys Glu Gly Ala Val Ala Asp Ala Arg Met Cys Lys Ala Glu Leu
    50                  55                  60
Ile Lys Lys Glu Ala Asp Ala Tyr Leu Phe Cys Glu Lys Ser Gly Ile
65                  70                  75                  80
Tyr Leu Thr Lys Lys Glu Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp
                85                  90                  95
Glu Ser Asn Thr Asp Gln Pro Phe Val Leu Tyr Pro Lys Asp Ile Leu
            100                 105                 110
Gly Ser Cys Asn Arg Ile Gly Glu Trp Leu Arg Asn Tyr Phe Arg Val
        115                 120                 125
Lys Glu Leu Gly Val Ile Ile Thr Asp Ser His Thr Thr Pro Met Arg
    130                 135                 140
Arg Gly Val Leu Gly Ile Gly Leu Cys Trp Tyr Gly Phe Ser Pro Leu
145                 150                 155                 160
His Asn Tyr Ile Gly Ser Leu Asp Cys Phe Gly Arg Pro Leu Gln Met
                165                 170                 175
Thr Gln Ser Asn Leu Val Asp Ala Leu Ala Val Ala Ala Val Val Cys
            180                 185                 190
Met Gly Glu Gly Asn Glu Gln Thr Pro Leu Ala Val Ile Glu Gln Ala
        195                 200                 205
Pro Asn Met Val Tyr His Ser Tyr Pro Thr Ser Arg Glu Glu Tyr Cys
    210                 215                 220
Ser Leu Arg Ile Asp Glu Thr Glu Asp Leu Tyr Gly Pro Phe Leu Gln
225                 230                 235                 240
Ala Val Thr Trp Ser Gln Glu Lys Lys
                245
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<210> 366
<211> 2418
<212> DNA
<213> Chlamydia pneumoniae

<400> 366

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ctagtctatg aggttgtaga caacagcatt gacgaagcca tggcaggtta ttgctctagg 180
attgatgttc gcattttaga ggacgggggt attgtcatcg tagataatgg ccgaggaatc 240
cctatagaag ttcacgaaag agagtctgca aaacaaggta gagaggtctc tgctttagaa 300
gtggttttaa cagtccttca tgctggagga aaattcgata aggatagcta taaagtatcc 360
ggaggcttgc acggagttgg ggtttcttgc gttaatgctc tttcggagaa attagttgcc 420
acggtcttta aagataagaa gtgttatcaa atggagttct ctaggggaat tcctgtaact 480
ccattgcagt atgtaagtgt tagtgatcgg cagggaacag aaatcgtttt ctaccctgat 540
cctaaaatat tttcgacttg tacttttgat cgctctattt taatgaaacg cttgcgagag 600
cttgctttct taaatcgtgg gatcacaata gtctttgaag atgatcgaga tgttagcttt 660
gacaaggtta ccttctttta tgagggaggg attcaatctt ttgtaagtta cctgaatcaa 720
aataaagaaa gccttttctc tgaaccgatt tatatttgtg gaactcgagt aggagatgat 780
ggagaaatcg agtttgaagc agccttacaa tggaattcag ggtattctga acttgtttat 840
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<213> Chlamydia pneumoniae

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<212> DNA
<213> Chlamydia pneumoniae

<400> 369

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<213> Chlamydia pneumoniae

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<213> Chlamydia pneumoniae

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<212> DNA
<213> Chlamydia pneumoniae

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<210> 374
<211> 5172
<212> DNA
<213> Chlamydia pneumoniae

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<212> DNA
<213> Chlamydia pneumoniae

<400> 375

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<213> Chlamydia pneumoniae

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tatattttag atgcacaagg tcactttaca aattattcag gctgtggaaa cactctcaat 900
acaaaccgcg cccccacgac ccaatggatt ctcgacatct tacgttattg ggtagaagaa 960
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cgtgacggca cagatgcgaa ctacagctac aatttcggaa cggaagggaa aacagaagac 1440
cctggcattc ttgaagttcg tgaaagacag ttacgaaatt ttttccttac tttgatggtc 1500
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cccatgacat ggcgccctgg aaatttctta gcatttaaaa taaaatcgcc aaaagcgcat 1800
gtatatgttg cttttcacgt gggagctcaa gaccaacttg cgaccttacc taaagcctcc 1860
agcaactttc ttccttatca aatagttgcc gagagtcagc aagggtttgt ccctcaaaat 1920
gtagcaacgc cgacagtgtc gctacagccc cataccacgc taattgcgat cagccatgcg 1980
aaagaggtta cctga 1995

<210> 382
<211> 987
<212> DNA
<213> Chlamydia pneumoniae

<400> 382
atggcattca aagaggtcgt tcgtgttgct gtcacaggag gcaaagggca gattgcgtat 60
aatttttat ttgcattagc ccatggagat gtttttggag tggatcgtgg tgtagattta 120
cggatctatg atgtgccggg tacagagaga gctctctcag ggtgcgtat ggagctcgat 180
gacggtgcat atcctctttt acatcgtctg cgtgtgacga catcgttaaa cgacgctttt 240
gatggtatcg atgcggcgtt tctgataggt gctgtgcctc gtggacccgg tatggagcga 300
ggagatcttt taaagcaaaa tggtcagatc ttttcgttac agggggccgc tttaaataca 360
gcagcaaaaa gagatgctaa gatttttgtt gtagggaacc ctgtcaatac gaattgctgg 420
attgctatga aacatgctcc cagattgcat cggaaaaatt tccatgcgat gttacgcttg 480
gatcagaatc gcatgcatag catgctcgct catcgtgctg aggttcctct agaggaggtc 540
tcccgtgttg tcatctgggg aaatcattct gcaaagcagg ttcctgactt cacacaagca 600
cgtatctcag ggaaacccgc agccgaggtt atcggagatc gagattggtt ggaaaacatt 660
ttagtacact ccgtgcagaa tcgtggaagc gctgtaattg aagcaagagg gaaatcttcg 720
gcagcatccg catctcgagc acttgccgag gccgcgcgat ctattttttg tcctaaaagt 780
gacgagtggt tttcttctgg agtgtgttcg gatcataatc cttatggtat tcctgaagac 840
ttgatttttg gttttccatg tcgtatgttg ccttctggag attatgaaat cattcctgga 900
ttgccttggg agccttttat cagaaataag attcaaattt ccctggatga aattgctcag 960
gaaaaagcta gcgtgtcttc gttataa 987

<210> 383
<211> 654
<212> DNA
<213> Chlamydia pneumoniae

<400> 383
atgaaaagag tcatttataa aaccatattt tgcgggttaa ctttacttac aagtttgagt 60
agttgttccc tggatcctaa aggatataac ctagagacaa aaaactcgag ggacttaaat 120
caagagtctg ttatactgaa ggaaaaccgt gaaacacctt ctcttgttaa gagactctct 180
cgtcgttctc gaagactctt cgctcgacgt gatcaaactc agaaggatac gctgcaagtg 240
caagctaact ttaagaccta cgcagaaaag atttcagagc aggacgaaag agacctttct 300
ttcgttgtct cgtctgctgc agaaaagtct tcaatttcgt tagctttgtc tcagggtgaa 360
attaaggatg ctttgtaccg tatccgagaa gtccaccctc tagctttaat agaagctctt 420
gctgaaaacc ctgccttgat agaagggatg aaaaagatgc aaggccgtga ttggatttgg 480
aatcttttct taacacaatt aagtgaagta ttttctcaag cttggtctca aggggttatc 540
tctgaagaag atatcgccgc atttgcctcc accttaggtt tggactccgg gaccgttgcg 600
tccattgtcc aaggggaaag gtggcccgag cttgtggata tagtgataac ttaa 654

<210> 384
<211> 813
<212> DNA
<213> Chlamydia pneumoniae

<400> 384
atgatcataa taaaaaacaa tgagctcatg ataagacgtt ttttcaaaac gcttttccct 60
ccgggtcctc aatactcttt atgttatgct tcgatcctga tcgttttgag ttcccttgtt 120
tgtgttccta cattttgttg gttatttctc cctgaactgt ctttatctaa attcaatcct 180
tctcccatta ggaacctatt tttagtttcc tccactctat ccaaagtccc tcctactgcg 240
attgcagaac atttacgtct ttctgcggat gcacctacat atctccatga attctctatt 300
aaagaagctg agtcgagctt gcatgctctt gggatttttt cctctttagt tatagaaaaa 360
tctcctgata ataagggcat tacaattttc tataccttac aaacacctat tgcttatgtt 420
gggaaccgat ctaatacgtt atgcaatctc gaggggagct gctttcttgg tcaaccgtac 480
ttcccctctc tgaatctccc tcagattttt ttctctcaag aagatttaaa aatgcaaaaa 540
ctccctaaag aaaaaatgct ttttaccaag attcttctta aggagcttgc tatggagtct 600
ccgaaaatca ttgatttatc tttatctgat gcataccctg gagaaattat agtgacgctc 660
tcttcaggca gtctgttaag acttccaatt aagaccttag atcgtgcctt agacctgtat 720
aagcacatga aaaaaagtcc tgtaatcgag agcgaaaaac aatatgtcta tgatttgcgt 780
tttccaaatt tcttattatt aaaagctcta tga 813

<210> 385
<211> 1956
<212> DNA
<213> Chlamydia pneumoniae

<400> 385
atggttaatc ctattggtcc aggtcctata gacgaaacag aacgcacacc tcccgcagat 60
ctttctgctc aaggattgga ggcgagtgca gcaaataaga gtgcggaagc tcaaagaata 120
gcaggtgcgg aagctaagcc taaagaatct aagaccgatt ctgtagagcg atggagcatc 180
ttgcgttctg cagtgaatgc tctcatgagt ctggcagata agctgggtat tgcttctagt 240
aacagctcgt cttctactag cagatctgca gacgtggact caacgacagc gaccgcacct 300
acgcctcctc cacccacgtt tgatgattat aagactcaag cgcaaacagc ttacgatact 360
atctttacct caacatcact agctgacata caggctgctt tggtgagcct ccaggatgct 420
gtcactaata taaaggatac agcggctact gatgaggaaa ccgcaatcgc tgcggagtgg 480
gaaactaaga atgccgatgc agttaaagtt ggcgcgcaaa ttacagaatt agcgaaatat 540
gcttcggata accaagcgat tcttgactct ttaggtaaac tgacttcctt cgacctctta 600
caggctgctc ttctccaatc tgtagcaaac aataacaaag cagctgagct tcttaaagag 660
atgcaagata acccagtagt cccagggaaa acgcctgcaa ttgctcaatc tttagttgat 720
cagacagatg ctacagcgac acagatagag aaagatggaa atgcgattag ggatgcatat 780
tttgcaggac agaacgctag tggagctgta gaaaatgcta aatctaataa cagtataagc 840
aacatagatt cagctaaagc agcaatcgct actgctaaga cacaaatagc tgaagctcag 900
aaaaagttcc ccgactctcc aattcttcaa gaagcggaac aaatggtaat acaggctgag 960
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gttggaggct ccaagcaaca aggaagtagt attggtagta ttcgtgtttc catgctgtta 1080
gatgatgctg aaaatgagac cgcttccatt ttgatgtctg ggtttcgtca gatgattcac 1140
atgttcaata cggaaaatcc tgattctcaa gctgcccaac aggagctcgc agcacaagct 1200

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agagcagcga aagccgctgg agatgacagt gctgctgcag cgctggcaga tgctcagaaa 1260
gctttagaag cggctctagg taaagctggg caacaacagg gcatactcaa tgctttagga 1320
cagatcgctt ctgctgctgt tgtgagcgca ggagttcctc ccgctgcagc aagttctata 1380
gggtcatctg taaaacagct ttacaagacc tcaaaatcta caggttctga ttataaaaca 1440
cagatatcag caggttatga tgcttacaaa tccatcaatg atgcctatgg tagggcacga 1500
aatgatgcga ctcgtgatgt gataaacaat gtaagtaccc ccgctctcac acgatccgtt 1560
cctagagcac gaacagaagc tcgaggacca gaaaaaacag atcaagccct cgctagggtg 1620
atttctggca atagcagaac tcttggagat gtctatagtc aagtttcggc actacaatct 1680
gtaatgcaga tcatccagtc gaatcctcaa gcgaataatg aggagatcag acaaaagctt 1740
acatcggcag tgacaaagcc tccacagttt ggctatcctt atgtgcaact ttctaatgac 1800
tctacacaga agttcatagc taaattagaa agtttgtttg ctgaaggatc taggacagca 1860
gctgaaataa aagcactttc ctttgaaacg aactccttgt ttattcagca ggtgctggtc 1920
aatatcggct ctctatattc tggttatctc caataa                           1956
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<210> 386
<211> 805
<212> PRT
<213> Chlamydia pneumoniae

<400> 386

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Met Asp Pro Lys Glu Lys Asn Tyr Asp Ala Ser Ala Ile Thr Val Leu
                5                   10                  15

Glu Gly Leu Gln Ala Val Arg Glu Arg Pro Gly Met Tyr Ile Gly Asp
            20                  25                  30

Thr Gly Ile Thr Gly Leu His His Leu Val Tyr Glu Val Val Asp Asn
        35                  40                  45

Ser Ile Asp Glu Ala Met Ala Gly Tyr Cys Ser Arg Ile Asp Val Arg
    50                  55                  60

Ile Leu Glu Asp Gly Gly Ile Val Ile Val Asp Asn Gly Arg Gly Ile
65                  70                  75                  80

Pro Ile Glu Val His Glu Arg Glu Ser Ala Lys Gln Gly Arg Glu Val
                85                  90                  95

Ser Ala Leu Glu Val Val Leu Thr Val Leu His Ala Gly Gly Lys Phe
            100                 105                 110

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
        115                 120                 125

Ser Cys Val Asn Ala Leu Ser Glu Lys Leu Val Ala Thr Val Phe Lys
    130                 135                 140

Asp Lys Lys Cys Tyr Gln Met Glu Phe Ser Arg Gly Ile Pro Val Thr
145                 150                 155                 160

Pro Leu Gln Tyr Val Ser Val Ser Asp Arg Gln Gly Thr Glu Ile Val
                165                 170                 175

Phe Tyr Pro Asp Pro Lys Ile Phe Ser Thr Cys Thr Phe Asp Arg Ser
            180                 185                 190

Ile Leu Met Lys Arg Leu Arg Glu Leu Ala Phe Leu Asn Arg Gly Ile
        195                 200                 205

Thr Ile Val Phe Glu Asp Asp Arg Asp Val Ser Phe Asp Lys Val Thr
```

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    210                 215                 220

Phe Phe Tyr Glu Gly Gly Ile Gln Ser Phe Val Ser Tyr Leu Asn Gln
225                 230                 235                 240

Asn Lys Glu Ser Leu Phe Ser Glu Pro Ile Tyr Ile Cys Gly Thr Arg
                245                 250                 255

Val Gly Asp Asp Gly Glu Ile Glu Phe Glu Ala Ala Leu Gln Trp Asn
            260                 265                 270

Ser Gly Tyr Ser Glu Leu Val Tyr Ser Tyr Ala Asn Asn Ile Pro Thr
        275                 280                 285

Arg Gln Gly Gly Thr His Leu Thr Gly Phe Ser Thr Ala Leu Thr Arg
    290                 295                 300

Val Ile Asn Thr Tyr Ile Lys Ala His Asn Leu Ala Lys Asn Asn Lys
305                 310                 315                 320

Leu Ala Leu Thr Gly Glu Asp Ile Arg Glu Gly Leu Thr Ala Val Ile
                325                 330                 335

Ser Val Lys Val Pro Asn Pro Gln Phe Glu Gly Gln Thr Lys Gln Lys
            340                 345                 350

Leu Gly Asn Ser Asp Val Ser Ser Val Ala Gln Gln Val Val Gly Glu
        355                 360                 365

Ala Leu Thr Ile Phe Phe Glu Glu Asn Pro Gln Ile Ala Arg Met Ile
    370                 375                 380

Val Asp Lys Val Phe Val Ala Ala Gln Ala Arg Glu Ala Ala Lys Lys
385                 390                 395                 400

Ala Arg Glu Leu Thr Leu Arg Lys Ser Ala Leu Asp Ser Ala Arg Leu
                405                 410                 415

Pro Gly Lys Leu Ile Asp Cys Leu Glu Lys Asp Pro Glu Lys Cys Glu
            420                 425                 430

Met Tyr Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
        435                 440                 445

Arg Asp Arg Arg Phe Gln Ala Ile Leu Pro Ile Arg Gly Lys Ile Leu
    450                 455                 460

Asn Val Glu Lys Ala Arg Leu Gln Lys Ile Phe Gln Asn Gln Glu Ile
465                 470                 475                 480

Gly Thr Ile Ile Ala Ala Leu Gly Cys Gly Ile Gly Ala Asp Asn Phe
                485                 490                 495

Asn Leu Ser Lys Leu Arg Tyr Arg Arg Ile Ile Ile Met Thr Asp Ala
            500                 505                 510

Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr
        515                 520                 525

Arg His Met Thr Ala Leu Ile Glu Asn Glu Cys Val Tyr Ile Ala Gln
    530                 535                 540
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Pro Pro Leu Tyr Lys Val Ser Lys Lys Lys Asp Phe Arg Tyr Ile Leu
545 550 555 560

Ser Glu Lys Glu Met Asp Ser Tyr Leu Leu Met Leu Gly Thr Asn Glu
565 570 575

Ser Ser Ile Leu Phe Lys Ser Thr Glu Arg Glu Leu Arg Gly Glu Ala
580 585 590

Leu Glu Ser Phe Ile Asn Val Ile Leu Asp Val Glu Ser Phe Ile Asn
595 600 605

Thr Leu Glu Lys Lys Ala Ile Pro Phe Ser Glu Phe Leu Glu Met Tyr
610 615 620

Lys Glu Gly Ile Gly Tyr Pro Leu Tyr Tyr Leu Ala Pro Ala Thr Gly
625 630 635 640

Met Gln Gly Gly Arg Tyr Leu Tyr Ser Asp Glu Glu Lys Glu Glu Ala
645 650 655

Leu Ala Gln Glu Glu Thr His Lys Phe Lys Ile Ile Glu Leu Tyr Lys
660 665 670

Val Ala Val Phe Val Asp Ile Gln Asn Gln Leu Lys Glu Tyr Gly Leu
675 680 685

Asp Ile Ser Ser Tyr Leu Ile Pro Gln Lys Asn Glu Ile Val Ile Gly
690 695 700

Asn Glu Asp Ser Pro Ser Cys Asn Tyr Ser Cys Tyr Thr Leu Glu Glu
705 710 715 720

Val Ile Asn Tyr Leu Lys Asn Leu Gly Arg Lys Gly Ile Glu Ile Gln
725 730 735

Arg Tyr Lys Gly Leu Gly Glu Met Asn Ala Asp Gln Leu Trp Asp Thr
740 745 750

Thr Met Asn Pro Glu Gln Arg Thr Leu Ile His Val Ser Leu Lys Asp
755 760 765

Ala Val Glu Ala Asp His Ile Phe Thr Met Leu Met Gly Glu Glu Val
770 775 780

Pro Pro Arg Arg Glu Phe Ile Glu Ser His Ala Leu Ser Ile Arg Ile
785 790 795 800

Asn Asn Leu Asp Ile
805

<210> 387
<211> 295
<212> PRT
<213> Chlamydia pneumoniae

<400> 387
Met Glu Lys Leu Leu Val Thr Asp Ile Asp Gly Thr Ile Thr His Gln
5 10 15

```
Ser His His Leu Asp Lys Lys Val Tyr Glu Arg Leu Tyr Ala Leu His
            20                  25                  30

Gln Ala Gly Trp Lys Leu Phe Phe Leu Thr Gly Arg Tyr Tyr Lys Tyr
        35                  40                  45

Ala Ala Arg Leu Phe Ser Asp Phe Asp Ala Pro Tyr Leu Leu Gly Cys
    50                  55                  60

Gln Asn Gly Ala Ser Val Trp Ser Ser Thr Ser Ser Asn Leu Leu Tyr
65                  70                  75                  80

Ser Lys Ser Leu Pro Ser Asp Leu Leu Cys Ile Leu Gln Asp Cys Met
                85                  90                  95

Glu Gly Ala Thr Ala Leu Phe Ser Val Glu Ser Gly Ala Pro Tyr Gly
            100                 105                 110

Asp His Tyr Tyr Arg Phe Ser Pro Thr Pro Ile Ala Gln Asp Leu His
        115                 120                 125

Glu Tyr Val Asp Pro Arg Tyr Phe Pro Asn Ala Lys Glu Arg Glu Ile
    130                 135                 140

Leu Phe Glu Thr Arg Ser Leu Lys Asp Asp Tyr Ala Phe Pro Ser Phe
145                 150                 155                 160

Ala Ala Ala Lys Val Phe Gly Leu Arg Asp Glu Val Ile Arg Ile Gln
                165                 170                 175

Lys Glu Leu Glu Arg Gln Glu Ala Leu Thr Ser Val Ala Thr Met Thr
            180                 185                 190

Leu Met Arg Trp Pro Phe Asp Phe Arg Tyr Ala Ile Leu Phe Leu Thr
        195                 200                 205

Asp Lys Ser Val Ser Lys Gly Lys Ala Leu Asp Arg Val Val Asn Ile
    210                 215                 220

Leu Tyr Asp Gly Lys Lys Pro Phe Val Met Ala Ser Gly Asp Asp Ala
225                 230                 235                 240

Asn Asp Leu Asp Leu Ile Glu Arg Gly Asp Phe Lys Ile Val Met Ser
                245                 250                 255

Ser Ala Pro Glu Glu Met His Val His Ala Asp Phe Leu Ala Pro Pro
            260                 265                 270

Ala Asp Lys Asn Gly Ile Leu Ser Ala Trp Glu Ala Gly Val Arg Tyr
        275                 280                 285

Tyr Asp Asp Leu Met Ser Leu
    290                 295
```

<210> 388
<211> 78
<212> PRT
<213> Chlamydia pneumoniae

<400> 388
Met Lys Glu Phe Leu Ala Tyr Ile Ile Lys Asn Leu Val Asp Arg Pro
5 10 15

Glu Glu Val Arg Ile Lys Glu Val Gln Gly Thr His Thr Ile Ile Tyr
20 25 30

Glu Leu Ser Val Ala Lys Pro Asp Ile Gly Lys Ile Ile Gly Lys Glu
35 40 45

Gly Arg Thr Ile Lys Ala Ile Arg Thr Leu Leu Val Ser Val Ala Ser
50 55 60

Arg Asn Asn Val Arg Val Ser Leu Glu Ile Met Glu Glu Lys
65 70 75

<210> 389
<211> 478
<212> PRT
<213> Chlamydia pneumoniae

<400> 389
Met Arg Asp Val Ser Glu Leu Phe Arg Thr His Phe Met His Tyr Ala
5 10 15

Ser Tyr Val Ile Leu Glu Arg Ala Ile Pro His Ile Leu Asp Gly Leu
20 25 30

Lys Pro Val Gln Arg Arg Leu Leu Trp Thr Leu Phe Leu Met Asp Asp
35 40 45

Gly Lys Met His Lys Val Ala Asn Ile Ala Gly Arg Thr Met Ala Leu
50 55 60

His Pro His Gly Asp Ala Pro Ile Val Glu Ala Leu Val Val Leu Ala
65 70 75 80

Asn Lys Gly Tyr Leu Ile Asp Thr Gln Gly Asn Phe Gly Asn Pro Leu
85 90 95

Thr Gly Asp Pro His Ala Ala Ala Arg Tyr Ile Glu Ala Arg Leu Ser
100 105 110

Pro Leu Ala Arg Glu Thr Leu Phe Asn Thr Asp Leu Ile Ala Phe His
115 120 125

Asp Ser Tyr Asp Gly Arg Glu Lys Glu Pro Asp Ile Leu Pro Ala Lys
130 135 140

Leu Pro Val Leu Leu Leu His Gly Val Asp Gly Ile Ala Val Gly Met
145 150 155 160

Thr Thr Lys Ile Phe Pro His Asn Phe Ala Glu Leu Leu Lys Ala Gln
165 170 175

Ile Ala Ile Leu Asn Asp Lys Lys Phe Thr Val Phe Pro Asp Phe Pro
180 185 190

Ser Gly Gly Leu Met Asp Pro Ser Glu Tyr Gln Asp Gly Leu Gly Ser
195 200 205

Ile Thr Leu Arg Ala Ser Ile Asp Ile Ile Asn Asp Lys Thr Leu Val
210 215 220

Val Lys Gln Ile Cys Pro Gln Ser Thr Thr Glu Thr Leu Ile Arg Ser
225 230 235 240

Ile Glu Asn Ala Ala Lys Arg Gly Thr Ile Lys Ile Asp Thr Ile Gln
245 250 255

Asp Phe Ser Thr Asp Val Pro His Ile Glu Ile Lys Leu Pro Lys Gly
260 265 270

Ser Arg Ala Lys Glu Met Leu Pro Leu Leu Phe Glu His Thr Glu Cys
275 280 285

Gln Val Ile Leu Tyr Ser Lys Pro Thr Val Ile Tyr Glu Asn Lys Pro
290 295 300

Val Glu Cys Ser Ile Ser Glu Ile Leu Lys Leu His Thr Thr Ala Leu
305 310 315 320

Gln Gly Tyr Leu Glu Lys Glu Leu Leu Leu Leu Gln Glu Gln Leu Thr
325 330 335

Leu Asp His Tyr His Lys Thr Leu Glu Tyr Ile Phe Ile Lys His Lys
340 345 350

Leu Tyr Asp Ser Val Arg Glu Val Leu Ala Ile Asn Lys Lys Ile Ser
355 360 365

Ala Asp Asp Leu His Gln Ala Val Leu His Ala Leu Glu Pro Trp Leu
370 375 380

His Glu Leu Ala Thr Pro Val Thr Lys Gln Asp Thr Ser Gln Leu Ala
385 390 395 400

Ser Leu Thr Ile Lys Lys Ile Leu Cys Phe Asn Glu Glu Ala Cys Thr
405 410 415

Lys Glu Leu Leu Ala Ile Glu Lys Lys Gln Ala Ala Ile Gln Lys Asp
420 425 430

Leu Gly Arg Ile Lys Glu Val Thr Val Lys Tyr Leu Lys Gly Leu Leu
435 440 445

Glu Arg His Gly His Leu Gly Glu Arg Lys Thr Gln Ile Thr Asn Phe
450 455 460

Lys Thr Ala Lys Thr Ser Ile Leu Lys Gln Gln Thr Leu Ile
465 470 475

<210> 390
<211> 257
<212> PRT
<213> Chlamydia pneumoniae

<400> 390
Met Ala Phe Tyr Ser Pro Ser Thr Ile Ser Lys Tyr Phe Ile Tyr Ser
5 10 15

Gly Ala Gly Asn Arg Phe Leu Leu Gly Glu Thr Leu Pro Glu Val Glu
20 25 30

Asp Val Arg Phe Leu Cys Gln Glu Thr Arg Val Asp Gly Phe Leu Tyr
35 40 45

Leu Lys Pro Ser Ser Cys Ala Asp Ala Gln Leu Ile Ile Phe Asn Ser
50 55 60

Asp Gly Ser Arg Pro Thr Met Cys Gly Asn Gly Leu Arg Cys Ala Ile
65 70 75 80

Ala His Leu Ala Ser Gln Lys Gly Lys Ser Asp Ile Ser Val Ser Thr
85 90 95

Asp Ser Gly Leu Tyr Ser Gly Tyr Phe Tyr Ser Trp Asp Arg Val Leu
100 105 110

Val Asp Met Thr Leu Ala Asp Trp Arg Ala Ser Val His Arg Leu Glu
115 120 125

Ser Arg Pro Asp Pro Leu Pro Lys Glu Val Val Cys Ile His Thr Gly
130 135 140

Val Pro His Ala Val Val Ile Leu Pro Glu Ile Ser Thr Leu Asp Leu
145 150 155 160

Ser Ile Leu Gly Pro Phe Leu Arg Tyr His Gln Thr Phe Ser Pro Asp
165 170 175

Gly Val Asn Val Asn Phe Val Gln Ile Leu Gly His Cys Gln Leu Arg
180 185 190

Val Arg Thr Tyr Glu Arg Gly Val Glu Gly Glu Thr Ala Ala Cys Gly
195 200 205

Thr Gly Ala Leu Ala Ser Ala Leu Val Val Ser Asn Ser Tyr Gly Trp
210 215 220

Lys Glu Ser Ile Gln Ile His Thr Trp Gly Gly Glu Leu Met Thr Val
225 230 235 240

Ser Gln Asn Arg Gly Arg Val Tyr Leu Gln Gly Ser Val Thr Arg Asp
245 250 255

Leu

<210> 391
<211> 191
<212> PRT
<213> Chlamydia pneumoniae

<400> 391
Met Ala Asp Gly Glu Val His Lys Leu Arg Asp Ile Ile Glu Lys Glu
5 10 15

Leu Leu Glu Ala Arg Arg Val Phe Phe Ser Glu Pro Val Thr Glu Lys
20 25 30

Ser Ala Ser Asp Ala Ile Lys Lys Leu Trp Tyr Leu Glu Leu Lys Asp
35 40 45

Pro Gly Lys Pro Ile Val Phe Val Ile Asn Ser Pro Gly Gly Ser Val
50 55 60

Asp Ala Gly Phe Ala Val Trp Asp Gln Ile Lys Met Leu Thr Ser Pro
65 70 75 80

Val Thr Thr Val Val Thr Gly Leu Ala Ala Ser Met Gly Ser Val Leu
85 90 95

Ser Leu Cys Ala Ala Pro Gly Arg Arg Phe Ala Thr Pro His Ser Arg
100 105 110

Ile Met Ile His Gln Pro Ser Ile Gly Gly Pro Ile Thr Gly Gln Ala
115 120 125

Thr Asp Leu Asp Ile His Ala Arg Glu Ile Leu Lys Thr Lys Ala Arg
130 135 140

Ile Ile Asp Val Tyr Val Glu Ala Thr Asn Gln Pro Arg Asp Ile Ile
145 150 155 160

Glu Lys Ala Ile Asp Arg Asp Met Trp Met Thr Ala Asn Glu Ala Lys
165 170 175

Asp Phe Gly Leu Leu Asp Gly Ile Leu Phe Ser Phe Asn Asp Leu
180 185 190

<210> 392
<211> 232
<212> PRT
<213> Chlamydia pneumoniae

<400> 392
Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Leu Lys Asn Tyr Asp
5 10 15

Phe Ser Lys Ser Tyr Ser Leu Arg Glu Ala Ile Asp Ile Leu Lys Gln
20 25 30

Cys Pro Pro Val Arg Phe Asp Gln Thr Val Asp Val Ser Ile Lys Leu
35 40 45

Gly Ile Asp Pro Lys Lys Ser Asp Gln Gln Ile Arg Gly Ala Val Phe
50 55 60

Leu Pro Asn Gly Thr Gly Lys Thr Leu Arg Ile Leu Val Phe Ala Ser
65 70 75 80

Gly Asn Lys Val Lys Glu Ala Val Glu Ala Gly Ala Asp Phe Met Gly
85 90 95

Ser Asp Asp Leu Val Glu Lys Ile Lys Ser Gly Trp Leu Glu Phe Asp
100 105 110

Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
115 120 125

Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Thr Gly Thr
130 135 140

Val Thr Thr Asp Val Ala Lys Ala Ile Ser Glu Leu Arg Lys Gly Lys
145 150 155 160

Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Gly
165 170 175

Lys Leu Ser Phe Glu Ser Ser Gln Ile Lys Glu Asn Ile Glu Ala Leu
180 185 190

Ser Ser Ala Leu Ile Lys Ala Lys Pro Pro Ala Ala Lys Gly Gln Tyr
195 200 205

Leu Val Ser Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Ile Ser Ile
210 215 220

Asp Thr Arg Glu Leu Met Ala Ser
225 230

<210> 393
<211> 122
<212> PRT
<213> Chlamydia pneumoniae

<400> 393
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
5 10 15

Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu
20 25 30

Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu
35 40 45

Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr
50 55 60

Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
65 70 75 80

Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
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Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
100 105 110

Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
115 120

<210> 394
<211> 1723
<212> PRT
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<400> 394
Met Lys Trp Leu Pro Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ala

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Leu Thr Ala Phe Gly Asp Pro Ala Ser Val Glu Ile Ser Thr Ser His
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Thr Gly Ser Gly Asp Pro Thr Ser Asp Ala Ala Leu Thr Gly Phe Thr
        35                  40                  45

Gln Ser Ser Thr Glu Thr Asp Gly Thr Thr Tyr Thr Ile Val Gly Asp
    50                  55                  60

Ile Thr Phe Ser Thr Phe Thr Asn Ile Pro Val Pro Val Val Thr Pro
65                  70                  75                  80

Asp Ala Asn Asp Ser Ser Ser Asn Ser Ser Lys Gly Gly Ser Ser Ser
                85                  90                  95

Ser Gly Ala Thr Ser Leu Ile Arg Ser Ser Asn Leu His Ser Asp Phe
            100                 105                 110

Asp Phe Thr Lys Asp Ser Val Leu Asp Leu Tyr His Leu Phe Phe Pro
        115                 120                 125

Ser Ala Ser Asn Thr Leu Asn Pro Ala Leu Leu Ser Ser Ser Ser Ser
    130                 135                 140

Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Ala Ser
145                 150                 155                 160

Ala Val Val Ala Ala Asp Pro Lys Gly Gly Ala Ala Phe Tyr Ser Asn
                165                 170                 175

Glu Ala Asn Gly Thr Leu Thr Phe Thr Thr Asp Ser Gly Asn Pro Gly
            180                 185                 190

Ser Leu Thr Leu Gln Asn Leu Lys Met Thr Gly Asp Gly Ala Ala Ile
        195                 200                 205

Tyr Ser Lys Gly Pro Leu Val Phe Thr Gly Leu Lys Asn Leu Thr Phe
    210                 215                 220

Thr Gly Asn Glu Ser Gln Lys Ser Gly Gly Ala Ala Tyr Thr Glu Gly
225                 230                 235                 240

Ala Leu Thr Thr Gln Ala Ile Val Glu Ala Val Thr Phe Thr Gly Asn
                245                 250                 255

Thr Ser Ala Gly Gln Gly Gly Ala Ile Tyr Val Lys Glu Ala Thr Leu
            260                 265                 270

Phe Asn Ala Leu Asp Ser Leu Lys Phe Glu Lys Asn Thr Ser Gly Gln
        275                 280                 285

Ala Gly Gly Gly Ile Tyr Thr Glu Ser Thr Leu Thr Ile Ser Asn Ile
    290                 295                 300

Thr Lys Ser Ile Glu Phe Ile Ser Asn Lys Ala Ser Val Pro Ala Pro
305                 310                 315                 320

Ala Pro Glu Pro Thr Ser Pro Ala Pro Ser Ser Leu Ile Asn Ser Thr
                325                 330                 335
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Thr Ile Asp Thr Ser Thr Leu Gln Thr Arg Ala Ala Ser Ala Thr Pro
340 345 350

Ala Val Ala Pro Val Ala Ala Val Thr Pro Thr Pro Ile Ser Thr Gln
355 360 365

Glu Thr Ala Gly Asn Gly Gly Ala Ile Tyr Ala Lys Gln Gly Ile Ser
370 375 380

Ile Ser Thr Phe Lys Asp Leu Thr Phe Lys Ser Asn Ser Ala Ser Val
385 390 395 400

Asp Ala Thr Leu Thr Val Asp Ser Ser Thr Ile Gly Glu Ser Gly Gly
405 410 415

Ala Ile Phe Ala Ala Asp Ser Ile Gln Ile Gln Gln Cys Thr Gly Thr
420 425 430

Thr Leu Phe Ser Gly Asn Thr Ala Asn Lys Ser Gly Gly Gly Ile Tyr
435 440 445

Ala Val Gly Gln Val Thr Leu Glu Asp Ile Ala Asn Leu Lys Met Thr
450 455 460

Asn Asn Thr Cys Lys Gly Glu Gly Gly Ala Ile Tyr Thr Lys Lys Ala
465 470 475 480

Leu Thr Ile Asn Asn Gly Ala Ile Leu Thr Thr Phe Ser Gly Asn Thr
485 490 495

Ser Thr Asp Asn Gly Gly Ala Ile Phe Ala Val Gly Gly Ile Thr Leu
500 505 510

Ser Asp Leu Val Glu Val Arg Phe Ser Lys Asn Lys Thr Gly Asn Tyr
515 520 525

Ser Ala Pro Ile Thr Lys Ala Ala Ser Asn Thr Ala Pro Val Val Ser
530 535 540

Ser Ser Thr Thr Ala Ala Ser Pro Ala Val Pro Ala Ala Ala Ala Ala
545 550 555 560

Pro Val Thr Asn Ala Ala Lys Gly Gly Ala Leu Tyr Ser Thr Glu Gly
565 570 575

Leu Thr Val Ser Gly Ile Thr Ser Ile Leu Ser Phe Glu Asn Asn Glu
580 585 590

Cys Gln Asn Gln Gly Gly Gly Ala Tyr Val Thr Lys Thr Phe Gln Cys
595 600 605

Ser Asp Ser His Arg Leu Gln Phe Thr Ser Asn Lys Ala Ala Asp Glu
610 615 620

Gly Gly Gly Leu Tyr Cys Gly Asp Asp Val Thr Leu Thr Asn Leu Thr
625 630 635 640

Gly Lys Thr Leu Phe Gln Glu Asn Ser Ser Glu Lys His Gly Gly Gly
645 650 655

Leu Ser Leu Ala Ser Gly Lys Ser Leu Thr Met Thr Ser Leu Glu Ser
660 665 670

Phe Cys Leu Asn Ala Asn Thr Ala Lys Glu Asn Gly Gly Gly Ala Asn
675 680 685

Val Pro Glu Asn Ile Val Leu Thr Phe Thr Tyr Thr Pro Thr Pro Asn
690 695 700

Glu Pro Ala Pro Val Gln Gln Pro Val Tyr Gly Glu Ala Leu Val Thr
705 710 715 720

Gly Asn Thr Ala Thr Lys Ser Gly Gly Gly Ile Tyr Thr Lys Asn Ala
725 730 735

Ala Phe Ser Asn Leu Ser Ser Val Thr Phe Asp Gln Asn Thr Ser Ser
740 745 750

Glu Asn Gly Gly Ala Leu Leu Thr Gln Lys Ala Ala Asp Lys Thr Asp
755 760 765

Cys Ser Phe Thr Tyr Ile Thr Asn Val Asn Ile Thr Asn Asn Thr Ala
770 775 780

Thr Gly Asn Gly Gly Gly Ile Ala Gly Gly Lys Ala His Phe Asp Arg
785 790 795 800

Ile Asp Asn Leu Thr Val Gln Ser Asn Gln Ala Lys Lys Gly Gly Gly
805 810 815

Val Tyr Leu Glu Asp Ala Leu Ile Leu Glu Lys Val Ile Thr Gly Ser
820 825 830

Val Ser Gln Asn Thr Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys
835 840 845

Asp Ile Gln Leu Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn
850 855 860

Lys Val Glu Thr Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly
865 870 875 880

Ile Tyr Ser Ser Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe
885 890 895

Gly Ile Thr Gly Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala
900 905 910

Asp Ile Gln Gly Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn
915 920 925

Gln Cys Asn Thr Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys
930 935 940

Lys Thr Ser Thr Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala
945 950 955 960

Ala Val Thr Ile Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn
965 970 975

Ser Ala Lys Ser Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp

980 985 990

Ser Cys Gly Gly Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn
995 1000 1005

Pro Glu Ile Thr Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile
1010 1015 1020

Gly Cys Ile Asp Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile
1025 1030 1035 1040

Ala Asp Asn Gly Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg
1045 1050 1055

Gly Gly Ala Ile Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala
1060 1065 1070

Thr Phe Ile Gly Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys
1075 1080 1085

Ser Thr Ala Leu Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn
1090 1095 1100

Asn Lys Val Thr Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn
1105 1110 1115 1120

Leu Gly Ala Ala Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile
1125 1130 1135

Ser Leu Ser Ala Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys
1140 1145 1150

Thr Ala Thr Asn Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr
1155 1160 1165

Ala Ile Glu Ala Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val
1170 1175 1180

Asn Val Ser Thr Lys Glu Thr Asn Ala Gln Glu Leu Lys Leu Asn Glu
1185 1190 1195 1200

Lys Ala Thr Ser Thr Gly Thr Ile Leu Phe Ser Gly Glu Leu His Glu
1205 1210 1215

Asn Lys Ser Tyr Ile Pro Gln Lys Val Thr Phe Ala His Gly Asn Leu
1220 1225 1230

Ile Leu Gly Lys Asn Ala Glu Leu Ser Val Val Ser Phe Thr Gln Ser
1235 1240 1245

Pro Gly Thr Thr Ile Thr Met Gly Pro Gly Ser Val Leu Ser Asn His
1250 1255 1260

Ser Lys Glu Ala Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe
1265 1270 1275 1280

Ser Glu Ile Val Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr
1285 1290 1295

Leu Lys Leu Val Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp
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Ile Thr Gly Thr Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln
1315 1320 1325

Asn Ser Tyr Leu Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp
1330 1335 1340

Asn Ser Ala Ser Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly
1345 1350 1355 1360

Asn Leu Gly Ala Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro
1365 1370 1375

Asn Ser Ser Gly Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr
1380 1385 1390

Leu Arg Trp Pro Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser
1395 1400 1405

Ile Trp Gly Ala Gln Asn Ser Leu Val Thr Val Lys Gln Gly Ile Leu
1410 1415 1420

Gly Asn Met Leu Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn
1425 1430 1435 1440

Phe Trp Ala Ser Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg
1445 1450 1455

Asn Ser Asp Ser Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val
1460 1465 1470

Asp Ala Lys Pro Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln
1475 1480 1485

Val Phe Gly His Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His
1490 1495 1500

Lys Gly Ser Gly His Ser Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile
1505 1510 1515 1520

Phe Tyr Phe Pro Ala Ile Arg Ser Arg Pro Ile Leu Phe Gln Gly Val
1525 1530 1535

Ala Thr Tyr Gly Tyr Met Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser
1540 1545 1550

Ile Glu Glu Lys Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe
1555 1560 1565

Asp Leu Arg Phe Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr
1570 1575 1580

Ala Arg Leu Thr Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln
1585 1590 1595 1600

Glu Lys Phe Thr Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys
1605 1610 1615

Ser Tyr Gly Asn Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala
1620 1625 1630

Leu Ala Trp Arg Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr
1635 1640 1645

Leu Pro Val Ile Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu
1650 1655 1660

Ser Thr Lys Glu Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn
1665 1670 1675 1680

Ala Ala Arg Ala Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp
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Thr Leu Tyr Gly Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val
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35 40 45
Gln Ser Ser Thr Glu Thr Asp Gly Thr Thr Tyr Thr Ile Val Gly Asp
50 55 60
Ile Thr Phe Ser Thr Phe Thr Asn Ile Pro Val Pro Val Val Thr Pro
65 70 75 80
Asp Ala Asn Asp Ser Ser Ser Asn Ser Ser Lys Gly Gly Ser Ser Ser
85 90 95
Ser Gly Ala Thr Ser Leu Ile Arg Ser Ser Asn Leu His Ser Asp Phe
100 105 110
Asp Phe Thr Lys Asp Ser Val Leu Asp Leu Tyr His Leu Phe Phe Pro
115 120 125
Ser Ala Ser Asn Thr Leu Asn Pro Ala Leu Leu Ser Ser Ser Ser Ser
130 135 140
Gly Gly Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Ala Ser
145 150 155 160
Ala Val Val Ala Ala Asp Pro Lys Gly Gly Ala Ala Phe Tyr Ser Asn
165 170 175
Glu Ala Asn Gly Thr Leu Thr Phe Thr Thr Asp Ser Gly Asn Pro Gly
180 185 190
Ser Leu Thr Leu Gln Asn Leu Lys Met Thr Gly Asp Gly Ala Ala Ile
195 200 205
Tyr Ser Lys Gly Pro Leu Val Phe Thr Gly Leu Lys Asn Leu Thr Phe
210 215 220
Thr Gly Asn Glu Ser Gln Lys Ser Gly Gly Ala Ala Tyr Thr Glu Gly
225 230 235 240
Ala Leu Thr Thr Gln Ala Ile Val Glu Ala Val Thr Phe Thr Gly Asn
245 250 255
Thr Ser Ala Gly Gln Gly Gly Ala Ile Tyr Val Lys Glu Ala Thr Leu
260 265 270
Phe Asn Ala Leu Asp Ser Leu Lys Phe Glu Lys Asn Thr Ser Gly Gln
275 280 285

Ala Gly Gly Gly Ile Tyr Thr Glu Ser Thr Leu Thr Ile Ser Asn Ile
290 295 300
Thr Lys Ser Ile Glu Phe Ile Ser Asn Lys Ala Ser Val Pro Ala Pro
305 310 315 320
Ala Pro Glu Pro Thr Ser Pro Ala Pro Ser Ser Leu Ile Asn Ser Thr
325 330 335
Thr Ile Asp Thr Ser Thr Leu Gln Thr Arg Ala Ala Ser Ala Thr Pro
340 345 350
Ala Val Ala Pro Val Ala Ala Val Thr Pro Thr Pro Ile Ser Thr Gln
355 360 365
Glu Thr Ala Gly Asn Gly Gly Ala Ile Tyr Ala Lys Gln Gly Ile Ser
370 375 380
Ile Ser Thr Phe Lys Asp Leu Thr Phe Lys Ser Asn Ser Ala Ser Val
385 390 395 400
Asp Ala Thr Leu Thr Val Asp Ser Ser Thr Ile Gly Glu Ser Gly Gly
405 410 415
Ala Ile Phe Ala Ala Asp Ser Ile Gln Ile Gln Gln Cys Thr Gly Thr
420 425 430
Thr Leu Phe Ser Gly Asn Thr Ala Asn Lys Ser Gly Gly Gly Ile Tyr
435 440 445
Ala Val Gly Gln Val Thr Leu Glu Asp Ile Ala Asn Leu Lys Met Thr
450 455 460
Asn Asn Thr Cys Lys Gly Glu Gly Gly Ala Ile Tyr Thr Lys Lys Ala
465 470 475 480
Leu Thr Ile Asn Asn Gly Ala Ile Leu Thr Thr Phe Ser Gly Asn Thr
485 490 495
Ser Thr Asp Asn Gly Gly Ala Ile Phe Ala Val Gly Gly Ile Thr Leu
500 505 510
Ser Asp Leu Val Glu Val Arg Phe Ser Lys Asn Lys Thr Gly Asn Tyr
515 520 525
Ser Ala Pro Ile Thr Lys Ala Ala Ser Asn Thr Ala Pro Val Val Ser
530 535 540
Ser Ser Thr Thr Ala Ala Ser Pro Ala Val Pro Ala Ala Ala Ala Ala
545 550 555 560
Pro Val Thr Asn Ala Ala Lys Gly Gly Ala Leu Tyr Ser Thr Glu Gly
565 570 575
Leu Thr Val Ser Gly Ile Thr Ser Ile Leu Ser Phe Glu Asn Asn Glu
580 585 590
Cys Gln Asn Gln Gly Gly Gly Ala Tyr Val Thr Lys Thr Phe Gln Cys
595 600 605
Ser Asp Ser His Arg Leu Gln Phe Thr Ser Asn Lys Ala Ala Asp Glu
610 615 620
Gly Gly Gly Leu Tyr Cys Gly Asp Asp Val Thr Leu Thr Asn Leu Thr
625 630 635 640
Gly Lys Thr Leu Phe Gln Glu Asn Ser Ser Glu Lys His Gly Gly Gly
645 650 655
Leu Ser Leu Ala Ser Gly Lys Ser Leu Thr Met Thr Ser Leu Glu Ser
660 665 670
Phe Cys Leu Asn Ala Asn Thr Ala Lys Glu Asn Gly Gly Gly Ala Asn
675 680 685
Val Pro Glu Asn Ile Val Leu Thr Phe Thr Tyr Thr Pro Thr Pro Asn
690 695 700
Glu Pro Ala Pro Val Gln Gln Pro Val Tyr Gly Glu Ala Leu Val Thr
705 710 715 720
Gly Asn Thr Ala Thr Lys Ser Gly Gly Gly Ile Tyr Thr Lys Asn Ala
725 730 735
Ala Phe Ser Asn Leu Ser Ser Val Thr Phe Asp Gln Asn Thr Ser Ser
740 745 750
Glu Asn Gly Gly Ala Leu Leu Thr Gln Lys Ala Ala Asp Lys Thr Asp
755 760 765
Cys Ser Phe Thr Tyr Ile Thr Asn Val Asn Ile Thr Asn Asn Thr Ala

770 775 780
Thr Gly Asn Gly Gly Gly Ile Ala Gly Gly Lys Ala His Phe Asp Arg
785 790 795 800
Ile Asp Asn Leu Thr Val Gln Ser Asn Gln Ala Lys Lys Gly Gly Gly
805 810 815
Val Tyr Leu Glu Asp Ala Leu Ile Leu Glu Lys Val Ile Thr Gly Ser
820 825 830
Val Ser Gln Asn Thr Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys
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Asp Ile Gln Leu Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn
850 855 860
Lys Val Glu Thr Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly
865 870 875 880
Ile Tyr Ser Ser Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe
885 890 895
Gly Ile Thr Gly Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala
900 905 910
Asp Ile Gln Gly Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn
915 920 925
Gln Cys Asn Thr Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys
930 935 940
Lys Thr Ser Thr Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala
945 950 955 960
Ala Val Thr Ile Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn
965 970 975
Ser Ala Lys Ser Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp
980 985 990
Ser Cys Gly Gly Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn
995 1000 1005
Pro Glu Ile Thr Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile
1010 1015 1020
Gly Cys Ile Asp Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile
1025 1030 1035 1040
Ala Asp Asn Gly Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg
1045 1050 1055
Gly Gly Ala Ile Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala
1060 1065 1070
Thr Phe Ile Gly Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys
1075 1080 1085
Ser Thr Ala Leu Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn
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Asn Lys Val Thr Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn
1105 1110 1115 1120
Leu Gly Ala Ala Ile Tyr Gly Asn Asn Glu Thr Ser Asp Ile Thr Ile
1125 1130 1135
Ser Leu Ser Ala Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys
1140 1145 1150
Thr Ala Thr Asn Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr
1155 1160 1165
Ala Ile Glu Ala Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val
1170 1175 1180
Asn Val Ser Thr Lys Glu Thr Asn Ala Gln Glu Leu Lys Leu Asn Glu
1185 1190 1195 1200
Lys Ala Thr Ser Thr Gly Thr Ile Leu Phe Ser Gly Glu Leu His Glu
1205 1210 1215
Asn Lys Ser Tyr Ile Pro Gln Lys Val Thr Phe Ala His Gly Asn Leu
1220 1225 1230
Ile Leu Gly Lys Asn Ala Glu Leu Ser Val Val Ser Phe Thr Gln Ser
1235 1240 1245
Pro Gly Thr Thr Ile Thr Met Gly Pro Gly Ser Val Leu Ser Asn His
1250 1255 1260

Ser Lys Glu Ala Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe
1265 1270 1275 1280
Ser Glu Ile Val Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr
1285 1290 1295
Leu Lys Leu Val Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp
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Ile Thr Gly Thr Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln
1315 1320 1325
Asn Ser Tyr Leu Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp
1330 1335 1340
Asn Ser Ala Ser Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly
1345 1350 1355 1360
Asn Leu Gly Ala Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro
1365 1370 1375
Asn Ser Ser Gly Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr
1380 1385 1390
Leu Arg Trp Pro Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser
1395 1400 1405
Ile Trp Gly Ala Gln Asn Ser Leu Val Thr Val Lys Gln Gly Ile Leu
1410 1415 1420
Gly Asn Met Leu Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn
1425 1430 1435 1440
Phe Trp Ala Ser Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg
1445 1450 1455
Asn Ser Asp Ser Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val
1460 1465 1470
Asp Ala Lys Pro Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln
1475 1480 1485
Val Phe Gly His Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His
1490 1495 1500
Lys Gly Ser Gly His Ser Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile
1505 1510 1515 1520
Phe Tyr Phe Pro Ala Ile Arg Ser Arg Pro Ile Leu Phe Gln Gly Val
1525 1530 1535
Ala Thr Tyr Gly Tyr Met Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser
1540 1545 1550
Ile Glu Glu Lys Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe
1555 1560 1565
Asp Leu Arg Phe Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr
1570 1575 1580
Ala Arg Leu Thr Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln
1585 1590 1595 1600
Glu Lys Phe Thr Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys
1605 1610 1615
Ser Tyr Gly Asn Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala
1620 1625 1630
Leu Ala Trp Arg Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr
1635 1640 1645
Leu Pro Val Ile Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu
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Ser Thr Lys Glu Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn
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Ala Ala Arg Ala Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp
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1715 1720

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Phe Leu Gln Ile Gly Lys Leu Ala Glu Glu Arg Glu Asn Ile Gly Leu
35 40 45

Glu Glu Val Phe Arg Glu Ile Phe Pro Ile Lys Ser Tyr Asn Glu Ala
50 55 60

Thr Val Leu Glu Tyr Leu Ser Tyr Asn Leu Gly Val Pro Lys Tyr Ser
65 70 75 80

Pro Glu Glu Cys Ile Arg Arg Gly Ile Thr Tyr Ser Val Thr Leu Lys
85 90 95

Val Arg Phe Arg Leu Thr Asp Glu Thr Gly Ile Lys Glu Glu Glu Val
100 105 110

Tyr Met Gly Thr Ile Pro Leu Met Thr Asp Lys Gly Thr Phe Ile Ile
115 120 125

Asn Gly Ala Glu Arg Val Val Val Ser Gln Val His Arg Ser Pro Gly
130 135 140

Ile Asn Phe Glu Gln Glu Lys His Ser Lys Gly Asn Ile Leu Phe Ser
145 150 155 160

Phe Arg Ile Ile Pro Tyr Arg Gly Ser Trp Leu Glu Ala Ile Phe Asp
165 170 175

Ile Asn Asp Leu Ile Tyr Ile His Ile Asp Arg Lys Lys Arg Arg Arg
180 185 190

Lys Ile Leu Ala Ile Thr Phe Ile Arg Ala Leu Gly Tyr Ser Ser Asp
195 200 205

Ala Asp Ile Ile Glu Glu Phe Phe Thr Ile Gly Glu Ser Ser Leu Arg
210 215 220

Ser Glu Lys Asp Phe Ala Leu Leu Val Gly Arg Ile Leu Ala Asp Asn
225 230 235 240

Ile Ile Asp Glu Ala Ser Ser Leu Val Tyr Gly Lys Ala Gly Glu Lys
245 250 255

Leu Ser Thr Ala Met Leu Lys Arg Met Leu Asp Ala Gly Ile Ala Ser
260 265 270

Val Lys Ile Ala Val Asp Ala Asp Glu Asn His Pro Ile Ile Lys Met
275 280 285

Leu Ala Lys Asp Pro Thr Asp Ser Tyr Glu Ala Ala Leu Lys Asp Phe
290 295 300

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Tyr Arg Arg Leu Arg Pro Gly Glu Pro Ala Thr Leu Ala Asn Ala Arg
305                 310                 315                 320

Ser Thr Ile Met Arg Leu Phe Phe Asp Pro Lys Arg Tyr Asn Leu Gly
                325                 330                 335

Arg Val Gly Arg Tyr Lys Leu Asn Arg Lys Leu Gly Phe Ser Ile Asp
            340                 345                 350

Asp Glu Ala Leu Ser Gln Val Thr Leu Arg Lys Glu Asp Val Ile Gly
        355                 360                 365

Ala Leu Lys Tyr Leu Ile Arg Leu Lys Met Gly Asp Glu Lys Ala Cys
    370                 375                 380

Val Asp Asp Ile Asp His Leu Ala Asn Arg Arg Val Arg Ser Val Gly
385                 390                 395                 400

Glu Leu Ile Gln Asn Gln Cys Arg Ser Gly Leu Ala Arg Met Glu Lys
                405                 410                 415

Ile Val Arg Glu Arg Met Asn Leu Phe Asp Phe Ser Ser Asp Thr Leu
            420                 425                 430

Thr Pro Gly Lys Val Val Ser Ala Lys Gly Leu Ala Ser Val Leu Lys
        435                 440                 445

Asp Phe Phe Gly Arg Ser Gln Leu Ser Gln Phe Met Asp Gln Thr Asn
    450                 455                 460

Pro Val Ala Glu Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
465                 470                 475                 480

Gly Gly Leu Asn Arg Glu Arg Ala Gly Phe Glu Val Arg Asp Val His
                485                 490                 495

Ala Ser His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu Gly Pro
            500                 505                 510

Asn Ile Gly Leu Ile Thr Ser Leu Ser Ser Phe Ala Lys Ile Asn Glu
        515                 520                 525

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Ile Val Arg Asp Gly Ile Val
    530                 535                 540

Thr Asp Glu Ile Glu Tyr Met Thr Ala Asp Val Glu Glu Glu Cys Val
545                 550                 555                 560

Ile Ala Gln Ala Ser Ala Ser Leu Asp Glu Tyr Asn Met Phe Thr Glu
                565                 570                 575

Pro Val Cys Trp Val Arg Tyr Ala Gly Glu Ala Phe Glu Ala Asp Thr
            580                 585                 590

Ser Thr Val Thr His Met Asp Val Ser Pro Lys Gln Leu Val Ser Ile
        595                 600                 605

Val Thr Gly Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala
    610                 615                 620
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Leu Met Gly Ser Asn Met Gln Arg Gln Ala Val Pro Leu Leu Lys Thr
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Glu Ala Pro Val Val Gly Thr Gly Leu Glu Cys Arg Ala Ala Lys Asp
645 650 655

Ser Gly Ala Ile Val Val Ala Glu Glu Asp Gly Val Val Asp Phe Val
660 665 670

Asp Gly Tyr Lys Val Val Val Ala Ala Lys His Asn Pro Thr Ile Lys
675 680 685

Arg Thr Tyr His Leu Lys Lys Phe Leu Arg Ser Asn Ser Gly Thr Cys
690 695 700

Ile Asn Gln Gln Pro Leu Cys Ala Val Gly Asp Val Ile Thr Lys Gly
705 710 715 720

Asp Val Ile Ala Asp Gly Pro Ala Thr Asp Arg Gly Glu Leu Ala Leu
725 730 735

Gly Lys Asn Val Leu Val Ala Phe Met Pro Trp Tyr Gly Tyr Asn Phe
740 745 750

Glu Asp Ala Ile Ile Ile Ser Glu Lys Leu Ile Arg Glu Asp Ala Tyr
755 760 765

Thr Ser Ile Tyr Ile Glu Glu Phe Glu Leu Thr Ala Arg Asp Thr Lys
770 775 780

Leu Gly Lys Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Asp Glu
785 790 795 800

Val Leu Ala Asn Leu Gly Glu Asp Gly Ile Ile Arg Ile Gly Ala Glu
805 810 815

Val Lys Pro Gly Asp Ile Leu Val Gly Lys Ile Thr Pro Lys Ser Glu
820 825 830

Thr Glu Leu Ala Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu
835 840 845

Lys Ala Ala Asp Val Lys Asp Ala Ser Leu Thr Val Pro Pro Gly Thr
850 855 860

Glu Gly Val Val Met Asp Val Lys Val Phe Ser Arg Lys Asp Arg Leu
865 870 875 880

Ser Lys Ser Asp Asp Glu Leu Val Glu Glu Ala Val His Leu Lys Asp
885 890 895

Leu Gln Lys Gly Tyr Lys Asn Gln Val Ala Thr Leu Lys Thr Glu Tyr
900 905 910

Arg Glu Lys Leu Gly Ala Leu Leu Leu Asn Glu Lys Ala Pro Ala Ala
915 920 925

Ile Ile His Arg Arg Thr Ala Glu Ile Val Val His Glu Gly Leu Leu
930 935 940

Phe Asp Gln Glu Thr Ile Glu Arg Ile Glu Gln Glu Asp Leu Val Asp

945 950 955 960

Leu Leu Met Pro Asn Cys Glu Met Tyr Glu Val Leu Lys Gly Leu Leu
965 970 975

Ser Asp Tyr Glu Thr Ala Leu Gln Arg Leu Glu Ile Asn Tyr Lys Thr
980 985 990

Glu Val Glu His Ile Arg Glu Gly Asp Ala Asp Leu Asp His Gly Val
995 1000 1005

Ile Arg Gln Val Lys Val Tyr Val Ala Ser Lys Arg Lys Leu Gln Val
1010 1015 1020

Gly Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Val Val Ser Lys
1025 1030 1035 1040

Ile Val Pro Glu Ala Asp Met Pro Tyr Leu Ser Asn Gly Glu Thr Val
1045 1050 1055

Gln Met Ile Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Leu Gly
1060 1065 1070

Gln Val Leu Glu Thr His Leu Gly Tyr Ala Ala Lys Thr Ala Gly Ile
1075 1080 1085

Tyr Val Lys Thr Pro Val Phe Glu Gly Phe Pro Glu Gln Arg Ile Trp
1090 1095 1100

Asp Met Met Ile Glu Gln Gly Leu Pro Glu Asp Gly Lys Ser Phe Leu
1105 1110 1115 1120

Tyr Asp Gly Lys Thr Gly Glu Arg Phe Asp Asn Lys Val Val Ile Gly
1125 1130 1135

Tyr Ile Tyr Met Leu Lys Leu Ser His Leu Ile Ala Asp Lys Ile His
1140 1145 1150

Ala Arg Ser Ile Gly Pro Tyr Ser Leu Val Thr Gln Gln Pro Leu Gly
1155 1160 1165

Gly Lys Ala Gln Met Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp
1170 1175 1180

Ala Leu Glu Ala Tyr Gly Val Ala His Met Leu Gln Glu Ile Leu Thr
1185 1190 1195 1200

Val Lys Ser Asp Asp Val Ser Gly Arg Thr Arg Ile Tyr Glu Ser Ile
1205 1210 1215

Val Lys Gly Glu Asn Leu Leu Arg Ser Gly Thr Pro Glu Ser Phe Asn
1220 1225 1230

Val Leu Ile Lys Glu Met Gln Gly Leu Gly Leu Asp Val Arg Pro Met
1235 1240 1245

Val Val Asp Ala
1250

<210> 397

<211> 224
<212> PRT
<213> Chlamydia pneumoniae

<400> 397
Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp Gln His
                5   10   15

Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys Leu Glu
            20   25   30

Lys Gln Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys
        35   40   45

Ala Phe Pro Cys Tyr Leu Ser Ala Leu His Ala Arg Cys Asp Asp Leu
    50   55   60

Gln Ile Arg Arg Gln Ile Leu Glu Asn Leu Met Asp Glu Glu Ala Gly
65   70   75   80

Asn Pro Asn His Ile Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly
                85   90   95

Val Ser Glu Glu Glu Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln
            100   105   110

Asp Met Val Ala Thr Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala
        115   120   125

Val Gly Leu Gly Ala Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val
    130   135   140

Cys Val Glu Lys Ile Arg Gly Leu Lys Glu Tyr Phe Gly Val Ser Ala
145   150   155   160

Arg Gly Tyr Ala Tyr Phe Thr Val His Gln Glu Ala Asp Ile Lys His
                165   170   175

Ala Ser Glu Glu Lys Glu Met Leu Gln Thr Leu Val Gly Arg Glu Asn
            180   185   190

Pro Asp Ala Val Leu Gln Gly Ser Gln Glu Val Leu Asp Thr Leu Trp
        195   200   205

Asn Phe Leu Ser Ser Phe Ile Asn Ser Thr Glu Pro Cys Ser Cys Lys
    210   215   220

<210> 398
<211> 556
<212> PRT
<213> Chlamydia pneumoniae

<400> 398
Met Ser Lys Leu Ile Arg Arg Val Val Thr Val Leu Ala Leu Thr Ser
                5   10   15

Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu Ala Ala Val Ala Glu
            20   25   30

Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu Thr Lys Pro Ala Pro

```
         35                  40                  45

Val Pro Met Thr Ala Lys Lys Val Arg Leu Val Arg Arg Asn Lys Gln
     50                  55                  60

Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys Asp Lys Glu Phe Tyr
 65                  70                  75                  80

Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu Ala Gln Gln Glu Ser
                 85                  90                  95

Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn Asp Asp Cys Asn Val
            100                 105                 110

Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr
        115                 120                 125

Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp Cys Val Asp Val Val
    130                 135                 140

Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro
145                 150                 155                 160

Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val Trp Lys Ile Asp Arg
                165                 170                 175

Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu
            180                 185                 190

Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu
        195                 200                 205

Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala Ile Cys Ile Lys Gln
    210                 215                 220

Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro Val Cys Tyr Lys Ile
225                 230                 235                 240

Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg Asn Val Thr Val Asp
                245                 250                 255

Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser Gly Gln Arg Val Leu
            260                 265                 270

Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp Lys Lys Val Phe Thr
        275                 280                 285

Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile Thr Asn Val Ala Thr
    290                 295                 300

Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala Asn Val Thr Thr Val
305                 310                 315                 320

Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser Gly Ala Asp Trp Ser
                325                 330                 335

Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser Val Ser Asn Pro Gly
            340                 345                 350

Asp Leu Val Leu His Asp Val Val Ile Gln Asp Thr Leu Pro Ser Gly
        355                 360                 365
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Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val
370 375 380

Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys
385 390 395 400

Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala
405 410 415

Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr Ser Cys Ala Glu Thr
420 425 430

Thr Thr His Trp Lys Gly Leu Ala Ala Thr His Met Cys Val Leu Asp
435 440 445

Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys
450 455 460

Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu
465 470 475 480

Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys
485 490 495

Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu
500 505 510

Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala
515 520 525

Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr
530 535 540

Ser Pro Val Ser Asp Thr Glu Asn Thr His Val Tyr
545 550 555

<210> 399
<211> 461
<212> PRT
<213> Chlamydia pneumoniae

<400> 399
Met Thr Gln Glu Phe Asp Cys Val Val Ile Gly Ala Gly Pro Ser Gly
5 10 15

Tyr Val Ala Ala Ile Thr Ala Ala Gln Ser Lys Leu Arg Thr Ala Leu
20 25 30

Ile Glu Glu Asp Gln Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile
35 40 45

Pro Ser Lys Ala Leu Ile Ala Gly Ala Asn Val Val Ser His Ile Lys
50 55 60

His Ala Glu Gln Phe Gly Ile His Val Asp Gly Tyr Thr Ile Asp Tyr
65 70 75 80

Pro Ala Met Ala Lys Arg Lys Asn Thr Val Val Gln Gly Ile Arg Gln
85 90 95

```
Gly Leu Glu Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Leu Lys Gly
            100                 105                 110

Thr Gly Ser Leu Val Ser Ser Thr Glu Val Lys Val Ile Gly Gln Asp
        115                 120                 125

Thr Thr Ile Ile Lys Ala Asn His Ile Ile Leu Ala Thr Gly Ser Glu
    130                 135                 140

Pro Arg Pro Phe Pro Gly Val Pro Phe Ser Ser Arg Ile Leu Ser Ser
145                 150                 155                 160

Thr Gly Ile Leu Glu Leu Glu Val Leu Pro Lys Lys Leu Ala Ile Ile
                165                 170                 175

Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu
            180                 185                 190

Gly Val Glu Ile Thr Val Ile Glu Ala Leu Asp His Ile Leu Ala Val
        195                 200                 205

Asn Asn Lys Glu Val Ser Gln Thr Val Thr Asn Lys Phe Thr Lys Gln
    210                 215                 220

Gly Ile Arg Ile Leu Thr Lys Ala Ser Ile Ser Ala Ile Glu Glu Ser
225                 230                 235                 240

Gln Asn Gln Val Arg Ile Thr Val Asn Asp Gln Val Glu Glu Phe Asp
                245                 250                 255

Tyr Val Leu Val Ala Ile Gly Arg Gln Phe Asn Thr Ala Ser Ile Gly
            260                 265                 270

Leu Asp Asn Ala Gly Val Ile Arg Asp Asp Arg Gly Val Ile Pro Val
        275                 280                 285

Asp Glu Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp
    290                 295                 300

Ile Thr Gly Lys Trp Leu Leu Ala His Val Ala Ser His Gln Gly Val
305                 310                 315                 320

Ile Ala Ala Lys Asn Ile Ser Gly His His Glu Val Met Asp Tyr Ser
                325                 330                 335

Ala Ile Pro Ser Val Ile Phe Thr His Pro Glu Ile Ala Met Val Gly
            340                 345                 350

Leu Ser Leu Gln Glu Ala Glu Gln Gln Asn Leu Pro Ala Lys Leu Thr
        355                 360                 365

Lys Phe Pro Phe Lys Ala Ile Gly Lys Ala Val Ala Leu Gly Ala Ser
    370                 375                 380

Asp Gly Phe Ala Ala Ile Val Ser His Glu Ile Thr Gln Gln Ile Leu
385                 390                 395                 400

Gly Ala Tyr Val Ile Gly Pro His Ala Ser Ser Leu Ile Gly Glu Met
                405                 410                 415
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Thr Leu Ala Ile Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr
420 425 430

Val His Ala His Pro Thr Leu Ser Glu Val Trp Ala Glu Gly Ala Leu
435 440 445

Leu Ala Thr Asn His Pro Leu His Phe Pro Pro Lys Ser
450 455 460

<210> 400
<211> 544
<212> PRT
<213> Chlamydia pneumoniae

<400> 400
Met Ala Ala Lys Asn Ile Lys Tyr Asn Glu Glu Ala Arg Lys Lys Ile
5 10 15

His Lys Gly Val Lys Thr Leu Ala Glu Ala Val Lys Val Thr Leu Gly
20 25 30

Pro Lys Gly Arg His Val Val Ile Asp Lys Ser Phe Gly Ser Pro Gln
35 40 45

Val Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Glu Asp
50 55 60

Lys His Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65 70 75 80

Thr Ala Asp Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
85 90 95

Glu Ala Ile Tyr Ser Glu Gly Leu Arg Asn Val Thr Ala Gly Ala Asn
100 105 110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Lys Val Val Val
115 120 125

Asp Glu Leu Lys Lys Ile Ser Lys Pro Val Gln His His Lys Glu Ile
130 135 140

Ala Gln Val Ala Thr Ile Ser Ala Asn Asn Asp Ser Glu Ile Gly Asn
145 150 155 160

Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Asn Gly Ser Ile Thr
165 170 175

Val Glu Glu Ala Lys Gly Phe Glu Thr Val Leu Asp Val Val Glu Gly
180 185 190

Met Asn Phe Asn Arg Gly Tyr Leu Ser Ser Tyr Phe Ser Thr Asn Pro
195 200 205

Glu Thr Gln Glu Cys Val Leu Glu Asp Ala Leu Ile Leu Ile Tyr Asp
210 215 220

Lys Lys Ile Ser Gly Ile Lys Asp Phe Leu Pro Val Leu Gln Gln Val
225 230 235 240

```
Ala Glu Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Glu Ile Glu Gly
                245                 250                 255

Glu Ala Leu Ala Thr Leu Val Val Asn Arg Leu Arg Ala Gly Phe Arg
            260                 265                 270

Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
        275                 280                 285

Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Gln Leu Val Ser Glu Glu
    290                 295                 300

Leu Gly Met Lys Leu Glu Asn Thr Thr Leu Ala Met Leu Gly Lys Ala
305                 310                 315                 320

Lys Lys Val Ile Val Thr Lys Glu Asp Thr Thr Ile Val Glu Gly Leu
                325                 330                 335

Gly Asn Lys Pro Asp Ile Gln Ala Arg Cys Asp Asn Ile Lys Lys Gln
            340                 345                 350

Ile Glu Asp Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg
        355                 360                 365

Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Arg Val Gly Ala Ala
    370                 375                 380

Thr Glu Ile Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Gln
385                 390                 395                 400

His Ala Thr Ile Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly Gly
                405                 410                 415

Thr Ala Leu Val Arg Cys Ile Pro Thr Leu Glu Ala Phe Leu Pro Met
            420                 425                 430

Leu Ala Asn Glu Asp Glu Ala Ile Gly Thr Arg Ile Ile Leu Lys Ala
        435                 440                 445

Leu Thr Ala Pro Leu Lys Gln Ile Ala Ser Asn Ala Gly Lys Glu Gly
    450                 455                 460

Ala Ile Ile Cys Gln Gln Val Leu Ala Arg Ser Ala Asn Glu Gly Tyr
465                 470                 475                 480

Asp Ala Leu Arg Asp Ala Tyr Thr Asp Met Ile Asp Ala Gly Ile Leu
                485                 490                 495

Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Glu Ser Ala Ala Ser Ile
            500                 505                 510

Ala Gly Leu Leu Leu Thr Thr Glu Ala Leu Ile Ala Asp Ile Pro Glu
        515                 520                 525

Glu Lys Ser Ser Ser Ala Pro Ala Met Pro Ser Ala Gly Met Asp Tyr
    530                 535                 540
```

<210> 401
<211> 664
<212> PRT

<213> Chlamydia pneumoniae

<400> 401
```
Met Glu Lys Val Ser Ser Tyr Pro Ser Val Pro Leu Pro Leu Gly Ala
                5                   10                  15

Ser Lys Ile Ser Pro Asn Arg Tyr Arg Phe Ala Leu Tyr Ala Ser Gln
            20                  25                  30

Ala Thr Glu Val Ile Leu Ala Leu Thr Asp Glu Asn Ser Glu Val Ile
        35                  40                  45

Glu Val Pro Leu Tyr Pro Asp Thr His Arg Thr Gly Ala Ile Trp His
    50                  55                  60

Ile Glu Ile Glu Gly Ile Ser Asp Gln Ser Ser Tyr Ala Phe Arg Val
65                  70                  75                  80

His Gly Pro Lys Lys His Gly Met Gln Tyr Ser Phe Lys Glu Tyr Leu
                85                  90                  95

Ala Asp Pro Tyr Ala Lys Asn Ile His Ser Pro Gln Ser Phe Gly Ser
            100                 105                 110

Arg Lys Lys Gln Gly Asp Tyr Ala Phe Cys Tyr Leu Lys Glu Glu Pro
        115                 120                 125

Phe Pro Trp Asp Gly Asp Gln Pro Leu His Leu Pro Lys Glu Glu Met
    130                 135                 140

Ile Ile Tyr Glu Met His Val Arg Ser Phe Thr Gln Ser Ser Ser Ser
145                 150                 155                 160

Arg Val His Ala Pro Gly Thr Phe Leu Gly Ile Ile Glu Lys Ile Asp
                165                 170                 175

His Leu His Lys Leu Gly Ile Asn Ala Val Glu Leu Leu Pro Ile Phe
            180                 185                 190

Glu Phe Asp Glu Thr Ala His Pro Phe Arg Asn Ser Lys Phe Pro Tyr
        195                 200                 205

Leu Cys Asn Tyr Trp Gly Tyr Ala Pro Leu Asn Phe Phe Ser Pro Cys
    210                 215                 220

Arg Arg Tyr Ala Tyr Ala Ser Asp Pro Cys Ala Pro Ser Arg Glu Phe
225                 230                 235                 240

Lys Thr Leu Val Lys Thr Leu His Gln Glu Gly Ile Glu Val Ile Leu
                245                 250                 255

Asp Val Val Phe Asn His Thr Gly Leu Gln Gly Thr Thr Cys Ser Leu
            260                 265                 270

Pro Trp Ile Asp Thr Pro Ser Tyr Tyr Ile Leu Asp Ala Gln Gly His
        275                 280                 285

Phe Thr Asn Tyr Ser Gly Cys Gly Asn Thr Leu Asn Thr Asn Arg Ala
    290                 295                 300

Pro Thr Thr Gln Trp Ile Leu Asp Ile Leu Arg Tyr Trp Val Glu Glu
```

```
305                 310                 315                 320

Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Val Phe Ser Arg
                325                 330                 335

Gly Pro Ser Gly Ser Pro Leu Gln Phe Ala Pro Val Leu Glu Ala Ile
            340                 345                 350

Ser Phe Asp Pro Leu Leu Ala Ser Thr Lys Ile Ile Ala Glu Pro Trp
        355                 360                 365

Asp Ala Gly Gly Leu Tyr Gln Val Gly Tyr Phe Pro Thr Leu Ser Pro
    370                 375                 380

Arg Trp Ser Glu Trp Asn Gly Pro Tyr Arg Asp Asn Val Lys Ala Phe
385                 390                 395                 400

Leu Asn Gly Asp Gln Asn Leu Ile Gly Thr Phe Ala Ser Arg Ile Ser
                405                 410                 415

Gly Ser Gln Asp Ile Tyr Pro His Gly Ser Pro Thr Asn Ser Ile Asn
            420                 425                 430

Tyr Val Ser Cys His Asp Gly Phe Thr Leu Cys Asp Thr Val Thr Tyr
        435                 440                 445

Asn His Lys His Asn Glu Ala Asn Gly Glu Asp Asn Arg Asp Gly Thr
    450                 455                 460

Asp Ala Asn Tyr Ser Tyr Asn Phe Gly Thr Glu Gly Lys Thr Glu Asp
465                 470                 475                 480

Pro Gly Ile Leu Glu Val Arg Glu Arg Gln Leu Arg Asn Phe Phe Leu
                485                 490                 495

Thr Leu Met Val Ser Gln Gly Ile Pro Met Ile Gln Ser Gly Asp Glu
            500                 505                 510

Tyr Ala His Thr Ala Glu Gly Asn Asn Asn Arg Trp Ala Leu Asp Ser
        515                 520                 525

Asn Ala Asn Tyr Phe Leu Trp Asp Gln Leu Thr Ala Lys Pro Thr Leu
    530                 535                 540

Met His Phe Leu Cys Asp Leu Ile Ala Phe Arg Lys Lys Tyr Lys Thr
545                 550                 555                 560

Leu Phe Asn Arg Gly Phe Leu Ser Asn Lys Glu Ile Ser Trp Val Asp
                565                 570                 575

Ala Met Gly Asn Pro Met Thr Trp Arg Pro Gly Asn Phe Leu Ala Phe
            580                 585                 590

Lys Ile Lys Ser Pro Lys Ala His Val Tyr Val Ala Phe His Val Gly
        595                 600                 605

Ala Gln Asp Gln Leu Ala Thr Leu Pro Lys Ala Ser Ser Asn Phe Leu
    610                 615                 620

Pro Tyr Gln Ile Val Ala Glu Ser Gln Gln Gly Phe Val Pro Gln Asn
625                 630                 635                 640
```

Val Ala Thr Pro Thr Val Ser Leu Gln Pro His Thr Thr Leu Ile Ala
645 650 655

Ile Ser His Ala Lys Glu Val Thr
660

<210> 402
<211> 328
<212> PRT
<213> Chlamydia pneumoniae

<400> 402
Met Ala Phe Lys Glu Val Val Arg Val Ala Val Thr Gly Gly Lys Gly
5 10 15

Gln Ile Ala Tyr Asn Phe Leu Phe Ala Leu Ala His Gly Asp Val Phe
20 25 30

Gly Val Asp Arg Gly Val Asp Leu Arg Ile Tyr Asp Val Pro Gly Thr
35 40 45

Glu Arg Ala Leu Ser Gly Val Arg Met Glu Leu Asp Asp Gly Ala Tyr
50 55 60

Pro Leu Leu His Arg Leu Arg Val Thr Thr Ser Leu Asn Asp Ala Phe
65 70 75 80

Asp Gly Ile Asp Ala Ala Phe Leu Ile Gly Ala Val Pro Arg Gly Pro
85 90 95

Gly Met Glu Arg Gly Asp Leu Leu Lys Gln Asn Gly Gln Ile Phe Ser
100 105 110

Leu Gln Gly Ala Ala Leu Asn Thr Ala Ala Lys Arg Asp Ala Lys Ile
115 120 125

Phe Val Val Gly Asn Pro Val Asn Thr Asn Cys Trp Ile Ala Met Lys
130 135 140

His Ala Pro Arg Leu His Arg Lys Asn Phe His Ala Met Leu Arg Leu
145 150 155 160

Asp Gln Asn Arg Met His Ser Met Leu Ala His Arg Ala Glu Val Pro
165 170 175

Leu Glu Glu Val Ser Arg Val Val Ile Trp Gly Asn His Ser Ala Lys
180 185 190

Gln Val Pro Asp Phe Thr Gln Ala Arg Ile Ser Gly Lys Pro Ala Ala
195 200 205

Glu Val Ile Gly Asp Arg Asp Trp Leu Glu Asn Ile Leu Val His Ser
210 215 220

Val Gln Asn Arg Gly Ser Ala Val Ile Glu Ala Arg Gly Lys Ser Ser
225 230 235 240

Ala Ala Ser Ala Ser Arg Ala Leu Ala Glu Ala Ala Arg Ser Ile Phe
245 250 255

```
Cys Pro Lys Ser Asp Glu Trp Phe Ser Ser Gly Val Cys Ser Asp His
            260                 265                 270

Asn Pro Tyr Gly Ile Pro Glu Asp Leu Ile Phe Gly Phe Pro Cys Arg
        275                 280                 285

Met Leu Pro Ser Gly Asp Tyr Glu Ile Ile Pro Gly Leu Pro Trp Glu
    290                 295                 300

Pro Phe Ile Arg Asn Lys Ile Gln Ile Ser Leu Asp Glu Ile Ala Gln
305                 310                 315                 320

Glu Lys Ala Ser Val Ser Ser Leu
                325


<210> 403
<211> 217
<212> PRT
<213> Chlamydia pneumoniae

<400> 403
Met Lys Arg Val Ile Tyr Lys Thr Ile Phe Cys Gly Leu Thr Leu Leu
                5                   10                  15

Thr Ser Leu Ser Ser Cys Ser Leu Asp Pro Lys Gly Tyr Asn Leu Glu
            20                  25                  30

Thr Lys Asn Ser Arg Asp Leu Asn Gln Glu Ser Val Ile Leu Lys Glu
        35                  40                  45

Asn Arg Glu Thr Pro Ser Leu Val Lys Arg Leu Ser Arg Arg Ser Arg
    50                  55                  60

Arg Leu Phe Ala Arg Arg Asp Gln Thr Gln Lys Asp Thr Leu Gln Val
65                  70                  75                  80

Gln Ala Asn Phe Lys Thr Tyr Ala Glu Lys Ile Ser Glu Gln Asp Glu
                85                  90                  95

Arg Asp Leu Ser Phe Val Val Ser Ser Ala Ala Glu Lys Ser Ser Ile
            100                 105                 110

Ser Leu Ala Leu Ser Gln Gly Glu Ile Lys Asp Ala Leu Tyr Arg Ile
        115                 120                 125

Arg Glu Val His Pro Leu Ala Leu Ile Glu Ala Leu Ala Glu Asn Pro
    130                 135                 140

Ala Leu Ile Glu Gly Met Lys Lys Met Gln Gly Arg Asp Trp Ile Trp
145                 150                 155                 160

Asn Leu Phe Leu Thr Gln Leu Ser Glu Val Phe Ser Gln Ala Trp Ser
                165                 170                 175

Gln Gly Val Ile Ser Glu Glu Asp Ile Ala Ala Phe Ala Ser Thr Leu
            180                 185                 190

Gly Leu Asp Ser Gly Thr Val Ala Ser Ile Val Gln Gly Glu Arg Trp
        195                 200                 205
```

Pro Glu Leu Val Asp Ile Val Ile Thr
    210   215

<210> 404
<211> 270
<212> PRT
<213> Chlamydia pneumoniae

<400> 404
Met Ile Ile Ile Lys Asn Asn Glu Leu Met Ile Arg Arg Phe Phe Lys
                5   10   15

Thr Leu Phe Pro Pro Gly Pro Gln Tyr Ser Leu Cys Tyr Ala Ser Ile
            20   25   30

Leu Ile Val Leu Ser Ser Leu Val Cys Val Pro Thr Phe Cys Trp Leu
        35   40   45

Phe Leu Pro Glu Leu Ser Leu Ser Lys Phe Asn Pro Ser Pro Ile Arg
    50   55   60

Asn Leu Phe Leu Val Ser Ser Thr Leu Ser Lys Val Pro Pro Thr Ala
65   70   75   80

Ile Ala Glu His Leu Arg Leu Ser Ala Asp Ala Pro Thr Tyr Leu His
                85   90   95

Glu Phe Ser Ile Lys Glu Ala Glu Ser Ser Leu His Ala Leu Gly Ile
            100   105   110

Phe Ser Ser Leu Val Ile Glu Lys Ser Pro Asp Asn Lys Gly Ile Thr
        115   120   125

Ile Phe Tyr Thr Leu Gln Thr Pro Ile Ala Tyr Val Gly Asn Arg Ser
    130   135   140

Asn Thr Leu Cys Asn Leu Glu Gly Ser Cys Phe Leu Gly Gln Pro Tyr
145   150   155   160

Phe Pro Ser Leu Asn Leu Pro Gln Ile Phe Phe Ser Gln Glu Asp Leu
                165   170   175

Lys Met Gln Lys Leu Pro Lys Glu Lys Met Leu Phe Thr Lys Ile Leu
            180   185   190

Leu Lys Glu Leu Ala Met Glu Ser Pro Lys Ile Ile Asp Leu Ser Leu
        195   200   205

Ser Asp Ala Tyr Pro Gly Glu Ile Ile Val Thr Leu Ser Ser Gly Ser
    210   215   220

Leu Leu Arg Leu Pro Ile Lys Thr Leu Asp Arg Ala Leu Asp Leu Tyr
225   230   235   240

Lys His Met Lys Lys Ser Pro Val Ile Glu Ser Glu Lys Gln Tyr Val
                245   250   255

Tyr Asp Leu Arg Phe Pro Asn Phe Leu Leu Leu Lys Ala Leu
            260   265   270

<210> 405
<211> 651
<212> PRT
<213> Chlamydia pneumoniae

<400> 405
```
Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr
                5                   10                  15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn
            20                  25                  30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
        35                  40                  45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
    50                  55                  60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
65                  70                  75                  80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
                85                  90                  95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
            100                 105                 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
        115                 120                 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
    130                 135                 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145                 150                 155                 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
                165                 170                 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
            180                 185                 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
        195                 200                 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
    210                 215                 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225                 230                 235                 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
                245                 250                 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
            260                 265                 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
        275                 280                 285
```

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Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
    290                 295                 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305                 310                 315                 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
                325                 330                 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
            340                 345                 350

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
        355                 360                 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
    370                 375                 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
385                 390                 395                 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
                405                 410                 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
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Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
        435                 440                 445

Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val
    450                 455                 460

Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr
465                 470                 475                 480

Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr
                485                 490                 495

Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser
            500                 505                 510

Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg
        515                 520                 525

Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn
    530                 535                 540

Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser
545                 550                 555                 560

Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile
                565                 570                 575

Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr
            580                 585                 590

Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys
        595                 600                 605
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Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys
    610                 615                 620

Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val
625                 630                 635                 640

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<210> 406
<211> 1074
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 406
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gaacaattgt ccattccata ttacacagtt tcctttteta aggaatataa agagcgagtg 240
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<210> 407
<211> 1827
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 407
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<211> 804
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 409
<211> 663
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 410
<211> 1470
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 411
<211> 234
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 411
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ctgaaagagg tgcagggaac caatacgatt atctacgaat tgactgttgc taagggagat 120
atcggtaaaa ttatcggtaa agaaggacgc actattaagg ctatccgtac tttattggtt 180
tccgtagcaa gtcgagataa tgtgaaagtc agcctagaaa ttatggaaga gcgg 234

<210> 412
<211> 1941
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 412
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gagaatgcgt ttagaaaaca gcccgctttc attcaacagg tgttggtaaa cattgcttct 1920
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<210> 413
<211> 693
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 413
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ccaggaactt gttgtagttg tcatcaatct tat 693

<210> 414
<211> 1599
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 414
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<210> 415
<211> 1395
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 415
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atcactgccg ctcaagcagg actcaaaact gcgctaatcg aaaagcgaga ggctggcgga 120
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<210> 416
<211> 366
<212> DNA
<213> Chlamydia trachomatis serovar D

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cccgaagcta gagctgcaga gttgactgag gaagaggttg gtcgactaaa cgctctttta 180
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aagaaa 366

<210> 417
<211> 1659
<212> DNA
<213> Chlamydia trachomatis serovar D

<400> 417
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<212> DNA
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<211> 5310
<212> DNA
<213> Chlamydia trachomatis serovar D

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<211> 5253
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 422
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<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 423
<211> 978
<212> DNA
<213> Chlamydia trachomatis serovar D

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<212> DNA
<213> Chlamydia trachomatis serovar D

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<211> 3756
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 426
<211> 894
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 427
<211> 894
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 428
<211> 459
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 429
<211> 1707
<212> DNA
<213> Chlamydia trachomatis serovar D

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<210> 430
<211> 1998
<212> DNA
<213> Chlamydia trachomatis serovar D

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cccagagagt ggggagccga tcattatcta gcttttgagt tgaaacacct gaactacagt 1800
ttattcgtag cgttttatag tgggaatgaa cgtattgaga tctctttacc taaacctaga 1860
aaagaacatt tggcctatga aaaaattgta gatagcacaa caggattctt ttctcagata 1920
ttatctccca aactctctct tgaaccttat agctctttgg tagccatcag cagaagaaaa 1980
acctccttgg aatctaga 1998

<210> 431
<211> 609
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 431

```
Met Gly Phe Trp Arg Thr Ser Ile Met Lys Met Asn Arg Ile Trp Leu
                5                   10                  15

Leu Leu Leu Thr Phe Ser Ser Ala Ile His Ser Pro Val Gln Gly Glu
            20                  25                  30

Ser Leu Val Cys Lys Asn Ala Leu Gln Asp Leu Ser Phe Leu Glu His
        35                  40                  45

Leu Leu Gln Val Lys Tyr Ala Pro Lys Thr Trp Lys Glu Gln Tyr Leu
    50                  55                  60

Gly Trp Asp Leu Val Gln Ser Ser Val Ser Ala Gln Gln Lys Leu Arg
65                  70                  75                  80

Thr Gln Glu Asn Pro Ser Thr Ser Phe Cys Gln Gln Val Leu Ala Asp
                85                  90                  95

Phe Ile Gly Gly Leu Asn Asp Phe His Ala Gly Val Thr Phe Phe Ala
            100                 105                 110

Ile Glu Ser Ala Tyr Leu Pro Tyr Thr Val Gln Lys Ser Ser Asp Gly
        115                 120                 125

Arg Phe Tyr Phe Val Asp Ile Met Thr Phe Ser Ser Glu Ile Arg Val
    130                 135                 140

Gly Asp Glu Leu Leu Glu Val Asp Gly Ala Pro Val Gln Asp Val Leu
145                 150                 155                 160

Ala Thr Leu Tyr Gly Ser Asn His Lys Gly Thr Ala Ala Glu Glu Ser
                165                 170                 175

Ala Ala Leu Arg Thr Leu Phe Ser Arg Met Ala Ser Leu Gly His Lys
            180                 185                 190

Val Pro Ser Gly Arg Thr Thr Leu Lys Ile Arg Arg Pro Phe Gly Thr
        195                 200                 205

Thr Arg Glu Val Arg Val Lys Trp Arg Tyr Val Pro Glu Gly Val Gly
    210                 215                 220

Asp Leu Ala Thr Ile Ala Pro Ser Ile Arg Ala Pro Gln Leu Gln Lys
225                 230                 235                 240

Ser Met Arg Ser Phe Phe Pro Lys Lys Asp Asp Ala Phe His Arg Ser
                245                 250                 255

Ser Ser Leu Phe Tyr Ser Pro Met Val Pro His Phe Trp Ala Glu Leu
            260                 265                 270

Arg Asn His Tyr Ala Thr Ser Gly Leu Lys Ser Gly Tyr Asn Ile Gly
        275                 280                 285

Ser Thr Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser
    290                 295                 300

Glu Gly Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly
305                 310                 315                 320

Lys Ser His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln
```

```
                325                 330                 335

Asp Met Glu Asp Phe Asp Pro Ser Gly Pro Pro Pro Trp Glu Glu Phe
            340                 345                 350

Ala Lys Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile
        355                 360                 365

Asp Gln Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu
    370                 375                 380

Leu Ser Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met
385                 390                 395                 400

Ile Leu Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu
                405                 410                 415

Leu Glu Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp
            420                 425                 430

Asn Met Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys
        435                 440                 445

Ser Phe Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu
    450                 455                 460

Leu Ser Thr Pro Ile Pro Leu Phe Gly Phe Glu Lys Ile His Pro His
465                 470                 475                 480

Pro Arg Val Gln Tyr Ser Lys Pro Ile Cys Val Leu Ile Asn Glu Gln
                485                 490                 495

Asp Phe Ser Cys Ala Asp Phe Phe Pro Val Val Leu Lys Asp Asn Asp
            500                 505                 510

Arg Ala Leu Ile Val Gly Thr Arg Thr Ala Gly Ala Gly Gly Phe Val
        515                 520                 525

Phe Asn Val Gln Phe Pro Asn Arg Thr Gly Ile Lys Thr Cys Ser Leu
    530                 535                 540

Thr Gly Ser Leu Ala Val Arg Glu His Gly Ala Phe Ile Glu Asn Ile
545                 550                 555                 560

Gly Val Glu Pro His Ile Asp Leu Pro Phe Thr Ala Asn Asp Ile Arg
                565                 570                 575

Tyr Lys Gly Tyr Ser Glu Tyr Leu Asp Lys Val Lys Lys Leu Val Cys
            580                 585                 590

Gln Leu Ile Asn Asn Asp Gly Thr Ile Ile Leu Ala Glu Asp Gly Ser
        595                 600                 605

Phe


<210> 432
<211> 268
<212> PRT
<213> Chlamydia trachomatis serovar D
```

<400> 432
Met Pro Pro Arg Ser Pro Ser Phe Leu Val His Ile Trp Arg Leu Phe
5 10 15

Phe Ala Lys Gly Pro Asn Tyr Ser Leu Pro Tyr Ala Phe Leu Cys Ile
20 25 30

Phe Val Ser Val Leu Val Phe Leu Pro Ile Gly Leu Trp Leu Thr Leu
35 40 45

Pro Ser Phe Leu Asn Phe Lys His Ser Leu Thr Pro Ile Lys Thr Leu
50 55 60

Phe Leu Thr Cys Thr Glu Pro Pro Cys Leu Pro Glu Pro Phe Phe Ser
65 70 75 80

Asp Ile Leu His Leu Ser Ala Asp Ser Pro Pro Ala Leu Gln Thr Phe
85 90 95

Ser Thr Lys Ser Ala Glu His Phe Leu Asn Glu Leu Gly Val Phe Ser
100 105 110

Phe Ile Ser Ile Glu Lys Val Pro Asp His Lys Gly Leu Ala Ile Ser
115 120 125

Tyr Ala Leu His Thr Pro Leu Ala Phe Leu Gly Asn Gln Thr His Thr
130 135 140

Phe Ile Gly Tyr Glu Gly Gln Thr Phe Pro Ala Leu Pro Phe Phe Gln
145 150 155 160

Ser Leu Glu Leu Pro Thr Val Phe Phe Ser Gln Gln Ala Leu Ser Gln
165 170 175

Thr Arg Ile Pro His Gln Thr Leu Ser Ile Val Thr Ser Leu Ile Asp
180 185 190

Gln Leu Gln Met Asp Pro Pro Ser Ile Ile Asp Leu Ser Gln Ile Asp
195 200 205

His Tyr Pro Gly Glu Phe Val Val Ser Leu Ser Ser Gly Thr Leu Leu
210 215 220

Arg Phe Arg Lys Asp Ser Phe Leu Pro Gly Ile Gln His Tyr Gln Gln
225 230 235 240

Ala Leu Ser Leu Gly Ala Phe Ser Pro Gln Gln Ala Val Ile Cys Asp
245 250 255

Leu Arg Cys Glu Asp Tyr Leu Leu Leu Lys Arg Lys
260 265

<210> 433
<211> 221
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 433
Met Lys Lys Phe Ile Tyr Lys Tyr Ser Phe Gly Ala Leu Leu Leu Leu

5 10 15

Ser Gly Leu Ser Gly Leu Ser Ser Cys Cys Ala Asn Ser Tyr Gly Ser
20 25 30

Thr Leu Ala Lys Asn Thr Ala Glu Ile Lys Glu Glu Ser Val Thr Leu
35 40 45

Arg Glu Lys Pro Asp Ala Gly Cys Lys Lys Lys Ser Ser Cys Tyr Leu
50 55 60

Arg Lys Phe Phe Ser Arg Lys Lys Pro Lys Glu Lys Thr Glu Pro Val
65 70 75 80

Leu Pro Asn Phe Lys Ser Tyr Ala Asp Pro Met Thr Asp Ser Glu Arg
85 90 95

Lys Asp Leu Ser Phe Val Val Ser Ala Ala Ala Asp Lys Ser Ser Ile
100 105 110

Ala Leu Ala Met Ala Gln Gly Glu Ile Lys Gly Ala Leu Ser Arg Ile
115 120 125

Arg Glu Ile His Pro Leu Ala Leu Leu Gln Ala Leu Ala Glu Asp Pro
130 135 140

Ala Leu Ile Ala Gly Met Lys Lys Met Gln Gly Arg Asp Trp Val Trp
145 150 155 160

Asn Ile Phe Ile Thr Glu Leu Ser Lys Val Phe Ser Gln Ala Ala Ser
165 170 175

Leu Gly Ala Phe Ser Val Ala Asp Val Ala Ala Phe Ala Ser Thr Leu
180 185 190

Gly Leu Asp Ser Gly Thr Val Thr Ser Ile Val Asp Gly Glu Arg Trp
195 200 205

Ala Glu Leu Ile Asp Val Val Ile Gln Asn Pro Ala Ile
210 215 220

<210> 434
<211> 490
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 434
Met Ser Asp Leu Ser Asp Leu Phe Lys Thr His Phe Thr Gln Tyr Ala
5 10 15

Ser Tyr Val Ile Leu Glu Arg Ala Ile Pro His Val Leu Asp Gly Leu
20 25 30

Lys Pro Val Gln Arg Arg Leu Leu Trp Thr Leu Phe Arg Met Asp Asp
35 40 45

Gly Lys Met His Lys Val Ala Asn Ile Ala Gly Arg Thr Met Ala Leu
50 55 60

His Pro His Gly Asp Ala Pro Ile Val Glu Ala Leu Val Val Leu Ala

```
65                  70                  75                  80

Asn Lys Gly Phe Leu Ile Glu Thr Gln Gly Asn Phe Gly Asn Pro Leu
                85                  90                  95

Thr Gly Asp Pro His Ala Ala Ala Arg Tyr Ile Glu Ala Arg Leu Ser
            100                 105                 110

Pro Leu Ala Lys Glu Val Leu Phe Asn Thr Asp Leu Met Thr Phe His
        115                 120                 125

Asp Ser Tyr Asp Gly Arg Glu Gln Glu Pro Asp Ile Leu Ala Ala Lys
    130                 135                 140

Ile Pro Leu Leu Leu Leu His Gly Val Asp Gly Ile Ala Val Gly Met
145                 150                 155                 160

Thr Thr Lys Ile Phe Pro His Asn Phe Cys Asp Leu Leu Glu Ala Gln
                165                 170                 175

Ile Ala Ile Leu Asn Asp Gln Pro Phe Ser Leu Leu Pro Asp Phe Pro
            180                 185                 190

Pro Gly Gly Thr Met Asp Ala Ser Asp Tyr Gln Asp Gly Leu Gly Ser
        195                 200                 205

Ile Val Leu Arg Ala Thr Ile Asp Ile Ile Asn Asp Lys Thr Leu Leu
    210                 215                 220

Ile Lys Glu Ile Cys Pro Ser Thr Thr Thr Glu Thr Leu Ile Arg Ser
225                 230                 235                 240

Ile Glu Asn Ala Ala Lys Arg Gly Ile Ile Lys Ile Asp Ser Ile Gln
                245                 250                 255

Asp Phe Ser Thr Asp Leu Pro His Ile Glu Ile Lys Leu Pro Lys Gly
            260                 265                 270

Ile Tyr Ala Lys Asp Leu Leu Arg Pro Leu Tyr Thr His Thr Glu Cys
        275                 280                 285

Gln Val Ile Leu Thr Ser Arg Pro Thr Ala Ile Tyr Gln Gly Lys Pro
    290                 295                 300

Trp Glu Thr Thr Ile Ser Glu Ile Leu Arg Leu Gln Thr Lys Thr Leu
305                 310                 315                 320

Gln Asn Tyr Leu Lys Lys Glu Leu Leu Ile Leu Glu Asp Ser Leu Ser
                325                 330                 335

Arg Glu Leu Tyr His Lys Thr Leu Glu Tyr Leu Phe Ile Lys His Lys
            340                 345                 350

Leu Tyr Asp Thr Val Arg Ser Met Leu Ser Lys Arg Lys Thr Ser Pro
        355                 360                 365

Ser Ser Ser Thr Ile His Asn Ala Val Leu Glu Ala Leu Thr Pro Phe
    370                 375                 380

Leu Asp Thr Leu Pro Ala Pro Asp Lys Gln Ala Thr Ala Gln Leu Ala
385                 390                 395                 400
```

Ala Leu Thr Ile Lys Lys Ile Leu Cys Phe Asp Glu Asn Ser Tyr Glu
405 410 415

Lys Glu Leu Ala Cys Leu Glu Lys Lys Arg Ser Ser Val Gln Lys Asp
420 425 430

Leu Ser Gln Leu Lys Lys Tyr Thr Val Leu Tyr Ile Lys Lys Leu Leu
435 440 445

Glu Thr Tyr Arg Gln Leu Gly His Arg Lys Thr Lys Ile Ala Lys Phe
450 455 460

Asp Asp Leu Pro Thr Glu Arg Val Ser Ala His Lys Lys Ala Lys Glu
465 470 475 480

Leu Ala Ala Leu Asp Gln Glu Glu Asn Phe
485 490

<210> 435
<211> 78
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 435
Met Lys Glu Phe Leu Ala Tyr Ile Val Lys Asn Leu Val Asp Lys Pro
5 10 15

Glu Glu Val His Leu Lys Glu Val Gln Gly Thr Asn Thr Ile Ile Tyr
20 25 30

Glu Leu Thr Val Ala Lys Gly Asp Ile Gly Lys Ile Ile Gly Lys Glu
35 40 45

Gly Arg Thr Ile Lys Ala Ile Arg Thr Leu Leu Val Ser Val Ala Ser
50 55 60

Arg Asp Asn Val Lys Val Ser Leu Glu Ile Met Glu Glu Arg
65 70 75

<210> 436
<211> 647
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 436
Met Glu Ser Gly Pro Glu Ser Val Ser Ser Asn Gln Ser Ser Met Asn
5 10 15

Pro Ile Ile Asn Gly Gln Ile Ala Ser Asn Ser Glu Thr Lys Glu Ser
20 25 30

Thr Lys Glu Ser Glu Ala Ser Pro Ser Ala Ser Ser Ser Val Ser Ser
35 40 45

Trp Ser Phe Leu Ser Ser Ala Lys His Ala Leu Ile Ser Leu Arg Asp
50 55 60

Ala Ile Leu Asn Lys Asn Ser Ser Pro Thr Asp Ser Leu Ser Gln Leu

```
65                  70                  75                  80

Glu Ala Ser Thr Ser Thr Ser Thr Val Thr Arg Val Ala Ala Arg Asp
                85                  90                  95

Tyr Asn Glu Ala Lys Ser Asn Phe Asp Thr Ala Lys Ser Gly Leu Glu
            100                 105                 110

Asn Ala Thr Thr Leu Ala Glu Tyr Glu Thr Lys Met Ala Asp Leu Met
        115                 120                 125

Ala Ala Leu Gln Asp Met Glu Arg Leu Ala Lys Gln Lys Ala Glu Val
    130                 135                 140

Thr Arg Ile Lys Glu Ala Leu Gln Glu Lys Gln Glu Val Ile Asp Lys
145                 150                 155                 160

Leu Asn Gln Leu Val Lys Leu Glu Lys Gln Asn Gln Thr Leu Lys Glu
                165                 170                 175

Thr Leu Thr Thr Thr Asp Ser Ala Asp Gln Ile Pro Ala Ile Asn Ser
            180                 185                 190

Gln Leu Glu Ile Asn Lys Asn Ser Ala Asp Gln Ile Ile Lys Asp Leu
        195                 200                 205

Glu Gly Gln Asn Ile Ser Tyr Glu Ala Val Leu Thr Asn Ala Gly Glu
    210                 215                 220

Val Ile Lys Ala Ser Ser Glu Ala Gly Ile Lys Leu Gly Gln Ala Leu
225                 230                 235                 240

Gln Ser Ile Val Asp Ala Gly Asp Gln Ser Gln Ala Ala Val Leu Gln
                245                 250                 255

Ala Gln Gln Asn Asn Ser Pro Asp Asn Ile Ala Ala Thr Lys Lys Leu
            260                 265                 270

Ile Asp Ala Ala Glu Thr Lys Val Asn Glu Leu Lys Gln Glu His Thr
        275                 280                 285

Gly Leu Thr Asp Ser Pro Leu Val Lys Lys Ala Glu Glu Gln Ile Ser
    290                 295                 300

Gln Ala Gln Lys Asp Ile Gln Glu Ile Lys Pro Ser Gly Ser Asp Ile
305                 310                 315                 320

Pro Ile Val Gly Pro Ser Gly Ser Ala Ala Ser Ala Gly Ser Ala Val
                325                 330                 335

Gly Ala Leu Lys Ser Ser Asn Asn Ser Gly Arg Ile Ser Leu Leu Leu
            340                 345                 350

Asp Asp Val Asp Asn Glu Met Ala Ala Ile Ala Met Gln Gly Phe Arg
        355                 360                 365

Ser Met Ile Glu Gln Phe Asn Val Asn Asn Pro Ala Thr Ala Lys Glu
    370                 375                 380

Leu Gln Ala Met Glu Ala Gln Leu Thr Ala Met Ser Asp Gln Leu Val
385                 390                 395                 400
```

```
Gly Ala Asp Gly Glu Leu Pro Ala Glu Ile Gln Ala Ile Lys Asp Ala
                405                 410                 415

Leu Ala Gln Ala Leu Lys Gln Pro Ser Thr Asp Gly Leu Ala Thr Ala
            420                 425                 430

Met Gly Gln Val Ala Phe Ala Ala Ala Lys Val Gly Gly Gly Ser Ala
        435                 440                 445

Gly Thr Ala Gly Thr Val Gln Met Asn Val Lys Gln Leu Tyr Lys Thr
    450                 455                 460

Ala Phe Ser Ser Thr Ser Ser Ser Ser Tyr Ala Ala Ala Leu Ser Asp
465                 470                 475                 480

Gly Tyr Ser Ala Tyr Lys Thr Leu Asn Ser Leu Tyr Ser Glu Ser Arg
                485                 490                 495

Ser Gly Val Gln Ser Ala Ile Ser Gln Thr Ala Asn Pro Ala Leu Ser
            500                 505                 510

Arg Ser Val Ser Arg Ser Gly Ile Glu Ser Gln Gly Arg Ser Ala Asp
        515                 520                 525

Ala Ser Gln Arg Ala Ala Glu Thr Ile Val Arg Asp Ser Gln Thr Leu
    530                 535                 540

Gly Asp Val Tyr Ser Arg Leu Gln Val Leu Asp Ser Leu Met Ser Thr
545                 550                 555                 560

Ile Val Ser Asn Pro Gln Val Asn Gln Glu Glu Ile Met Gln Lys Leu
                565                 570                 575

Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr Pro Ala Val Gln
            580                 585                 590

Asn Ser Ala Asp Ser Leu Gln Lys Phe Ala Ala Gln Leu Glu Arg Glu
        595                 600                 605

Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Arg Glu Asn Ala Phe
    610                 615                 620

Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val Asn Ile Ala Ser
625                 630                 635                 640

Leu Phe Ser Gly Tyr Leu Ser
                645


<210> 437
<211> 231
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 437
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
                 5                  10                  15

Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
            20                  25                  30
```

```
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
        35                  40                  45

Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
    50                  55                  60

Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
65                  70                  75                  80

Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
                85                  90                  95

Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
            100                 105                 110

Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
        115                 120                 125

Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
    130                 135                 140

Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145                 150                 155                 160

Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
                165                 170                 175

Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
            180                 185                 190

Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
        195                 200                 205

Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
    210                 215                 220

Cys Ser Cys His Gln Ser Tyr
225                 230


<210> 438
<211> 533
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 438
Met Ser Asn Ser Phe Arg Asp Gln Glu Gln Gly Leu Gln Ala Val Phe
                5                   10                  15

Arg Ala Ala Arg Val Ile Ser His Met Phe Ser Gln Thr Ile Gly Pro
            20                  25                  30

Tyr Gly Phe Ser Thr Ile Val His Asn Val Gln Asp Thr Arg Thr Thr
        35                  40                  45

Gln Asp Ser Gln Ser Met Leu Lys Asp Ile Leu Phe Pro Asp Val Phe
    50                  55                  60

Glu Asn Ile Gly Met Lys Leu Ile Arg Asp Thr Ala Leu Arg Thr Arg
65                  70                  75                  80
```

```
Met Arg Phe Gly Asp Gly Ala Lys Thr Thr Ala Leu Leu Ile Glu Ala
                85                  90                  95

Leu Leu Ala Glu Gly Met Thr Gly Ile Gln Lys Gly Leu Asp Pro His
            100                 105                 110

Glu Ile His Arg Gly Met Leu Leu Ala Glu Lys Lys Ile Gln Glu Val
        115                 120                 125

Phe Tyr Arg Glu Thr Phe Pro Leu Ser Asp Leu Glu His Thr Val Tyr
    130                 135                 140

Val Ser Ser Ile Ala Arg Arg Cys Asn Ser Glu Ile Ala Ser Val Leu
145                 150                 155                 160

Ser Ser Ala Val Gly Tyr Gly Gly Lys Asn Gly Tyr Tyr Ile Val Glu
                165                 170                 175

Glu His Glu Glu His Glu Thr Tyr Trp His Ala Glu Glu His Ala Val
            180                 185                 190

Trp Asp Phe Gly Tyr Ala Ser Pro Tyr Phe Ile Thr His Ala Glu Thr
        195                 200                 205

Gly Thr Val Glu Tyr Ser Gln Val Tyr Ile Leu Val Ser Glu Gln Pro
    210                 215                 220

Leu His Tyr Ser Asn Pro Ser Phe Leu Thr Phe Leu Gln Ser Val Val
225                 230                 235                 240

Gln Ala Gly Lys Thr Pro Leu Val Ile Leu Ala Glu Ala Phe Asp Lys
                245                 250                 255

Glu Leu Leu Ala Met Leu Glu Met Asn Gln Ile Glu Arg Val Phe Pro
            260                 265                 270

Val Cys Ala Val Lys Val Ser Gly Lys His Ala Arg Glu Ser Leu Glu
        275                 280                 285

Asp Ile Ala Val Leu Thr Gly Ala Thr Leu Leu Ser Glu Met Asp Phe
    290                 295                 300

Glu Asp Ser Glu Glu Glu Arg Ile Thr Asn Arg Leu Gly Phe Val Ala
305                 310                 315                 320

Gly Ile Cys Val Ser Ser Thr Ser Leu Cys Val Pro Arg Glu Thr Asp
                325                 330                 335

Asn Lys Gln Arg Met Ala Glu His Cys Ala Phe Leu Gln Asp Lys Leu
            340                 345                 350

Ser Phe Ser Gln Glu Glu Glu Ala Ser Ala Arg Leu Arg Arg Arg Leu
        355                 360                 365

Ala Arg Leu Ser Ser Gly Glu Val Cys Ile His Ile Ala Ala Asp Cys
    370                 375                 380

Ile Pro Gln Glu Glu Ile Gly Tyr Ile Thr Ser Ser Ile Arg Ala Met
385                 390                 395                 400
```

Thr Glu Ser Leu Arg Ser Gly Cys Leu Pro Gly Gly Gly Cys Ala Phe
405 410 415

Ile Arg Ala Ala Arg Glu Ile Ser Val Pro Leu Ala Leu Ser Pro Ser
420 425 430

Glu Arg Phe Gly Phe Leu Ala Val Leu Ser Ala Ala Glu Lys Pro Phe
435 440 445

Arg Ala Ile Val Thr Arg Ser Arg Arg Val Glu Glu Glu Val Phe Ser
450 455 460

Glu Val Phe Ser Gln Ala Asp Trp Arg Val Gly Phe Asn Gly Val Ser
465 470 475 480

Gly Phe Val Glu Asp Ile Val Ser Gln Gly Ile Cys Asp Gly Ala Ser
485 490 495

Cys Ile Gln Tyr Ala Leu Ser His Ala Val Gly Thr Thr Gly Leu Leu
500 505 510

Leu Thr Ser Ala Leu Phe Ile Ala Ser Gln Glu Pro Met Leu Arg Glu
515 520 525

Glu Asn Ser Glu Glu
530

<210> 439
<211> 465
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 439
Met Asn Glu Ala Phe Asp Cys Val Val Ile Gly Ala Gly Pro Gly Gly
5 10 15

Tyr Val Ala Ala Ile Thr Ala Ala Gln Ala Gly Leu Lys Thr Ala Leu
20 25 30

Ile Glu Lys Arg Glu Ala Gly Gly Thr Cys Leu Asn Arg Gly Cys Ile
35 40 45

Pro Ser Lys Ala Leu Leu Ala Gly Ala Glu Val Val Thr Gln Ile Arg
50 55 60

His Ala Asp Gln Phe Gly Ile His Val Glu Gly Phe Ser Ile Asn Tyr
65 70 75 80

Pro Ala Met Val Gln Arg Lys Asp Ser Val Val Arg Ser Ile Arg Asp
85 90 95

Gly Leu Asn Gly Leu Ile Arg Ser Asn Lys Ile Thr Val Phe Ser Gly
100 105 110

Arg Gly Ser Leu Ile Ser Ser Thr Glu Val Lys Ile Leu Gly Glu Asn
115 120 125

Pro Ser Val Ile Lys Ala His Ser Ile Ile Leu Ala Thr Gly Ser Glu
130 135 140

Pro Arg Ala Phe Pro Gly Ile Pro Phe Ser Ala Glu Ser Pro Arg Ile
145 150 155 160

Leu Cys Ser Thr Gly Val Leu Asn Leu Lys Glu Ile Pro Gln Lys Met
165 170 175

Ala Ile Ile Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe
180 185 190

His Thr Leu Gly Ser Glu Val Ser Val Ile Glu Ala Ser Ser Gln Ile
195 200 205

Leu Ala Leu Asn Asn Pro Asp Ile Ser Lys Thr Met Phe Asp Lys Phe
210 215 220

Thr Arg Gln Gly Leu Arg Phe Val Leu Glu Ala Ser Val Ser Asn Ile
225 230 235 240

Glu Asp Ile Gly Asp Arg Val Arg Leu Thr Ile Asn Gly Asn Val Glu
245 250 255

Glu Tyr Asp Tyr Val Leu Val Ser Ile Gly Arg Arg Leu Asn Thr Glu
260 265 270

Asn Ile Gly Leu Asp Lys Ala Gly Val Ile Cys Asp Glu Arg Gly Val
275 280 285

Ile Pro Thr Asp Ala Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala
290 295 300

Ile Gly Asp Ile Thr Gly Lys Trp Gln Leu Ala His Val Ala Ser His
305 310 315 320

Gln Gly Ile Ile Ala Ala Arg Asn Ile Ala Gly His Lys Glu Glu Ile
325 330 335

Asp Tyr Ser Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala
340 345 350

Ser Val Gly Leu Ser Pro Thr Ala Ala Gln Gln Gln Lys Ile Pro Val
355 360 365

Lys Val Thr Lys Phe Pro Phe Arg Ala Ile Gly Lys Ala Val Ala Met
370 375 380

Gly Glu Ala Asp Gly Phe Ala Ala Ile Ile Ser His Glu Thr Thr Gln
385 390 395 400

Gln Ile Leu Gly Ala Tyr Val Ile Gly Pro His Ala Ser Ser Leu Ile
405 410 415

Ser Glu Ile Thr Leu Ala Val Arg Asn Glu Leu Thr Leu Pro Cys Ile
420 425 430

Tyr Glu Thr Ile His Ala His Pro Thr Leu Ala Glu Val Trp Ala Glu
435 440 445

Ser Ala Leu Leu Ala Val Asp Thr Pro Leu His Met Pro Pro Ala Lys
450 455 460

Lys

465

<210> 440
<211> 122
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 440
```
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
                5                   10                  15

Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Leu Ser Lys Glu
            20                  25                  30

Ile Ile Ala Arg Leu Gln Leu Asn Pro Glu Ala Arg Ala Ala Glu Leu
        35                  40                  45

Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln Ser Asp Tyr
    50                  55                  60

Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
65                  70                  75                  80

Leu Ile Thr Ile His Ala Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
                85                  90                  95

Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
            100                 105                 110

Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
        115                 120
```

<210> 441
<211> 553
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 441
```
Met Arg Ile Gly Asp Pro Met Asn Lys Leu Ile Arg Arg Ala Val Thr
                5                   10                  15

Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
            20                  25                  30

Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
        35                  40                  45

Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg
    50                  55                  60

Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro
65                  70                  75                  80

Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly
                85                  90                  95

Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr
            100                 105                 110
```

Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu
115 120 125

Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
130 135 140

Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr
145 150 155 160

Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln
165 170 175

Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
180 185 190

Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser
195 200 205

Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro
210 215 220

Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val
225 230 235 240

Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val
245 250 255

Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr
260 265 270

Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe
275 280 285

Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr
290 295 300

Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu
305 310 315 320

Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys
325 330 335

Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val
340 345 350

Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val
355 360 365

Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr
370 375 380

Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val
385 390 395 400

Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser
405 410 415

Cys Ser Asp Cys Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr
420 425 430

Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp

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        435                 440                 445

Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn
    450                 455                 460

Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser
465                 470                 475                 480

Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile
                485                 490                 495

Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys
            500                 505                 510

Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp
        515                 520                 525

Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val
    530                 535                 540

Ser Asp Thr Glu Asn Thr His Ile Tyr
545                 550
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<210> 442
<211> 192
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 442

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Met Pro Glu Gly Glu Met Met His Lys Leu Gln Asp Val Ile Asp Arg
                5                   10                  15

Lys Leu Leu Asp Ser Arg Arg Ile Phe Phe Ser Glu Pro Val Thr Glu
            20                  25                  30

Lys Ser Ala Thr Glu Ala Ile Lys Lys Leu Trp Tyr Leu Glu Leu Thr
        35                  40                  45

Asn Pro Gly Gln Pro Ile Val Phe Val Ile Asn Ser Pro Gly Gly Ser
    50                  55                  60

Val Asp Ala Gly Phe Ala Val Trp Asp Gln Ile Lys Met Ile Ser Ser
65                  70                  75                  80

Pro Leu Thr Thr Val Val Thr Gly Leu Ala Ala Ser Met Gly Ser Val
                85                  90                  95

Leu Ser Leu Cys Ala Val Pro Gly Arg Arg Phe Ala Thr Pro His Ala
            100                 105                 110

Arg Ile Met Ile His Gln Pro Ser Ile Gly Gly Thr Ile Thr Gly Gln
        115                 120                 125

Ala Thr Asp Leu Asp Ile His Ala Arg Glu Ile Leu Lys Thr Lys Ala
    130                 135                 140

Arg Ile Ile Asp Val Tyr Val Glu Ala Thr Gly Gln Ser Arg Glu Val
145                 150                 155                 160

Ile Glu Lys Ala Ile Asp Arg Asp Met Trp Met Ser Ala Asn Glu Ala
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165 170 175

Met Glu Phe Gly Leu Leu Asp Gly Ile Leu Phe Ser Phe Asn Asp Leu
180 185 190

<210> 443
<211> 275
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 443
Met Gly Phe Ser Ser Leu Leu Thr Thr Cys Arg Tyr Leu Leu Tyr Ser
5 10 15

Gly Ala Gly Asn Ser Phe Ile Leu Gly Glu Ser Met Pro Ser Leu Glu
20 25 30

Asp Val Leu Phe Leu Cys Gln Glu Glu Met Val Asp Gly Phe Leu Cys
35 40 45

Val Glu Ser Ser Glu Ile Ala Asp Ala Lys Leu Thr Val Phe Asn Ser
50 55 60

Asp Gly Ser Ile Ala Ser Met Cys Gly Asn Gly Leu Arg Cys Ala Met
65 70 75 80

Ala His Val Ala Gln Cys Phe Gly Leu Glu Asp Val Ser Ile Glu Thr
85 90 95

Glu Arg Gly Val Tyr Gln Gly Lys Phe Phe Ser Met Asn Arg Val Leu
100 105 110

Val Asp Met Thr Leu Pro Asp Trp Lys Lys Ala Glu Arg Lys Leu Thr
115 120 125

His Val Leu Pro Gly Met Pro Glu Gln Val Phe Phe Ile Asp Thr Gly
130 135 140

Val Pro His Val Val Val Phe Val Ser Asp Leu Ser Lys Val Pro Val
145 150 155 160

Gln Glu Trp Gly Ser Phe Leu Arg Tyr His Glu Asp Phe Ala Pro Glu
165 170 175

Gly Val Asn Val Asp Phe Val Gln Arg Lys Lys Asp Asp Leu Leu Leu
180 185 190

Val Tyr Thr Tyr Glu Arg Gly Cys Glu Arg Glu Thr Leu Ser Cys Gly
195 200 205

Thr Gly Met Leu Ala Ser Ala Leu Val Ala Ala Asp Ile Phe Ser Leu
210 215 220

Gly Gln Asp Phe Ser Ile Ala Val Cys Ser Arg Ser Arg Asn Leu Ile
225 230 235 240

Lys Ile Phe Ser Glu Lys Gly Lys Val Phe Leu Glu Gly Pro Val Ser
245 250 255

Leu Leu Asn Arg Ser Glu Asn Phe Gly Trp Leu Glu Pro Lys Ser Arg

260 265 270

Arg Phe Gly
275

<210> 444
<211> 1770
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 444
Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Ala Leu Ser Ser
5 10 15

Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr Asp Cys
20 25 30

Asn Val Ser Lys Leu Gly Tyr Ser Thr Ser Gln Ala Phe Thr Asp Met
35 40 45

Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val Ser Phe
50 55 60

Tyr Asp Phe Ser Thr Ser Ser Arg Leu Pro Arg Lys His Leu Ser Ser
65 70 75 80

Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser Ser Ser
85 90 95

Gly Glu Thr Asp Glu Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly Ile
100 105 110

Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu
115 120 125

Ser Asn Gln Ser Ile Glu Leu His Asp Asn Ser Ile Phe Phe Gly Glu
130 135 140

Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala
145 150 155 160

Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu
165 170 175

Val Glu Val Asn Ile Ala Val Glu Lys Gly Gly Ser Val Tyr Ala Lys
180 185 190

Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn
195 200 205

Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu
210 215 220

Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala
225 230 235 240

Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu Ala
245 250 255

Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu

260 265 270

Thr Glu Gln Thr Glu Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu Thr
275 280 285

Glu Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro Asp
290 295 300

Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser Leu Thr
305 310 315 320

Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile Ala Thr
325 330 335

Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys Thr Asn
340 345 350

Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His Gly Gly
355 360 365

Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr Ser Glu
370 375 380

Ser Ile Thr Thr Pro Pro Leu Ile Gly Glu Val Ile Phe Ser Glu Asn
385 390 395 400

Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys Leu Ser Leu
405 410 415

Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys Glu Ser
420 425 430

Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Ile Thr Asp Thr
435 440 445

Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser Thr Pro Glu
450 455 460

Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Lys
465 470 475 480

Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln
485 490 495

Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn
500 505 510

Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly
515 520 525

Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu
530 535 540

Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys Leu Thr
545 550 555 560

Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn
565 570 575

Ser Ala Ala Lys Glu Gly Gly Ala Ile His Ser Lys Thr Val Thr Leu
580 585 590

Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala
595 600 605

Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu
610 615 620

Gly Glu Glu Ser Thr Ala Thr Glu Asp Pro Asn Ser Asn Thr Glu Gly
625 630 635 640

Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp
645 650 655

Thr Gly Thr Gly Asp Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr
660 665 670

Gly Asn Ala Glu Ser Glu Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn
675 680 685

Glu Glu Asn Thr Leu Pro Asn Ser Asn Ile Asp Gln Ser Asn Glu Asn
690 695 700

Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser
705 710 715 720

Val Ser Ser Ser Ser Glu Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly
725 730 735

Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn
740 745 750

Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val
755 760 765

Ser Asn Ser Ser Gly Ser Glu Glu Pro Val Thr Ser Ser Ser Asp Ser
770 775 780

Asp Val Thr Ala Ser Ser Asp Asn Pro Asp Ser Ser Ser Ser Gly Asp
785 790 795 800

Ser Ala Gly Asp Ser Glu Glu Pro Thr Glu Pro Glu Ala Gly Ser Thr
805 810 815

Thr Glu Thr Leu Thr Leu Ile Gly Gly Gly Ala Ile Tyr Gly Glu Thr
820 825 830

Val Lys Ile Glu Asn Phe Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys
835 840 845

Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser Ser Lys Ser Asp Val Leu
850 855 860

Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser
865 870 875 880

Ser Arg Arg Thr Val Thr Phe Ser Gly Asn Thr Val Ser Ser Gln Ser
885 890 895

Thr Thr Gly Gln Val Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr
900 905 910

Ile Ala Thr Pro Val Val Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala
915 920 925

Asn Asn Thr Thr Asp Thr Gln Arg Lys Asp Thr Phe Gly Gly Ala Ile
930 935 940

Gly Ala Thr Ser Ala Val Ser Leu Ser Gly Gly Ala His Phe Leu Glu
945 950 955 960

Asn Val Ala Asp Leu Gly Ser Ala Ile Gly Leu Val Pro Gly Thr Gln
965 970 975

Asn Thr Glu Thr Val Lys Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys
980 985 990

Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr Ala Pro Val Val Ser Ile
995 1000 1005

Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly
1010 1015 1020

Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser
1025 1030 1035 1040

Val Leu Phe Thr Gly Asn Leu Val Thr Leu Thr Leu Ser Thr Thr Thr
1045 1050 1055

Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala
1060 1065 1070

Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn
1075 1080 1085

Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn
1090 1095 1100

Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys
1105 1110 1115 1120

Ser Ile Ala Gly Asp Val Lys Leu Thr Met Gln Ala Ala Lys Gly Lys
1125 1130 1135

Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly
1140 1145 1150

Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp
1155 1160 1165

Ser Glu Thr Val Asn Ser Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser
1170 1175 1180

Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln Asn Val Val Leu His
1185 1190 1195 1200

Ser Gly Ser Leu Val Leu Lys Pro Asn Thr Glu Leu His Val Ile Ser
1205 1210 1215

Phe Glu Gln Lys Glu Gly Ser Ser Leu Val Met Thr Pro Gly Ser Val
1220 1225 1230

Leu Ser Asn Gln Thr Val Ala Asp Gly Ala Leu Val Ile Asn Asn Met

1235 1240 1245

Thr Ile Asp Leu Ser Ser Val Glu Lys Asn Gly Ile Ala Glu Gly Asn
1250 1255 1260

Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile Asp Thr Thr Thr Gly Gly
1265 1270 1275 1280

Ser Gly Gly Thr Pro Ser Thr Asp Ser Glu Ser Asn Gln Asn Ser Asp
1285 1290 1295

Asp Thr Glu Glu Gln Asn Asn Asn Asp Ala Ser Asn Gln Gly Glu Ser
1300 1305 1310

Ala Asn Gly Ser Ser Ser Pro Ala Val Ala Ala Ala His Thr Ser Arg
1315 1320 1325

Thr Arg Asn Phe Ala Ala Ala Ala Thr Ala Thr Pro Thr Thr Thr Pro
1330 1335 1340

Thr Ala Thr Thr Thr Thr Ser Asn Gln Val Ile Leu Gly Gly Glu Ile
1345 1350 1355 1360

Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe Gln Asn Pro Ala Leu Arg
1365 1370 1375

Ser Asp Gln Gln Ile Ser Leu Leu Val Leu Pro Thr Asp Ser Ser Lys
1380 1385 1390

Met Gln Ala Gln Lys Ile Val Leu Thr Gly Asp Ile Ala Pro Gln Lys
1395 1400 1405

Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro Asp Gln Leu Gln Asn Gly
1410 1415 1420

Thr Ile Ser Val Leu Trp Lys Phe Asp Ser Tyr Arg Gln Trp Ala Tyr
1425 1430 1435 1440

Val Pro Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln
1445 1450 1455

Met Leu Met Val Thr Val Lys Gln Gly Leu Leu Asn Asp Lys Met Asn
1460 1465 1470

Leu Ala Arg Phe Glu Glu Val Ser Tyr Asn Asn Leu Trp Ile Ser Gly
1475 1480 1485

Leu Gly Thr Met Leu Ser Gln Val Gly Thr Pro Thr Ser Glu Glu Phe
1490 1495 1500

Thr Tyr Tyr Ser Arg Gly Ala Ser Val Ala Leu Asp Ala Lys Pro Ala
1505 1510 1515 1520

His Asp Val Ile Val Gly Ala Ala Phe Ser Lys Met Ile Gly Lys Thr
1525 1530 1535

Lys Ser Leu Lys Arg Glu Asn Asn Tyr Thr His Lys Gly Ser Glu Tyr
1540 1545 1550

Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys Pro Phe His Phe Val Ile
1555 1560 1565

Asn Lys Lys Thr Glu Lys Ser Leu Pro Leu Leu Leu Gln Gly Val Ile
    1570   1575   1580

Ser Tyr Gly Tyr Ile Lys His Asp Thr Val Thr His Tyr Pro Thr Ile
1585   1590   1595   1600

Arg Glu Arg Asn Lys Gly Glu Trp Glu Asp Leu Gly Trp Leu Thr Ala
                1605   1610   1615

Leu Arg Val Ser Ser Val Leu Arg Thr Pro Ala Gln Gly Asp Thr Lys
            1620   1625   1630

Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys
        1635   1640   1645

Gln Phe Thr Glu Thr Glu Tyr Asp Pro Arg Tyr Phe Asp Asn Cys Thr
    1650   1655   1660

Tyr Arg Asn Leu Ala Ile Pro Met Gly Leu Ala Phe Glu Gly Glu Leu
1665   1670   1675   1680

Ser Gly Asn Asp Ile Leu Met Tyr Asn Arg Phe Ser Val Ala Tyr Met
                1685   1690   1695

Leu Ser Ile Tyr Arg Asn Ser Pro Thr Cys Lys Tyr Gln Val Leu Ser
            1700   1705   1710

Ser Gly Glu Gly Gly Glu Ile Ile Cys Gly Val Pro Thr Arg Asn Ser
        1715   1720   1725

Ala Arg Gly Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Leu Trp Thr
    1730   1735   1740

Leu Tyr Gly Ser Tyr Thr Ile Glu Ala Asp Ala His Thr Leu Ala His
1745   1750   1755   1760

Met Met Asn Cys Gly Ala Arg Met Thr Phe
                1765   1770

<210> 445
<211> 1751
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 445
Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser
                5   10   15

Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
            20   25   30

Val Gly Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Val Gly Glu Ala
        35   40   45

Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
    50   55   60

Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser Asn Ser Ser
65   70   75   80

Ser Ser Asn Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
85 90 95

Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr Asn Ala His
100 105 110

Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
115 120 125

Thr Leu Ser Glu Ile Lys Ile Thr Gly Glu Gly Gly Ala Ile Phe Ser
130 135 140

Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Gly Leu Thr Ile Gln Asn
145 150 155 160

Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Glu Ser Thr Ile
165 170 175

Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Ser Asn Ser Ala Glu
180 185 190

Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
195 200 205

Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
210 215 220

Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn Leu Gln Ser
225 230 235 240

His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
245 250 255

Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
260 265 270

Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
275 280 285

Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val
290 295 300

Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
305 310 315 320

Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
325 330 335

Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly
340 345 350

Ala Leu Tyr Val Glu Gly Asp Ile Asn Phe Gln Asp Leu Glu Glu Ile
355 360 365

Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
370 375 380

Leu Pro Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp Ala Ser
385 390 395 400

Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asn Ser Gly
405 410 415

Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val Pro Ala
420 425 430

Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser Ile Thr
435 440 445

Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr Asp Val
450 455 460

Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn Ser His
465 470 475 480

Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly Gly Ile
485 490 495

Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys Thr Leu
500 505 510

Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe Ile Lys
515 520 525

Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe Cys Leu
530 535 540

Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val Thr Lys
545 550 555 560

Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile
565 570 575

Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly
580 585 590

Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu
595 600 605

Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly
610 615 620

Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln
625 630 635 640

Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Glu Ser Ala Pro Val
645 650 655

Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser Leu
660 665 670

Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Lys
675 680 685

Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val
690 695 700

Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile
705 710 715 720

Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser

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                725                 730                 735

Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu Ser
            740                 745                 750

Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu Val
        755                 760                 765

Gly Lys Glu Gly Gly Gly Leu His Ala Lys Thr Val Asn Ile Ser Asn
    770                 775                 780

Leu Lys Ser Gly Phe Ser Phe Ser Asn Asn Lys Ala Asn Ser Ser Ser
785                 790                 795                 800

Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala Ser
                805                 810                 815

Leu Gln Ala Ala Ala Ala Ala Val Pro Ser Ser Pro Ala Thr Pro Thr
            820                 825                 830

Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr Phe
        835                 840                 845

Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile Asp
    850                 855                 860

Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile Tyr
865                 870                 875                 880

Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser Tyr
                885                 890                 895

Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr Gly
            900                 905                 910

Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn Cys
        915                 920                 925

Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Met Ala Thr Pro Lys Thr
    930                 935                 940

Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile Gly
945                 950                 955                 960

Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg Phe
                965                 970                 975

Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala Asn
            980                 985                 990

Ala Asn Thr Pro Ser Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr Glu
        995                 1000                1005

Lys Ile Thr Leu Glu Asn Gly Ser Phe Ile Phe Glu Arg Asn Gln Ala
    1010                1015                1020

Asn Lys Arg Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly Asn
1025                1030                1035                1040

Asn Ile Thr Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala Ile
                1045                1050                1055
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Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu Phe
1060 1065 1070

Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser Gly
1075 1080 1085

Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp Pro
1090 1095 1100

Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu Ala
1105 1110 1115 1120

Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn Gln
1125 1130 1135

Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val Lys
1140 1145 1150

Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Cys
1155 1160 1165

Val His Thr Ser Thr Lys Lys Ile Gly Ser Thr Gln Asn Val Tyr Glu
1170 1175 1180

Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly Thr
1185 1190 1195 1200

Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln
1205 1210 1215

Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr Glu
1220 1225 1230

Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile Met
1235 1240 1245

Lys Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala Leu
1250 1255 1260

Val Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro Gln
1265 1270 1275 1280

Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr Thr
1285 1290 1295

Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr Asn
1300 1305 1310

Pro Lys Arg Ile Ser Ala Ala Ala Pro Ser Gly Ser Ala Ala Thr Thr
1315 1320 1325

Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr Gly Asp Leu Thr Leu
1330 1335 1340

Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser Asp
1345 1350 1355 1360

Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val Gln
1365 1370 1375

Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly Tyr
1380 1385 1390

Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu Gln
1395 1400 1405

Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro Arg
1410 1415 1420

Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser Met
1425 1430 1435 1440

Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala Arg
1445 1450 1455

Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly Thr
1460 1465 1470

Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr Tyr
1475 1480 1485

Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp Phe
1490 1495 1500

Ile Leu Gly Ala Ala Phe Ser Lys Met Val Gly Lys Thr Lys Ala Ile
1505 1510 1515 1520

Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr Gln
1525 1530 1535

Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys Gln
1540 1545 1550

His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr Gly
1555 1560 1565

His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro Ser Ile His Glu Arg
1570 1575 1580

Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu Ala Asp Leu Arg Ile
1585 1590 1595 1600

Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile Thr
1605 1610 1615

Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr
1620 1625 1630

Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg Asn
1635 1640 1645

Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn Cys
1650 1655 1660

Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser Ile
1665 1670 1675 1680

Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn Glu
1685 1690 1695

Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg Ala

1700 1705 1710

Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr Gly
1715 1720 1725

Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu Ser Gln Met Thr Ser
1730 1735 1740

Cys Gly Ala Arg Met Ile Phe
1745 1750

<210> 446
<211> 660
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 446
Met Ser Glu Lys Arg Lys Ser Asn Lys Ile Ile Gly Ile Asp Leu Gly
5 10 15

Thr Thr Asn Ser Cys Val Ser Val Met Glu Gly Gly Gln Pro Lys Val
20 25 30

Ile Ala Ser Ser Glu Gly Thr Arg Thr Thr Pro Ser Ile Val Ala Phe
35 40 45

Lys Gly Gly Glu Thr Leu Val Gly Ile Pro Ala Lys Arg Gln Ala Val
50 55 60

Thr Asn Pro Glu Lys Thr Leu Ala Ser Thr Lys Arg Phe Ile Gly Arg
65 70 75 80

Lys Phe Ser Glu Val Glu Ser Glu Ile Lys Thr Val Pro Tyr Lys Val
85 90 95

Ala Pro Asn Ser Lys Gly Asp Ala Val Phe Asp Val Glu Gln Lys Leu
100 105 110

Tyr Thr Pro Glu Glu Ile Gly Ala Gln Ile Leu Met Lys Met Lys Glu
115 120 125

Thr Ala Glu Ala Tyr Leu Gly Glu Thr Val Thr Glu Ala Val Ile Thr
130 135 140

Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Ala Ser Thr Lys Asp Ala
145 150 155 160

Gly Arg Ile Ala Gly Leu Asp Val Lys Arg Ile Ile Pro Glu Pro Thr
165 170 175

Ala Ala Ala Leu Ala Tyr Gly Ile Asp Lys Glu Gly Asp Lys Lys Ile
180 185 190

Ala Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu
195 200 205

Ile Gly Asp Gly Val Phe Glu Val Leu Ser Thr Asn Gly Asp Thr His
210 215 220

Leu Gly Gly Asp Asp Phe Asp Gly Val Ile Ile Asn Trp Met Leu Asp

225 230 235 240

Glu Phe Lys Lys Gln Glu Gly Ile Asp Leu Ser Lys Asp Asn Met Ala
245 250 255

Leu Gln Arg Leu Lys Asp Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser
260 265 270

Gly Val Ser Ser Thr Glu Ile Asn Gln Pro Phe Ile Thr Ile Asp Ala
275 280 285

Asn Gly Pro Lys His Leu Ala Leu Thr Leu Thr Arg Ala Gln Phe Glu
290 295 300

His Leu Ala Ser Ser Leu Ile Glu Arg Thr Lys Gln Pro Cys Ala Gln
305 310 315 320

Ala Leu Lys Asp Ala Lys Leu Ser Ala Ser Asp Ile Asp Asp Val Leu
325 330 335

Leu Val Gly Gly Met Ser Arg Met Pro Ala Val Gln Ala Val Val Lys
340 345 350

Glu Ile Phe Gly Lys Glu Pro Asn Lys Gly Val Asn Pro Asp Glu Val
355 360 365

Val Ala Ile Gly Ala Ala Ile Gln Gly Gly Val Leu Gly Gly Glu Val
370 375 380

Lys Asp Val Leu Leu Leu Asp Val Ile Pro Leu Ser Leu Gly Ile Glu
385 390 395 400

Thr Leu Gly Gly Val Met Thr Pro Leu Val Glu Arg Asn Thr Thr Ile
405 410 415

Pro Thr Gln Lys Lys Gln Ile Phe Ser Thr Ala Ala Asp Asn Gln Pro
420 425 430

Ala Val Thr Ile Val Val Leu Gln Gly Glu Arg Pro Met Ala Lys Asp
435 440 445

Asn Lys Glu Ile Gly Arg Phe Asp Leu Thr Asp Ile Pro Pro Ala Pro
450 455 460

Arg Gly His Pro Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly
465 470 475 480

Ile Leu His Val Ser Ala Lys Asp Ala Ala Ser Gly Arg Glu Gln Lys
485 490 495

Ile Arg Ile Glu Ala Ser Ser Gly Leu Lys Glu Asp Glu Ile Gln Gln
500 505 510

Met Ile Arg Asp Ala Glu Leu His Lys Glu Glu Asp Lys Gln Arg Lys
515 520 525

Glu Ala Ser Asp Val Lys Asn Glu Ala Asp Gly Met Ile Phe Arg Ala
530 535 540

Glu Lys Ala Val Lys Asp Tyr His Asp Lys Ile Pro Ala Glu Leu Val
545 550 555 560

Lys Glu Ile Glu Glu His Ile Glu Lys Val Arg Gln Ala Ile Lys Glu
565 570 575

Asp Ala Ser Thr Thr Ala Ile Lys Ala Ala Ser Asp Glu Leu Ser Thr
580 585 590

His Met Gln Lys Ile Gly Glu Ala Met Gln Ala Gln Ser Ala Ser Ala
595 600 605

Ala Ala Ser Ser Ala Ala Asn Ala Gln Gly Gly Pro Asn Ile Asn Ser
610 615 620

Glu Asp Leu Lys Lys His Ser Phe Ser Thr Arg Pro Pro Ala Gly Gly
625 630 635 640

Ser Ala Ser Ser Thr Asp Asn Ile Glu Asp Ala Asp Val Glu Ile Val
645 650 655

Asp Lys Pro Glu
660

<210> 447
<211> 326
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 447
Met Val Ser Gln Thr Val Ser Val Ala Val Thr Gly Gly Thr Gly Gln
5 10 15

Ile Ala Tyr Ser Phe Leu Phe Ser Leu Ala His Gly Asp Val Phe Gly
20 25 30

Leu Asp Cys Gly Ile Asp Leu Arg Ile Tyr Asp Ile Pro Gly Thr Glu
35 40 45

Arg Ala Leu Ser Gly Val Arg Met Glu Leu Asp Asp Gly Ala Phe Pro
50 55 60

Leu Leu Gln Arg Val Gln Val Thr Thr Ser Leu His Asp Ala Phe Asp
65 70 75 80

Gly Ile Asp Ala Ala Phe Leu Ile Gly Ser Val Pro Arg Gly Pro Gly
85 90 95

Met Glu Arg Arg Asp Leu Leu Lys Lys Asn Gly Glu Ile Phe Ala Thr
100 105 110

Gln Gly Lys Ala Leu Asn Thr Thr Ala Lys Arg Asp Ala Lys Ile Phe
115 120 125

Val Val Gly Asn Pro Val Asn Thr Asn Cys Trp Ile Ala Met Asn His
130 135 140

Ala Pro Arg Leu Leu Arg Lys Asn Phe His Ala Met Leu Arg Leu Asp
145 150 155 160

Gln Asn Arg Met His Ser Met Leu Ser His Arg Ala Glu Val Pro Leu
165 170 175

```
Ser Ala Val Ser Gln Val Val Val Trp Gly Asn His Ser Ala Lys Gln
            180                 185                 190

Val Pro Asp Phe Thr Gln Ala Leu Ile Asn Asp Arg Pro Ile Ala Glu
        195                 200                 205

Thr Ile Ala Asp Arg Asp Trp Leu Glu Asn Ile Met Val Pro Ser Val
    210                 215                 220

Gln Ser Arg Gly Ser Ala Val Ile Glu Ala Arg Gly Lys Ser Ser Ala
225                 230                 235                 240

Ala Ser Ala Ala Arg Ala Leu Ala Glu Ala Ala Arg Ser Ile Tyr Gln
                245                 250                 255

Pro Lys Glu Gly Glu Trp Phe Ser Ser Gly Val Cys Ser Asp His Asn
            260                 265                 270

Pro Tyr Gly Leu Pro Glu Asp Leu Ile Phe Gly Phe Pro Cys Arg Met
        275                 280                 285

Leu Ala Thr Gly Glu Tyr Glu Val Ile Pro Arg Leu Pro Trp Asp Ala
    290                 295                 300

Phe Ile Arg Gly Lys Met Gln Ile Ser Leu Asp Glu Ile Leu Gln Glu
305                 310                 315                 320

Lys Ala Ser Val Ser Leu
                325


<210> 448
<211> 232
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 448
Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp
1               5                   10                  15

Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln
            20                  25                  30

Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu
        35                  40                  45

Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser
    50                  55                  60

Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala
65                  70                  75                  80

Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly
                85                  90                  95

Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp
            100                 105                 110

Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly
        115                 120                 125
```

```
Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr
    130                 135                 140

Val Thr Thr Asp Val Val Lys Thr Val Ala Glu Leu Arg Lys Gly Lys
145                 150                 155                 160

Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala
                165                 170                 175

Lys Leu Ser Phe Asp Ser Ala Gln Ile Lys Glu Asn Val Glu Ala Leu
            180                 185                 190

Cys Ala Ala Leu Val Lys Ala Lys Pro Ala Thr Ala Lys Gly Gln Tyr
        195                 200                 205

Leu Val Asn Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Val Thr Val
    210                 215                 220

Asp Thr Arg Glu Leu Ile Ala Leu
225                 230


<210> 449
<211> 1252
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 449
Met Phe Lys Cys Pro Glu Arg Val Ser Ile Lys Lys Lys Glu Asp Ile
                5                   10                  15

Leu Asp Leu Pro Asn Leu Val Glu Val Gln Ile Lys Ser Tyr Lys Gln
            20                  25                  30

Phe Leu Gln Ile Gly Lys Leu Ala Glu Glu Arg Glu Asn Ile Gly Leu
        35                  40                  45

Glu Glu Val Phe Arg Glu Ile Phe Pro Ile Lys Ser Tyr Asn Glu Ala
    50                  55                  60

Thr Ile Leu Glu Tyr Leu Ser Tyr Asn Leu Gly Val Pro Lys Tyr Ser
65                  70                  75                  80

Pro Glu Glu Cys Ile Arg Arg Gly Ile Thr Tyr Ser Val Thr Leu Lys
                85                  90                  95

Val Arg Phe Arg Leu Thr Asp Glu Thr Gly Ile Lys Glu Glu Glu Val
            100                 105                 110

Tyr Met Gly Thr Ile Pro Ile Met Thr Asp Lys Gly Thr Phe Ile Ile
        115                 120                 125

Asn Gly Ala Glu Arg Val Val Val Ser Gln Val His Arg Ser Pro Gly
    130                 135                 140

Ile Asn Phe Glu Gln Glu Lys His Ser Lys Gly Asn Val Leu Phe Ser
145                 150                 155                 160

Phe Arg Ile Ile Pro Tyr Arg Gly Ser Trp Leu Glu Ala Val Phe Asp
                165                 170                 175
```

```
Ile Asn Asp Leu Ile Tyr Ile His Ile Asp Arg Lys Lys Arg Arg Arg
            180                 185                 190

Lys Ile Leu Ala Met Thr Phe Ile Arg Ala Leu Gly Tyr Ser Thr Asp
        195                 200                 205

Ala Asp Ile Ile Glu Glu Phe Phe Ser Val Glu Glu Arg Ser Leu Arg
    210                 215                 220

Leu Glu Lys Asp Phe Val Ala Leu Val Gly Lys Val Leu Ala Asp Asn
225                 230                 235                 240

Val Val Asp Ala Asp Ser Ser Leu Val Tyr Gly Lys Ala Gly Glu Lys
                245                 250                 255

Leu Ser Thr Ala Met Leu Lys Arg Ile Leu Asp Ala Gly Val Gln Ser
            260                 265                 270

Leu Lys Ile Ala Val Gly Ala Asp Glu Asn His Pro Ile Ile Lys Met
        275                 280                 285

Leu Ala Lys Asp Pro Thr Asp Ser Tyr Glu Ala Ala Leu Lys Asp Phe
    290                 295                 300

Tyr Arg Arg Leu Arg Pro Gly Glu Pro Ala Thr Leu Val Asn Ala Arg
305                 310                 315                 320

Ser Thr Ile Met Arg Leu Phe Phe Asp Ala Lys Arg Tyr Asn Leu Gly
                325                 330                 335

Arg Val Gly Arg Tyr Lys Leu Asn Lys Lys Leu Gly Phe Pro Leu Asp
            340                 345                 350

Asp Glu Thr Leu Ser Gln Val Thr Leu Arg Lys Glu Asp Val Ile Gly
        355                 360                 365

Ala Leu Lys Tyr Leu Ile Arg Leu Arg Met Gly Asp Glu Lys Thr Ser
    370                 375                 380

Ile Asp Asp Ile Asp His Leu Ala Asn Arg Arg Val Arg Ser Val Gly
385                 390                 395                 400

Glu Leu Ile Gln Asn His Cys Arg Ser Gly Leu Ala Arg Met Glu Lys
                405                 410                 415

Ile Val Arg Glu Arg Met Asn Leu Phe Asp Phe Ser Ser Asp Thr Leu
            420                 425                 430

Thr Pro Gly Lys Ile Ile Ser Ala Lys Gly Leu Val Ser Val Leu Lys
        435                 440                 445

Asp Phe Phe Ser Arg Ser Gln Leu Ser Gln Phe Met Asp Gln Thr Asn
    450                 455                 460

Pro Val Ala Glu Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
465                 470                 475                 480

Gly Gly Leu Asn Arg Glu Arg Ala Gly Phe Glu Val Arg Asp Val His
                485                 490                 495
```

```
Ala Ser His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu Gly Pro
            500                 505                 510

Asn Ile Gly Leu Ile Thr Ser Leu Ser Ser Phe Ala Lys Ile Asn Glu
        515                 520                 525

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Val Val Arg Asp Gly Ile Val
    530                 535                 540

Thr Asp Glu Ile Glu Tyr Met Thr Ala Asp Val Glu Glu Glu Cys Val
545                 550                 555                 560

Ile Ala Gln Ala Ser Ala Glu Leu Asp Glu Tyr Asp Met Phe Lys Thr
                565                 570                 575

Pro Val Cys Trp Ala Arg Tyr Lys Gly Glu Ala Phe Glu Ala Asp Thr
            580                 585                 590

Ser Thr Val Thr His Met Asp Val Ser Pro Lys Gln Leu Val Ser Val
        595                 600                 605

Val Thr Gly Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala
    610                 615                 620

Leu Met Gly Ser Asn Met Gln Arg Gln Ala Val Pro Leu Leu Lys Thr
625                 630                 635                 640

Glu Ala Ala Ile Val Gly Thr Gly Leu Glu Gly Arg Ala Ala Lys Asp
                645                 650                 655

Ser Gly Ala Ile Ile Val Ala Gln Glu Asp Gly Val Val Glu Tyr Val
            660                 665                 670

Asp Ser Tyr Glu Ile Val Val Ala Lys Lys Asn Asn Pro Thr Leu Lys
        675                 680                 685

Asp Arg Tyr Gln Leu Lys Lys Phe Leu Arg Ser Asn Ser Gly Thr Cys
    690                 695                 700

Ile Asn Gln Thr Pro Leu Cys Ser Val Gly Asp Val Val Thr His Gly
705                 710                 715                 720

Asp Val Leu Ala Asp Gly Pro Ala Thr Asp Lys Gly Glu Leu Ala Leu
                725                 730                 735

Gly Lys Asn Val Leu Val Ala Phe Met Pro Trp Tyr Gly Tyr Asn Phe
            740                 745                 750

Glu Asp Ala Ile Ile Ile Ser Glu Arg Leu Ile Lys Gln Asp Ala Tyr
        755                 760                 765

Thr Ser Ile Tyr Ile Glu Glu Phe Glu Leu Thr Ala Arg Asp Thr Lys
    770                 775                 780

Leu Gly Lys Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu
785                 790                 795                 800

Val Leu Ala Asn Leu Gly Glu Asp Gly Val Val Arg Ile Gly Ala Glu
                805                 810                 815

Val Lys Pro Gly Asp Ile Leu Val Gly Lys Ile Thr Pro Lys Ser Glu
```

```
          820                 825                 830

Thr Glu Leu Ala Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu
        835                 840                 845

Lys Ala Ala Asp Val Lys Asp Ala Ser Leu Thr Val Pro Pro Gly Thr
    850                 855                 860

Glu Gly Val Val Met Asp Val Lys Val Phe Ser Arg Lys Asp Arg Leu
865                 870                 875                 880

Ser Lys Ser Asp Asp Glu Leu Val Glu Glu Ala Val His Leu Lys Asp
                885                 890                 895

Leu Gln Lys Glu Tyr Lys Ser Gln Leu Ala Gln Leu Lys Val Glu His
            900                 905                 910

Arg Glu Lys Leu Gly Ala Leu Leu Leu Asn Glu Lys Ala Pro Ala Ala
        915                 920                 925

Ile Ile His Arg Arg Ser Ala Asp Ile Leu Val Gln Glu Gly Ala Ile
    930                 935                 940

Phe Asp Gln Glu Thr Ile Glu Leu Leu Glu Arg Glu Ser Leu Val Asp
945                 950                 955                 960

Leu Leu Met Ala Pro Cys Asp Met Tyr Asp Val Leu Lys Asp Ile Leu
                965                 970                 975

Ser Ser Tyr Glu Thr Ala Val Gln Arg Leu Glu Val Asn Tyr Lys Thr
            980                 985                 990

Glu Ala Glu His Ile Lys Glu Gly Asp Ala Asp Leu Asp His Gly Val
        995                 1000                1005

Ile Arg Gln Val Lys Val Tyr Val Ala Ser Lys Arg Lys Leu Gln Val
    1010                1015                1020

Gly Asp Lys Met Ala Gly Arg His Gly Asn Lys Gly Val Val Ser Lys
1025                1030                1035                1040

Ile Val Pro Glu Ala Asp Met Pro Phe Leu Ala Asn Gly Glu Thr Val
                1045                1050                1055

Gln Met Ile Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Leu Gly
            1060                1065                1070

Gln Val Leu Glu Thr His Leu Gly Tyr Ala Ala Lys Thr Ala Gly Ile
        1075                1080                1085

Tyr Val Lys Thr Pro Val Phe Glu Gly Phe Pro Glu Ser Arg Ile Trp
    1090                1095                1100

Asp Met Met Ile Glu Gln Gly Leu Pro Glu Asp Gly Lys Ser Tyr Leu
1105                1110                1115                1120

Phe Asp Gly Lys Thr Gly Glu Arg Phe Asp Ser Lys Val Val Val Gly
                1125                1130                1135

Tyr Ile Tyr Met Leu Lys Leu Ser His Leu Ile Ala Asp Lys Ile His
            1140                1145                1150
```

```
Ala Arg Ser Ile Gly Pro Tyr Ser Leu Val Thr Gln Gln Pro Leu Gly
        1155                1160                1165

Gly Lys Ala Gln Met Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp
    1170                1175                1180

Ala Leu Glu Ala Tyr Gly Val Ala His Met Leu Gln Glu Ile Leu Thr
1185                1190                1195                1200

Val Lys Ser Asp Asp Val Ser Gly Arg Thr Arg Ile Tyr Glu Ser Ile
                1205                1210                1215

Val Lys Gly Glu Asn Leu Leu Arg Ser Gly Thr Pro Glu Ser Phe Asn
            1220                1225                1230

Val Leu Ile Lys Glu Met Gln Gly Leu Gly Leu Asp Val Arg Pro Met
        1235                1240                1245

Val Val Asp Ala
    1250
```

<210> 450
<211> 298
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 450

```
Met Leu Lys Ile Asp Leu Thr Gly Lys Ile Ala Phe Ile Ala Gly Ile
                  5                  10                  15

Gly Asp Asp Asn Gly Tyr Gly Trp Gly Ile Ala Lys Met Leu Ala Glu
             20                  25                  30

Ala Gly Ala Thr Ile Leu Val Gly Thr Trp Val Pro Ile Tyr Lys Ile
         35                  40                  45

Phe Ser Gln Ser Leu Glu Leu Gly Lys Phe Asn Ala Ser Arg Glu Leu
     50                  55                  60

Ser Asn Gly Glu Leu Leu Thr Phe Ala Lys Ile Tyr Pro Met Asp Ala
 65                  70                  75                  80

Ser Phe Asp Thr Pro Glu Asp Ile Pro Gln Glu Ile Leu Glu Asn Lys
                 85                  90                  95

Arg Tyr Lys Asp Leu Ser Gly Tyr Thr Val Ser Glu Val Val Glu Gln
            100                 105                 110

Val Lys Lys His Phe Gly His Ile Asp Ile Leu Val His Ser Leu Ala
        115                 120                 125

Asn Ser Pro Glu Ile Ala Lys Pro Leu Leu Asp Thr Ser Arg Lys Gly
    130                 135                 140

Tyr Leu Ala Ala Leu Ser Thr Ser Ser Tyr Ser Phe Ile Ser Leu Leu
145                 150                 155                 160

Ser His Phe Gly Pro Ile Met Asn Ala Gly Ala Ser Thr Ile Ser Leu
                165                 170                 175
```

```
Thr Tyr Leu Ala Ser Met Arg Ala Val Pro Gly Tyr Gly Gly Gly Met
            180                 185                 190

Asn Ala Ala Lys Ala Ala Leu Glu Ser Asp Thr Lys Val Leu Ala Trp
        195                 200                 205

Glu Ala Gly Arg Arg Trp Gly Val Arg Val Asn Thr Ile Ser Ala Gly
    210                 215                 220

Pro Leu Ala Ser Arg Ala Gly Lys Ala Ile Gly Phe Ile Glu Arg Met
225                 230                 235                 240

Val Asp Tyr Tyr Gln Asp Trp Ala Pro Leu Pro Ser Pro Met Glu Ala
                245                 250                 255

Glu Gln Val Gly Ala Ala Ala Ala Phe Leu Val Ser Pro Leu Ala Ser
            260                 265                 270

Ala Ile Thr Gly Glu Thr Leu Tyr Val Asp His Gly Ala Asn Val Met
        275                 280                 285

Gly Ile Gly Pro Glu Met Phe Pro Lys Asp
    290                 295


<210> 451
<211> 298
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 451
Met Ser Leu Gln Lys Leu Leu Val Thr Asp Ile Asp Gly Thr Ile Thr
                5                   10                  15

His Gln Ser His Leu Leu His Asp Arg Val Val Lys Ala Leu His Gln
            20                  25                  30

Tyr Tyr Asp Ser Gly Trp Gln Leu Phe Phe Leu Thr Gly Arg Tyr Phe
        35                  40                  45

Ser Tyr Ala Tyr Pro Leu Phe Gln Asn Phe Ser Val Pro Phe Leu Leu
    50                  55                  60

Gly Ser Gln Asn Gly Ser Ser Val Trp Ser Ser Thr Asp Lys Glu Phe
65                  70                  75                  80

Ile Tyr Phe Arg Ser Leu Ser Arg Asp Phe Leu Tyr Val Leu Glu Lys
                85                  90                  95

Tyr Phe Glu Asp Leu Asp Leu Ile Ala Cys Ile Glu Ser Gly Ala Ser
            100                 105                 110

Asn Arg Asp Val Tyr Phe Arg Lys Gly Leu Gly Lys Thr Ser Gln Glu
        115                 120                 125

Leu Lys Ala Ile Leu Asp Ala Val Tyr Phe Pro Thr Pro Glu Ala Ala
    130                 135                 140

Arg Leu Leu Val Asp Val Gln Gly His Leu Ser Glu Glu Phe Ser Tyr
145                 150                 155                 160
```

```
Glu Asp Phe Ala Ile Ala Lys Phe Phe Gly Glu Arg Glu Glu Val Lys
                165                 170                 175

Lys Ile Met Asp Arg Phe Ile Gln Ser Pro Glu Val Ser Ser Gln Val
            180                 185                 190

Thr Met Asn Tyr Met Arg Trp Pro Phe Asp Phe Lys Tyr Ala Val Leu
        195                 200                 205

Leu Leu Thr Leu Lys Asp Val Ser Lys Gly Phe Ala Val Asp Gln Val
    210                 215                 220

Val Gln Thr Phe Tyr Lys Glu Asn Lys Pro Phe Ile Met Ala Ser Gly
225                 230                 235                 240

Asp Asp Ala Asn Asp Ile Asp Leu Leu Ser Arg Gly Asp Phe Lys Ile
                245                 250                 255

Val Ile Gln Thr Ala Pro Glu Glu Met His Gly Leu Ala Asp Phe Leu
            260                 265                 270

Ala Pro Pro Ala Lys Asp Phe Gly Ile Leu Ser Ala Trp Glu Ala Gly
        275                 280                 285

Glu Leu Arg Tyr Lys Gln Leu Val Asn Pro
    290                 295


<210> 452
<211> 153
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 452
Met Leu Arg Leu Phe Gln His Ile Leu Cys Phe Leu Glu Glu Asp Pro
                5                   10                  15

Ser Phe Val Asp Val Pro Gln Glu Leu Ser Phe Val Asn Glu Ala Phe
            20                  25                  30

Ser Gly Ser Met Arg Trp Glu Val Gly Arg Met Leu Gly Ser Leu Leu
        35                  40                  45

Leu Leu Leu Gly Ile Phe Gly Gly Gly Cys Leu Leu Phe Arg Arg Phe
    50                  55                  60

Leu Arg Ser Arg Gly His Leu Pro Ser Gly Asn Ser Ser Ile Lys Ile
65                  70                  75                  80

Leu Asp Gln Arg Val Leu Ala Ser Lys Thr Ser Ile Tyr Val Ile Lys
                85                  90                  95

Val Ala Asn Lys Thr Leu Val Val Ala Glu Arg Gly Glu Arg Val Thr
            100                 105                 110

Leu Leu Ser Glu Phe Pro Pro Asn Thr Asp Leu Asn Glu Leu Ile Gln
        115                 120                 125

Lys Asp Gln Lys Lys Pro Ser Thr Pro Arg Gly Glu Met Leu Ser Gly
    130                 135                 140
```

Phe Leu Lys Gln Phe Lys Glu Lys Lys
145 150

<210> 453
<211> 569
<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 453
Met Pro Lys Gln Ala Asp Tyr Thr Trp Gly Ala Lys Lys Asn Leu Asp
1 5 10 15

Thr Ile Ala Cys Leu Pro Glu Asp Val Lys Gln Phe Lys Asp Leu Leu
20 25 30

Tyr Ala Met Tyr Gly Phe Thr Ala Thr Glu Glu Glu Pro Thr Ser Glu
35 40 45

Val His Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Ser Lys
50 55 60

Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile Pro
65 70 75 80

Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Thr Val Gly Ala Glu
85 90 95

Val Glu Val Tyr Leu Asp Gln Thr Glu Asp Asp Glu Gly Lys Val Val
100 105 110

Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile Leu
115 120 125

Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg Lys
130 135 140

Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu Pro
145 150 155 160

Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr Val
165 170 175

Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Asp Arg Arg
180 185 190

Asn Val Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile Ser
195 200 205

Lys Lys Ala Glu Leu Ile Glu Gln Ile Thr Ile Gly Glu Arg Arg Lys
210 215 220

Gly Ile Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu Asp
225 230 235 240

Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg Ile
245 250 255

Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val Ile
260 265 270

Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu Lys
275 280 285

Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro Pro
290 295 300

Gly Lys Arg Val Arg Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly Ala
305 310 315 320

Phe Ile Glu Ile Glu Glu Gly Ile Glu Gly Leu Ile His Val Ser Glu
325 330 335

Met Ser Trp Val Lys Asn Ile Val Asp Pro Asn Glu Val Val Asn Lys
340 345 350

Gly Asp Glu Val Glu Val Val Val Leu Ser Ile Gln Lys Asp Glu Gly
355 360 365

Lys Ile Ser Leu Gly Leu Lys Gln Thr Lys His Asn Pro Trp Asp Asn
370 375 380

Ile Glu Glu Lys Tyr Pro Ile Gly Leu Arg Val Thr Ala Glu Ile Lys
385 390 395 400

Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile Glu
405 410 415

Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser His
420 425 430

Pro Ser Glu Leu Phe Lys Lys Gly Asn Thr Val Glu Ala Val Ile Leu
435 440 445

Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln Leu
450 455 460

Thr Pro Asn Pro Trp Asp Glu Ile Glu Val Met Phe Pro Val Gly Ser
465 470 475 480

Asp Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe Val
485 490 495

Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu Ser
500 505 510

Glu Lys Pro Phe Ala Lys Ile Glu Asp Val Leu Ser Ile Gly Asp Lys
515 520 525

Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val Ser
530 535 540

Leu Ser Ile Lys Glu Phe Leu Val His Gly Gly Asp Ala Gly His Asp
545 550 555 560

Ala Glu Glu Glu Ser Ser Asp Arg Asp
565

<210> 454
<211> 666

<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 454
Met Glu Ser Leu Ser Val Arg Ser Thr Ile Pro Leu Pro Leu Gly Ala
1   5   10   15

Lys Lys Leu Ser Ala Asp Arg Tyr Arg Phe Ser Leu Phe Ser Ser Gln
            20   25   30

Ala Gln Gln Val Thr Leu Val Leu Leu Asp Pro Leu Ser Glu Ile His
        35   40   45

Glu Ile Pro Leu Ser Ser Thr Asp His Arg Thr Gly Ala Ile Trp His
    50   55   60

Ile Glu Ile Ala Gly Ile Ser Ser Glu Trp Ser Tyr Ala Tyr Lys Leu
65   70   75   80

Arg Gly Thr Asp Leu Ser Ser Gln Lys Phe Ala Thr Asp Ser Tyr Ile
                85   90   95

Ala Asp Pro Tyr Ser Lys Asn Ile Tyr Ser Pro Gln Leu Phe Gly Ser
            100   105   110

Pro Lys Gln Glu Lys Asp Tyr Ala Phe Ser Tyr Leu Lys His Glu Asp
        115   120   125

Phe Asp Trp Glu Gly Asp Thr Pro Leu His Leu Pro Lys Glu Asn Tyr
    130   135   140

Phe Ile Tyr Glu Met His Val Arg Ser Phe Thr Arg Asp Pro Ser Ser
145   150   155   160

Gln Val Ser His Pro Gly Thr Phe Leu Gly Ile Ile Glu Lys Ile Asp
                165   170   175

His Leu Lys Gln Leu Gly Val His Ala Val Glu Leu Leu Pro Ile Phe
            180   185   190

Glu Phe Asp Glu Thr Val His Pro Phe Lys Asn Gln Asp Phe Pro His
        195   200   205

Leu Cys Asn Tyr Trp Gly Tyr Ser Ser Val Asn Phe Phe Cys Pro Ser
    210   215   220

Arg Arg Tyr Thr Tyr Gly Ala Asp Pro Cys Ala Pro Ala Arg Glu Phe
225   230   235   240

Lys Thr Leu Val Lys Ala Leu His Arg Ala Gly Ile Glu Val Ile Leu
                245   250   255

Asp Val Val Phe Asn His Thr Gly Phe Glu Gly Thr Ser Cys Pro Leu
            260   265   270

Pro Trp Ile Asp Leu Glu Ser Tyr Tyr Met Val Asn Asp His Gly Asp
        275   280   285

Leu Met Asn Phe Ser Gly Cys Gly Asn Thr Val Asn Thr Asn Thr Pro
    290   295   300

```
Thr Thr Leu Lys Trp Ile Leu Asp Ala Leu Arg Tyr Trp Val Gln Glu
305                 310                 315                 320

Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Val Phe Ser Arg
                325                 330                 335

Asp Pro Gln Gly Val Pro Leu Pro Leu Thr Pro Ile Leu Gln Ala Ile
            340                 345                 350

Ser Ser Asp Ser Ile Leu Ser Glu Thr Lys Leu Ile Ala Glu Pro Trp
        355                 360                 365

Asp Ala Gly Gly Leu Tyr Gln Leu Gly His Phe Pro Ser Ile Ser Thr
    370                 375                 380

Arg Trp Ser Glu Trp Asn Gly Cys Tyr Arg Asp His Val Lys Ala Phe
385                 390                 395                 400

Leu Asn Gly Asp Ala His Gln Val Ser Ser Phe Ala Ser Arg Ile Ser
                405                 410                 415

Gly Ser His Asp Ile Tyr Pro Asn Gly Lys Pro Thr Asn Ser Ile Asn
            420                 425                 430

Tyr Ile Cys Ser His Asp Gly Phe Thr Leu Tyr Asp Thr Val Ala Tyr
        435                 440                 445

Asn Asp Lys His Asn Glu Glu Asn Gly Glu Tyr Asn Arg Asp Gly Thr
    450                 455                 460

Ser Ala Asn Tyr Ser Tyr Asn Phe Gly Cys Glu Gly Glu Thr Thr Asp
465                 470                 475                 480

Pro Thr Ile Cys Ala Leu Arg Glu Arg Gln Met Lys Asn Phe Phe Leu
                485                 490                 495

Ala Leu Phe Leu Ser Gln Gly Ile Pro Met Ile Gln Ser Gly Asp Glu
            500                 505                 510

Tyr Gly His Thr Ala Tyr Gly Asn Asn Asn His Trp Cys Leu Asp Thr
        515                 520                 525

Lys Ile Asn Tyr Phe Leu Trp Asp Arg Leu Ala Glu Arg Lys Glu Leu
    530                 535                 540

Phe Ser Phe Leu Cys Gln Val Ile Ala Leu Arg Lys Ala Tyr Thr Glu
545                 550                 555                 560

Leu Phe Asn Thr Ser Phe Leu Ser Glu Asp Thr Ile Thr Trp Leu Asn
                565                 570                 575

Thr Lys Gly Ser Pro Arg Glu Trp Gly Ala Asp His Tyr Leu Ala Phe
            580                 585                 590

Glu Leu Lys His Leu Asn Tyr Ser Leu Phe Val Ala Phe Tyr Ser Gly
        595                 600                 605

Asn Glu Arg Ile Glu Ile Ser Leu Pro Lys Pro Arg Lys Glu His Leu
    610                 615                 620

Ala Tyr Glu Lys Ile Val Asp Ser Thr Thr Gly Phe Phe Ser Gln Ile
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625 630 635 640

Leu Ser Pro Lys Leu Ser Leu Glu Pro Tyr Ser Ser Leu Val Ala Ile
645 650 655

Ser Arg Arg Lys Thr Ser Leu Glu Ser Arg
660 665

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<211> 882
<212> DNA
<213> Chlamydia pneumoniae

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<210> 456
<211> 1185
<212> DNA
<213> Chlamydia pneumoniae

<400> 456
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<210> 457
<211> 1656
<212> DNA

<213> Chlamydia pneumoniae

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<211> 294
<212> DNA
<213> Chlamydia pneumoniae

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tttactgaag agattgtagt aactgctagc cctactgtgg aaagaaagag atcagaacat 240
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<210> 459
<211> 618
<212> DNA
<213> Chlamydia pneumoniae

<400> 459
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<210> 460
<211> 1809
<212> DNA
<213> Chlamydia pneumoniae

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<211> 975
<212> DNA
<213> Chlamydia pneumoniae

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<210> 462
<211> 1980
<212> DNA
<213> Chlamydia pneumoniae

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<210> 463
<211> 1236
<212> DNA
<213> Chlamydia pneumoniae

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<210> 464
<211> 1215
<212> DNA
<213> Chlamydia pneumoniae

<400> 464
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<211> 1632
<212> DNA
<213> Chlamydia pneumoniae

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```
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```

<210> 466
<211> 312
<212> DNA
<213> Chlamydia pneumoniae

<400> 466

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tcgcactatg cagaacaagc cttaaaatct cacggcttcc tgatgggctg ctggctttct    180
ataaagagaa tcggaaagtg tggcccctgg catcctggag gcattgacat ggtccctaag    240
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```

<210> 467
<211> 1089
<212> DNA
<213> Chlamydia pneumoniae

<400> 467

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catttatttt ccggaccttt gattgcgaaa agtagtcgta aggtctacct ttctgaagat    180
tttttaaacg agatatctca agcatctttg gacgacttga tttcgttgtt caaagatgag    240
cgctatatgt atggtcggcc gataaaactt tgggcgttga gtgtagcgat agcttcccac    300
cacatagaca tcactcctgt gctttcgaag cctttgacct atacagagtt gaaaggatct    360
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<210> 468
<211> 1308
<212> DNA
<213> Chlamydia pneumoniae

<400> 468

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tctcctgaac aagcaaaacg ggccatggac ctttctattg cccaacttct ttttgatggt    180
ctgactagag aaactcatcg cgaatccaat gatttggaat tagcgattgc cagtcgctat    240
acagtctctg aagacttttg ctcttatacg ttctttatca aagacagcgc tttatggagc    300
```

```
gacggaacac caatcacctc cgaagatatc cgtaacgctt gggagtatgc acaggagaac    360
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acgattcatc tcgactcgcc caaccccgat tttcctaagc ttcttgcctt tcctgcattt    480
gctatcttta aaccagaaaa cccgaagctc tttagcggtc cgtatactct tgtagagtat    540
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<210> 469
<211> 1749
<212> DNA
<213> Chlamydia pneumoniae

<400> 469

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cgatggattg tctcttcagg aaccgcctct tctctgattg tttctttagg cagtttcttc    300
tctttaggaa gtctatgggc agcaacgttt gcgtgcctcc ttcttttctt tgtgaacttt    360
ttgatggttt caaagggttc ggaaagaatc gcagaggtcc gttcgcggtt tttcttagag    420
gctcttccag caaaacagat ggctttagat tctgatcttg tttctggaag agcttcttat    480
aaggctgtca aaaaacaaaa aaatgccctt atagaagaag gggatttctt ctctgccatg    540
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gttccttaa                                                           1749
```

<210> 470
<211> 516
<212> DNA
<213> Chlamydia pneumoniae

<400> 470

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gaaactgaag aattggaagc tatgaaacag cagtttgtaa aaaatgctga gaaaatagaa 180
gaagaactca cttctattta taataagttg caagatgaag attacatgga aagcctatcg 240
gattctgcct ctgaagagtt gcgaaagaaa ttcgaagatc tttcaggaga gtacaatgcg 300
taccagtctc agtactatca atctatcaat caaagtaatg taaaacgcat tcaaaaactc 360
attcaagaag taaaaatagc tgcagaatca gtgcggtcca aagaaaaact agaagctatc 420
cttaatgaag aagctgtctt agcaatagca cctgggactg ataaaacaac cgaaattatt 480
gctattctta acgaatcttt caaaaaacaa aactag 516

<210> 471
<211> 1083
<212> DNA
<213> Chlamydia pneumoniae

<400> 471
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catattgctt ttttagataa tgagaaatac tctagctttc taaaaaacac caaagctggt 180
gctattattt tatctagatc tcaggcaatg caacatgccc acctaaagaa aaactttctt 240
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acacatcggt tgattgctaa aattcggaac cttcctaaaa ctgaagaaag actaagtaag 1020
ttagaaaaac aagtaagaga tctatcgact cccagccttg ctgagattcc ttcagagatc 1080
taa 1083

<210> 472
<211> 1200
<212> DNA
<213> Chlamydia pneumoniae

<400> 472
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gagatgaaca tgattcaaca atctcaggac ctgacaaatc ccgcagcagc aacacgcacg 180
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<210> 473
<211> 675
<212> DNA
<213> Chlamydia pneumoniae

<400> 473
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aaagattact atttacatat taaagcattt ccttgttacc tttcagcgct gcatgctcgc 180
tgtgatgact tgcagattcg tagacaaatt cttgagaatc tcatggatga agaagctgga 240
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cgaggctatg catactttac tgtacatcaa gaagctgata ttaaacatgc cagcgaagag 540
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<210> 474
<211> 741
<212> DNA
<213> Chlamydia pneumoniae

<400> 474
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<210> 475
<211> 1062
<212> DNA
<213> Chlamydia pneumoniae

<400> 475
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gaaagcttga tcatactgga aaacctgacc aaacaacaaa atcagaaact tcgaatgatt 960
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<210> 476
<211> 561
<212> DNA
<213> Chlamydia pneumoniae

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gcaggtcttg atttagttga agttgcttca aatagcgagc ctcctgtatg taagatcatg 180
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agtcagggtt tagaggatat tggtttcgtt gaagctgaac ccaaactagc aggtcgttcc 480
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gcccaagatg aaaaccaata a 561

<210> 477
<211> 3135
<212> DNA
<213> Chlamydia pneumoniae

<400> 477
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<211> 1041
<212> DNA
<213> Chlamydia pneumoniae

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<210> 479
<211> 984
<212> DNA
<213> Chlamydia pneumoniae

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gctaccgctg ttttgatcaa aggatcctta gaccctcatg cgtatgagat ggttaaaggg 240
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gacaattatt ttagcacctt taaacataat gtctgcctta tcacagaaga attaggaggg     960
gtggctcttg aatgtcaaag atga                                             984
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<210> 480
<211> 444
<212> DNA
<213> Chlamydia pneumoniae

<400> 480

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atagaagaag atggaaattc cggagatctt gcagtatcga cactactagg tactcttcct     180
gaaaacgtat ttcgcgagcg tattttcaaa gctgctctct ctgtaaatgg ctcgttccaa     240
tccagcatca agggaattct aggctacggt gaggtcactc aacagctcta tctttcagat     300
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<210> 481
<211> 1581
<212> DNA
<213> Chlamydia pneumoniae

<400> 481

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<210> 482
<211> 1908
<212> DNA

<213> Chlamydia pneumoniae

<400> 482
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<210> 483
<211> 945
<212> DNA
<213> Chlamydia pneumoniae

<400> 483
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<210> 484
<211> 3723

<212> DNA
<213> Chlamydia pneumoniae

<400> 484
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<211> 1731
<212> DNA
<213> Chlamydia pneumoniae

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ttacgtcgcc aaacctctca gaatatatcc acgatttatg gtccggacaa tgaaaatatt 1320
gatcccgaat ttccttacc ctggatgcct aaaaaagaag aagaaataga ccatagctta 1380
gaacctgtta caaagttgga acccggttca agagaagagt tgttgttggt agaggggggtc 1440
aacccaacct taagagaact caatatgaga attgcacttc tacaacaaca actatcaagt 1500
gtccgaaaat ggagacaccc tcgaggggaa cattacggga atgttatcta ttcagataca 1560
gaactcgatc gtattcagat gctagaaggc gcattttata atcacctcag ggaagctcaa 1620
gaggaaatca cccagtctct cggagacctt gttgacattc aaaaccgtat tttagggatc 1680
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<210> 486
<211> 4224
<212> DNA
<213> Chlamydia pneumoniae

<400> 486
atgaaatatt ctttaccttg gctacttacc tcttcggctt tagttttctc cctacatcca 60
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agcgcagcat tcactgccaa ggaaacttcg gatgcttcag gaactaccta cactctcact 180
agcgatgttt ctattacgaa tgtatctgca attactcctg cagataaaag ctgttttaca 240
aacacaggag gagcattgag ttttgttgga gctgatcact cattggttct gcaaaccata 300
gcgcttacgc atgatggtgc tgcaattaac aataccaaca cagctctttc tttctcagga 360
ttctcgtcac tcttaatcga ctcagctcca gcaacaggaa cttcgggcgg caagggtgct 420
atttgtgtga caaatacaga gggaggtact gcgactttta ctgacaatgc cagtgtcacc 480
ctccaaaaaa atacttcaga aaaagatgga gctgcagttt ctgcctacag catcgatctt 540
gctaagacta cgacagcagc tctcttagat caaaatacta gcacaaaaaa tggcgggggcc 600
ctctgtagta cagcaaacac tacagtccaa ggaaactcag gaacggtgac cttctcctca 660
aatactgcta cagataaagg tgggggggatc tactcaaaag aaaaggatag cacgctagat 720

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gccaatacag gagtcgttac cttcaaatct aatactgcaa agacgggggg tgcttggagc     780
tctgatgaca atcttgctct taccggcaac actcaagtac tttttcagga aaataaaaca     840
accggctcag cagcacaggc aaataacccg gaaggttgtg gtggggcaat ctgttgttat     900
cttgctacag caacagacaa aactggatta gccatttctc agaatcaaga aatgagcttc     960
actagtaata caacaactgc gaatggtgga gcgatctacg ctactaaatg tactctggat    1020
ggaaacacaa ctcttacctt cgatcagaat actgcgacag caggatgtgg cggagctatc    1080
tatacagaaa ctgaagattt ttctcttaag ggaagtacgg gaaccgtgac cttcagcaca    1140
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accaacctgc tcttttcagg gaacaaagct acgggcccga gtaattcttc agcaaatcaa    1260
gagggttgcg gtggggcaat cctagccttt attgattcag gatccgtaag cgataaaaca    1320
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ggtggtgcga tctatgctac caaatgtact ctaactggaa acggctccct gacctttgac    1440
ggcaatactg ctggaacttc aggagggcg atctatacag aaactgaaga ttttactctt    1500
acaggaagta caggaaccgt gaccttcagc acaaatacag caaagacagg cggcgcctta    1560
tattctaaag gcaacaactc tctgtctggt aataccaacc tgctcttttc agggaacaaa    1620
gctacgggcc cgagtaattc ttcagcaaat caagaggggtt gcggtggggc aatcctatcg    1680
tttcttgagt cagcatctgt aagtactaaa aaaggactct ggattgaaga taacgaaaac    1740
gtgagtctct ctggtaatac tgcaacagta agtggcggtg cgatctatgc gaccaagtgt    1800
gctctgcatg gaaacacgac tcttaccttt gatggcaata ctgccgaaac tgcaggagga    1860
gcgatctata cagaaaccga agattttact cttacgggaa gtacgggaac cgtgaccttc    1920
agcacaaata cagcaaagac agcaggggct ctacatacta aaggaaatac ttcctttacc    1980
aaaaataagg ctcttgtatt ttctggaaat tcagcaacag caacagcaac aacaactaca    2040
gatcaagaag gttgtggtgg agcgatcctc tgtaatatct cagagtctga catagctaca    2100
aaaagcttaa ctcttactga aaatgagagt ttaagtttca ttaacaatac ggcaaaaaga    2160
agtggtggtg gtatttatgc tcctaagtgt gtaatctcag gcagtgaatc cataaacttt    2220
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gctaacggtc ctgtctcctt taccaataat tctggaggca agggaggcgc catttatata    2340
gccgatagcg gagaactttc cttagaggct attgatgggg atattacttt ctcagggaac    2400
cgagcgactg agggaacttc aactcccaac tcgatccatt taggtgcagg ggctaagatc    2460
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ggcagcatcg atctaaagaa tctctctgta aatctggatg ctttagatgg caagcgtatg    2940
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ccagagcttc gtgcgacttt agttcctaat agcctttgga atgcttatgt aaacatccat    3300
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aacaacacac aagggaaatc agactgggac agccatagct tcgctgttga agtcggtggt    3780
tctcttcctg tagatctaaa ctacagatac cttaccagct actctcccta tgtgaaactc    3840
caagttgtga gtgtaaatca aaaaggattc caagaggttg ctgctgatcc acgtatcttt    3900
gacgctagcc atctggtcaa cgtgtctatc cctatgggac tcaccttcaa acacgaatca    3960
gcaaagcccc ccagtgcttt gcttcttact ttaggttacg ctgtagatgc ttaccgggat    4020
caccctcact gcctgacctc cttaacaaat ggcacctcgt ggtctacgtt tgctacaaac    4080
ttatcacgac aagctttctt tgctgaggct tctggacatc tgaagttact tcatggtctt    4140
gactgcttcg cttctggaag ttgtgaactg cgcagctcct caagaagcta taatgcaaac    4200
tgtggaactc gttattcttt ctaa                                           4224
```

<210> 487

<211> 804
<212> DNA
<213> Chlamydia pneumoniae

<400> 487
atgggcaatt caggtttcta tttacaagat actcaaaaca ctattttcgc agataacatt 60
cgtcttggtc aaatgaccac agttcttaaa aaagacgagg ttattatagg cacagataca 120
actccaacag taacaaaatt tagtggcgat aagggaattg taattactac agactcaacc 180
ataacaccat ctagcactac tttttctttg gatatggaag ctgtaatcaa agaagtaaca 240
gataaaatct taactcaaat tgaagatgag ttagtcaaag acattataaa aaacataact 300
caaagtctaa tagaagaagt aattaagaaa atacacattg atccttcttt ctcatattct 360
agagcattta aagatgttaa tataactaat aaaattcagt gcaatggtct atttacaaaa 420
gaaaatatag ggaatttaga cggaggaaca gaaatagctt cgtcttcagt aacacctgat 480
aatgctaata gtatgttctt aatttgtgcg gatattatag ccacacgcat ggaaggaaca 540
gtggccttgg cgttagttaa agaaggagat ttatctcctt gctctattag ttatggatac 600
tccgctggat atccgaatat aatttcacta agagcaaccg tcggaaacaa aacaactgct 660
ccagttaaat tctctttgag agcaggaggg atggatagtg gtgttgtgtg ggtaaatgct 720
atgccaaatg gagaaaaaat tttaggagtt gacgcagttt cgaagattac tatcttagaa 780
gtaaaaccac aaacaaatgg ttaa 804

<210> 488
<211> 306
<212> DNA
<213> Chlamydia pneumoniae

<400> 488
atgaataaca gacaaaacac taatgacttt atcagaattg tgaaggatgt tgaaaaggcg 60
tttccagaac tagatatcaa agtaaaaata gataaagaaa aagttacttt tttgacttct 120
ccaacagagc tttatcacaa aagtatatct gtcatactca atttactaaa cagcattgaa 180
tcatctctag accttttccc agactctcca gtagttgaag aattagaaaa aaataatctt 240
aagctcaaaa aagctctgat catgctaatt ctatcaagaa aagacatgtt ctcaaaaaca 300
gaataa 306

<210> 489
<211> 806
<212> DNA
<213> Chlamydia pneumoniae

<400> 489
gtgaaaacaa tagcattttg ctcatttaaa ggagggactg gtaaaactac cttgtctctc 60
aatgttggtt gtaatttagc ccaatatagc aacaaaaagg ttttgcttgt ggatttagat 120
ccacaagcaa accttactac aggtcttggt gtacaatctt gttatgaatc taatttgaac 180
gacattttta gaagttcagg aaacgtaagg gatatcattc aagatacgaa gatagaaaac 240
ttacacatag taccttctag tattctcata gaggagtttc gagaatttaa tagaaatagt 300
gtactggata caagtcattt gcgttcatct ttacaactta ttgaatccaa ttatgatctg 360
tgtattttag acactccacc aagtctgggg acgctcaccg aagaagcctt tattgcatca 420
gatcatttga ttgtttgtct tactcctgaa ccattttcca tattaggatt acagaaaatc 480
aaagagtttt gttcagtgtt acctaaaaag aaagacttat cagtgttagg aatagttttt 540
tctttttggg acggaaggaa ttcaacaaat tcaacctact tgaacattat agaatctatc 600
tacgaaggga aagtgttatc tagtaaagta cgaagagaca taacattaag cagatctctt 660
ttaaaagaaa catccatagc taacgcatac cctaattcta gagcaagtca tgacatactg 720
cgtctaacaa aggagataga agataaacta ttcaataaag aaatgtctgc ccaggaagtg 780
ttgtgagtaa gttagtcaaa gaagca 806

<210> 490
<211> 293
<212> PRT
<213> Chlamydia pneumoniae

<400> 490
Met Ser Lys His Thr Ser Glu Ser Arg Ile Ala Gln Asp Met Leu Glu

```
1               5                   10                  15
Arg Tyr Ser Gly Ser Ser Val Lys Gln Phe Cys Pro Tyr Leu Leu Leu
            20                  25                  30
Thr Asn Phe Ser Tyr Tyr Ile Gln Thr Phe Ala Lys Leu His Gly Val
        35                  40                  45
Pro Val Phe Glu Gly Ser Met Phe Ser Ala Ala His Ala Pro His Leu
    50                  55                  60
Lys Thr Ser Ile Leu Asp Phe Lys Leu Gly Ser Pro Gly Ala Ala Leu
65                  70                  75                  80
Thr Ile Asp Leu Cys Ser Phe Leu Pro Asp Leu Lys Ala Ala Leu Met
                85                  90                  95
Leu Gly Met Cys Gly Gly Leu Arg Ser His Tyr Gln Val Gly Asp Tyr
            100                 105                 110
Phe Val Pro Val Ala Ser Ile Arg Gly Glu Gly Thr Ser Asp Ala Tyr
        115                 120                 125
Phe Pro Pro Glu Val Pro Ala Leu Ala Asn Phe Val Val Gln Lys Ala
    130                 135                 140
Thr Thr Glu Val Leu Glu Asp Lys Lys Ala Asn Tyr His Ile Gly Ile
145                 150                 155                 160
Thr His Thr Thr Asn Ile Arg Phe Trp Glu Phe Asn Lys Lys Phe Arg
                165                 170                 175
Lys Lys Leu Tyr Glu Thr Lys Ala Gln Ser Ala Glu Met Glu Cys Ala
            180                 185                 190
Thr Leu Phe Ala Ala Gly Tyr Arg Arg Asn Leu Pro Ile Gly Ala Leu
        195                 200                 205
Leu Leu Ile Ser Asp Leu Pro Leu Arg Lys Glu Gly Ile Lys Thr Lys
    210                 215                 220
Ser Ser Gly Asn Phe Ile Phe Asn Thr Tyr Thr Glu Asp His Ile Leu
225                 230                 235                 240
Thr Gly Gln Glu Val Ile Glu Asn Leu Glu Lys Val Met Leu Lys Arg
                245                 250                 255
Ala Ala Ser Asp His Lys Lys Asp Gln Gln Tyr Arg Gly Leu Pro His
            260                 265                 270
Met Glu Val Gly Glu Ala Asp Asp Thr Met Ala Ser Gly Ser Glu Thr
        275                 280                 285
Ser Asp Ser Asp Tyr
    290
```

<210> 491
<211> 394
<212> PRT
<213> Chlamydia pneumoniae

<400> 491

```
Met Ser Lys Glu Thr Phe Gln Arg Asn Lys Pro His Ile Asn Ile Gly
1               5                   10                  15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
            20                  25                  30
Thr Arg Ala Leu Ser Gly Asp Gly Leu Ala Ser Phe Arg Asp Tyr Ser
        35                  40                  45
Ser Ile Asp Asn Thr Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
    50                  55                  60
Ala Ser His Val Glu Tyr Glu Thr Pro Asn Arg His Tyr Ala His Val
65                  70                  75                  80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
                85                  90                  95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Thr Asp Gly Ala
            100                 105                 110
Met Pro Gln Thr Lys Glu His Ile Leu Leu Ala Arg Gln Val Gly Val
        115                 120                 125
Pro Tyr Ile Val Val Phe Leu Asn Lys Val Asp Met Ile Ser Gln Glu
```

```
    130                 135                 140
Asp Ala Glu Leu Ile Asp Leu Val Glu Met Glu Leu Ser Glu Leu Leu
145                 150                 155                 160
Glu Glu Lys Gly Tyr Lys Gly Cys Pro Ile Ile Arg Gly Ser Ala Leu
                165                 170                 175
Lys Ala Leu Glu Gly Asp Ala Asn Tyr Ile Glu Lys Val Arg Glu Leu
            180                 185                 190
Met Gln Ala Val Asp Asp Asn Ile Pro Thr Pro Glu Arg Glu Ile Asp
        195                 200                 205
Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
    210                 215                 220
Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser
225                 230                 235                 240
Asp Lys Val Gln Leu Val Gly Leu Gly Glu Thr Lys Glu Thr Ile Val
                245                 250                 255
Thr Gly Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly
            260                 265                 270
Glu Asn Val Gly Leu Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu
        275                 280                 285
Arg Gly Met Val Val Cys Gln Pro Asn Ser Val Lys Pro His Thr Lys
    290                 295                 300
Phe Lys Ser Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His
305                 310                 315                 320
Lys Pro Phe Phe Ser Gly Tyr Arg Pro Gln Phe Phe Phe Arg Thr Thr
                325                 330                 335
Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Thr Glu Met Val Met
            340                 345                 350
Pro Gly Asp Asn Val Glu Leu Asp Val Glu Leu Ile Gly Thr Val Ala
        355                 360                 365
Leu Glu Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile
    370                 375                 380
Gly Ala Gly Thr Ile Ser Lys Ile Asn Ala
385                 390

<210> 492
<211> 560
<212> PRT
<213> Chlamydia pneumoniae

<220>
<221> VARIANT
<222> 553,554,555,556,558,559,560
<223> Xaa = Any Amino Acid

<400> 492
Met Pro Gln Lys Val Leu Ile Thr Ser Ala Leu Pro Tyr Ala Asn Gly
 1               5                  10                  15
Pro Leu His Phe Gly His Ile Ala Gly Val Tyr Leu Pro Ala Asp Val
            20                  25                  30
Tyr Ala Arg Phe Arg Arg Leu Leu Gly Asp Asp Val Leu Tyr Ile Cys
        35                  40                  45
Gly Ser Asp Glu Phe Gly Ile Ala Ile Thr Leu Asn Ala Asp Arg Glu
    50                  55                  60
Gly Leu Gly Tyr Gln Glu Tyr Val Asp Met Tyr His Lys Leu His Lys
65                  70                  75                  80
Asp Thr Phe Glu Lys Leu Gly Phe Ala Leu Asp Phe Phe Ser Arg Thr
                85                  90                  95
Thr Asn Pro Phe His Ala Glu Leu Val Gln Asp Phe Tyr Ser Gln Leu
            100                 105                 110
Lys Ala Ser Gly Leu Ile Glu Asn Arg Ile Ser Glu Gln Leu Tyr Ser
        115                 120                 125
```

```
Glu Gln Glu Gln Arg Phe Leu Ala Asp Arg Tyr Val Glu Gly Thr Cys
    130                 135                 140
Pro Arg Cys Gly Phe Asp His Ala Arg Gly Asp Glu Cys Gln Ser Cys
145                 150                 155                 160
Gly Ala Asp Tyr Glu Ala Ile Asp Leu Ile Gly Pro Lys Ser Lys Ile
                165                 170                 175
Ser Gly Val Glu Leu Val Lys Lys Glu Thr Glu His Ser Tyr Phe Leu
            180                 185                 190
Leu Asp Arg Met Lys Asp Ala Leu Leu Ser Phe Ile Gln Gly Cys Tyr
        195                 200                 205
Leu Pro Asp His Val Arg Lys Phe Val Val Asp Tyr Ile Glu His Val
    210                 215                 220
Arg Ser Arg Ala Ile Thr Arg Asp Leu Ser Trp Gly Ile Pro Val Pro
225                 230                 235                 240
Asp Phe Pro Gly Lys Val Phe Tyr Val Trp Phe Asp Ala Pro Ile Gly
                245                 250                 255
Tyr Ile Ser Gly Thr Met Glu Trp Ala Ala Ser Gln Gly Asn Pro Asp
            260                 265                 270
Glu Trp Lys Arg Phe Trp Leu Glu Asp Gly Val Glu Tyr Val Gln Phe
        275                 280                 285
Ile Gly Lys Asp Asn Leu Pro Phe His Ser Val Val Phe Pro Ala Met
    290                 295                 300
Glu Leu Gly Gln Lys Leu Asp Tyr Lys Lys Val Asp Ala Leu Val Val
305                 310                 315                 320
Ser Glu Phe Tyr Leu Leu Glu Gly Arg Gln Phe Ser Lys Ser Glu Gly
                325                 330                 335
Asn Tyr Val Asp Met Asp Lys Phe Leu Ser Ser Tyr Ser Leu Asp Lys
            340                 345                 350
Leu Arg Tyr Val Leu Ala Ala Thr Ala Pro Glu Thr Ser Asp Ser Glu
        355                 360                 365
Phe Thr Phe Leu Asp Phe Lys Thr Arg Cys Asn Ser Glu Leu Val Gly
    370                 375                 380
Lys Phe Gly Asn Phe Ile Asn Arg Val Leu Ala Phe Ala Glu Lys Asn
385                 390                 395                 400
His Tyr Asp Lys Leu Ser Tyr His Ser Val Val Leu Glu Asp Ser Asp
                405                 410                 415
Arg Ala Phe Leu Glu Glu Ala Arg Gln Leu Val Arg Asp Ala Glu Lys
            420                 425                 430
Cys Tyr Arg Glu Tyr Ser Leu Arg Lys Ala Thr Ser Val Ile Met Ser
        435                 440                 445
Leu Ala Ala Leu Gly Asn Val Tyr Phe Asn Gln Gln Ala Pro Trp Lys
    450                 455                 460
Leu Leu Lys Glu Gly Thr Arg Glu Arg Val Glu Ala Ile Leu Phe Cys
465                 470                 475                 480
Ala Cys Tyr Cys Gln Lys Leu Leu Ala Leu Ile Ser Tyr Pro Ile Ile
                485                 490                 495
Pro Glu Ser Ala Val Ala Ile Trp Glu Met Ile Ser Pro Lys Ser Leu
            500                 505                 510
Glu Asn Cys Asn Leu Asp Thr Met Tyr Ala Arg Asp Leu Trp Lys Glu
        515                 520                 525
Glu Ile Leu Asp Val Ile Asn Glu Glu Phe His Leu Lys Ser Pro Arg
    530                 535                 540
Leu Leu Phe Thr Thr Val Glu Thr Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa
545                 550                 555                 560
```

<210> 493
<211> 97
<212> PRT
<213> Chlamydia pneumoniae

<400> 493

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Met Ile Lys Lys Asp Arg Phe Thr Asn Glu Lys Leu Asn Lys Leu Phe
 1               5                  10                  15
Asp Ser Pro Phe Ser Leu Val Asn Tyr Ala Ile Lys Gln Ala Lys Ile
            20                  25                  30
Lys Ile Ala Lys Gly Asp Val Arg Ser Ser Asn Val Ala Ile Glu Thr
        35                  40                  45
Leu Val Leu Leu Asp Arg Glu Gly Ile Gln Pro Glu Phe Thr Glu Glu
    50                  55                  60
Ile Val Val Thr Ala Ser Pro Thr Val Glu Arg Lys Arg Ser Glu His
65                  70                  75                  80
Thr Asn Ser Arg Lys Lys Asp Pro Ser Ala Tyr Thr Trp Ser Asp Val
                85                  90                  95
Lys
```

<210> 494
<211> 205
<212> PRT
<213> Chlamydia pneumoniae

<400> 494

```
Met Asn Lys Ile Leu Val Asp Ser Pro Phe Ser Pro Asp His Gln Lys
 1               5                  10                  15
Cys Cys Pro Lys Leu Phe Thr Ile Ser Ala Pro Ala Gly Val Gly Lys
            20                  25                  30
Thr Thr Leu Val Arg Met Leu Glu Gln Glu Phe Ser Ser Ala Phe Ala
        35                  40                  45
Glu Thr Ile Ser Val Thr Thr Arg Lys Pro Arg Glu Gly Glu Val Pro
    50                  55                  60
Gly Lys Asp Tyr His Phe Val Ser His Glu Glu Phe Gln Arg Leu Leu
65                  70                  75                  80
Asp Arg Gln Ala Leu Leu Glu Trp Val Phe Leu Phe Gly Glu Cys Tyr
                85                  90                  95
Gly Thr Ser Met Leu Glu Ile Glu Arg Ile Trp Ser Leu Gly Lys His
            100                 105                 110
Ala Val Ala Val Ile Asp Ile Gln Gly Ala Leu Phe Ile Arg Ser Arg
        115                 120                 125
Met Pro Ser Val Ser Ile Phe Ile Ala Pro Pro Ser Gln Glu Glu Leu
    130                 135                 140
Glu Arg Arg Leu Ala Ser Arg Gly Ser Glu Glu Gly Ser Gln Arg Lys
145                 150                 155                 160
Glu Arg Leu Glu His Ser Leu Ile Glu Leu Ala Ala Ala Asn Gln Phe
                165                 170                 175
Asp Tyr Val Ile Ile Asn Asp Asp Leu Asn Gln Ala Tyr Arg Val Leu
            180                 185                 190
Lys Ser Ile Phe Ile Ala Glu Glu His Arg Asn Ile Leu
        195                 200                 205
```

<210> 495
<211> 602
<212> PRT
<213> Chlamydia pneumoniae

<400> 495

```
Met Lys Glu Tyr Lys Ile Glu Asn Ile Arg Asn Phe Ser Ile Ile Ala
 1               5                  10                  15
His Ile Asp His Gly Lys Ser Thr Ile Ala Asp Arg Leu Leu Glu Ser
            20                  25                  30
Thr Ser Thr Val Glu Glu Arg Glu Met Arg Glu Gln Leu Leu Asp Ser
        35                  40                  45
Met Asp Leu Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala His Pro Val
```

```
    50                  55                  60
Thr Met Thr Tyr Leu Tyr Glu Gly Glu Val Tyr Gln Leu Asn Leu Ile
65                  70                  75                  80
Asp Thr Pro Gly His Val Asp Phe Ser Tyr Glu Val Ser Arg Ser Leu
                85                  90                  95
Ser Ala Cys Glu Gly Ala Leu Leu Ile Val Asp Ala Ala Gln Gly Val
            100                 105                 110
Gln Ala Gln Ser Leu Ala Asn Val Tyr Leu Ala Leu Glu Arg Asp Leu
        115                 120                 125
Glu Ile Ile Pro Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Asp Pro
    130                 135                 140
Val Arg Ile Ala Gln Gln Ile Glu Asp Tyr Ile Gly Leu Asp Thr Thr
145                 150                 155                 160
Asn Ile Ile Ala Cys Ser Ala Lys Thr Gly Gln Gly Ile Pro Ala Ile
                165                 170                 175
Leu Lys Ala Ile Ile Asp Leu Val Pro Pro Pro Lys Ala Pro Ala Glu
            180                 185                 190
Thr Glu Leu Lys Ala Leu Val Phe Asp Ser His Tyr Asp Pro Tyr Val
        195                 200                 205
Gly Ile Met Val Tyr Val Arg Ile Ile Ser Gly Glu Leu Lys Lys Gly
    210                 215                 220
Asp Arg Ile Thr Phe Met Ala Ala Lys Gly Ser Ser Phe Glu Val Leu
225                 230                 235                 240
Gly Ile Gly Ala Phe Leu Pro Lys Ala Thr Phe Ile Glu Gly Ser Leu
                245                 250                 255
Arg Pro Gly Gln Val Gly Phe Phe Ile Ala Asn Leu Lys Lys Val Lys
            260                 265                 270
Asp Val Lys Ile Gly Asp Thr Val Thr Lys Thr Lys His Pro Ala Lys
        275                 280                 285
Thr Pro Leu Glu Gly Phe Lys Glu Ile Asn Pro Val Val Phe Ala Gly
    290                 295                 300
Ile Tyr Pro Ile Asp Ser Ser Asp Phe Asp Thr Leu Lys Asp Ala Leu
305                 310                 315                 320
Gly Arg Leu Gln Leu Asn Asp Ser Ala Leu Thr Ile Glu Gln Glu Ser
                325                 330                 335
Ser His Ser Leu Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu
            340                 345                 350
His Leu Glu Ile Ile Phe Glu Arg Ile Ile Arg Glu Phe Asp Leu Asp
        355                 360                 365
Ile Ile Ala Thr Ala Pro Ser Val Ile Tyr Lys Val Val Leu Lys Asn
    370                 375                 380
Gly Lys Val Leu Asp Ile Asp Asn Pro Ser Gly Tyr Pro Asp Pro Ala
385                 390                 395                 400
Ile Ile Glu His Val Glu Glu Pro Trp Val His Val Asn Ile Ile Thr
                405                 410                 415
Pro Gln Glu Tyr Leu Ser Asn Ile Met Asn Leu Cys Leu Asp Lys Arg
            420                 425                 430
Gly Ile Cys Val Lys Thr Glu Met Leu Asp Gln His Arg Leu Val Leu
        435                 440                 445
Ala Tyr Glu Leu Pro Leu Asn Glu Ile Val Ser Asp Phe Asn Asp Lys
    450                 455                 460
Leu Lys Ser Val Thr Lys Gly Tyr Gly Ser Phe Asp Tyr Arg Leu Gly
465                 470                 475                 480
Asp Tyr Arg Lys Gly Ser Ile Ile Lys Leu Glu Val Leu Ile Asn Glu
                485                 490                 495
Glu Pro Ile Asp Ala Phe Ser Cys Leu Val His Arg Asp Lys Ala Glu
            500                 505                 510
Ser Arg Gly Arg Ser Ile Cys Glu Lys Leu Val Asp Val Ile Pro Gln
        515                 520                 525
Gln Leu Phe Lys Ile Pro Ile Gln Ala Ala Ile Asn Lys Lys Val Ile
    530                 535                 540
```

Ala Arg Glu Thr Ile Arg Ala Leu Ser Lys Asn Val Thr Ala Lys Cys
545 550 555 560
Tyr Gly Gly Asp Ile Thr Arg Lys Arg Lys Leu Trp Glu Lys Gln Lys
565 570 575
Lys Gly Lys Lys Arg Met Lys Glu Phe Gly Lys Val Ser Ile Pro Asn
580 585 590
Thr Ala Phe Ile Glu Val Leu Lys Leu Asp
595 600

<210> 496
<211> 324
<212> PRT
<213> Chlamydia pneumoniae

<400> 496
Met Glu Leu Leu Pro His Glu Lys Gln Val Val Glu Tyr Glu Lys Ala
1 5 10 15
Ile Ala Glu Phe Lys Glu Lys Asn Lys Lys Asn Ser Leu Leu Ser Ser
20 25 30
Ser Glu Ile Gln Lys Leu Glu Lys Arg Leu Asp Lys Leu Lys Glu Lys
35 40 45
Ile Tyr Ser Asp Leu Thr Pro Trp Glu Arg Val Gln Ile Cys Arg His
50 55 60
Pro Ser Arg Pro Arg Thr Val Asn Tyr Ile Glu Gly Met Cys Glu Glu
65 70 75 80
Phe Val Glu Leu Cys Gly Asp Arg Thr Phe Arg Asp Asp Pro Ala Val
85 90 95
Val Gly Gly Phe Val Lys Ile Gln Gly Gln Arg Phe Val Leu Ile Gly
100 105 110
Gln Glu Lys Gly Cys Asp Thr Ala Ser Arg Leu His Arg Asn Phe Gly
115 120 125
Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg Leu Gly Lys Leu
130 135 140
Ala Glu Lys Phe Gly Leu Pro Val Val Phe Leu Val Asp Thr Pro Gly
145 150 155 160
Ala Tyr Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln Gly Trp Ala Ile
165 170 175
Ala Lys Asn Leu Phe Glu Leu Ser Arg Leu Ala Thr Pro Val Ile Ile
180 185 190
Val Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu Gly Met Ala Val
195 200 205
Gly Asp Ser Val Ala Met Leu Glu His Ser Tyr Tyr Ser Val Ile Ser
210 215 220
Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro Lys Lys Asn Ser
225 230 235 240
Glu Ala Ala Ser Met Leu Lys Met His Gly Glu Asn Leu Lys Gln Phe
245 250 255
Gly Ile Ile Asp Thr Val Ile Lys Glu Pro Ile Gly Gly Ala His His
260 265 270
Asp Pro Ala Leu Val Tyr Ser Asn Val Arg Glu Phe Ile Ile Gln Glu
275 280 285
Trp Leu Arg Leu Lys Asp Leu Ala Ile Glu Glu Leu Leu Glu Lys Arg
290 295 300
Tyr Glu Lys Phe Arg Ser Ile Gly Leu Tyr Glu Thr Thr Ser Glu Ser
305 310 315 320
Gly Pro Glu Ala

<210> 497
<211> 659
<212> PRT

<213> Chlamydia pneumoniae

<400> 497

```
Met Lys Leu Leu Leu Lys Ala Val Leu Arg His Lys Asn His Leu Val
 1               5                  10                  15
Ile Leu Gly Cys Ser Leu Leu Ala Ile Leu Gly Leu Thr Phe Ser Ser
            20                  25                  30
Gln Met Glu Ile Phe Ser Leu Gly Met Ile Ala Lys Thr Gly Pro Asp
        35                  40                  45
Ala Phe Leu Leu Phe Gly Arg Lys Glu Ser Gly Lys Leu Val Lys Val
    50                  55                  60
Ser Glu Leu Ser Gln Lys Asp Ile Leu Glu Asn Trp Gln Ala Ile Ser
65                  70                  75                  80
Lys Asp Ser Glu Thr Leu Thr Val Ser Asp Ala Thr Thr Tyr Ile Ala
                85                  90                  95
Glu His Gly Lys Ser Thr Ala Ser Leu Thr Ser Lys Leu Ser Lys Phe
            100                 105                 110
Val Arg Asn Tyr Ile Asp Val Ser Arg Phe Arg Gly Leu Ala Ile Phe
        115                 120                 125
Leu Ile Cys Val Ala Ile Phe Lys Ala Val Thr Leu Phe Phe Gln Arg
    130                 135                 140
Phe Leu Gly Gln Val Val Ala Ile Arg Val Ser Arg Asp Leu Arg Gln
145                 150                 155                 160
Asp Tyr Phe Lys Ala Leu Gln Gln Leu Pro Met Thr Phe Phe His Asp
                165                 170                 175
His Asp Ile Gly Asn Leu Ser Asn Arg Val Met Thr Asp Ser Ala Ser
            180                 185                 190
Ile Ala Leu Ala Val Asn Ser Leu Met Ile Asn Tyr Ile Gln Ala Pro
        195                 200                 205
Ile Thr Phe Ile Leu Thr Leu Gly Val Cys Leu Ser Ile Ser Trp Lys
    210                 215                 220
Phe Ser Ile Leu Ile Cys Val Ala Phe Pro Ile Phe Ile Leu Pro Ile
225                 230                 235                 240
Val Val Ile Ala Arg Lys Ile Lys Asn Leu Ala Lys Arg Ile Gln Lys
                245                 250                 255
Ser Gln Asp Ser Phe Ser Ser Val Leu Tyr Asp Phe Leu Ala Gly Val
            260                 265                 270
Met Thr Val Lys Val Phe Arg Thr Glu Lys Phe Ala Phe Thr Lys Tyr
        275                 280                 285
Cys Glu His Asn Asn Lys Ile Ser Ala Leu Glu Glu Lys Ser Ala Ala
    290                 295                 300
Tyr Gly Leu Leu Pro Arg Pro Leu Leu His Thr Ile Ala Ser Leu Phe
305                 310                 315                 320
Phe Ala Phe Val Val Val Ile Gly Ile Tyr Lys Phe Ala Ile Pro Pro
                325                 330                 335
Glu Glu Leu Ile Val Phe Cys Gly Leu Leu Tyr Leu Ile Tyr Asp Pro
            340                 345                 350
Ile Lys Lys Phe Gly Asp Glu Asn Thr Ser Ile Met Arg Gly Cys Ala
        355                 360                 365
Ala Ala Glu Arg Phe Tyr Glu Val Leu Asn His Pro Asp Leu His Ser
    370                 375                 380
Gln Lys Glu Arg Glu Ile Glu Phe Leu Gly Leu Ser Asn Thr Ile Thr
385                 390                 395                 400
Phe Glu Asn Val Ser Phe Gly Tyr Gln Glu Asp Lys His Ile Leu Lys
                405                 410                 415
Asn Leu Ser Phe Thr Leu His Lys Gly Glu Ala Leu Gly Ile Val Gly
            420                 425                 430
Pro Thr Gly Ser Gly Lys Thr Thr Leu Val Lys Leu Leu Pro Arg Leu
        435                 440                 445
Tyr Glu Val Ser Gln Gly Lys Ile Leu Ile Asp Ser Leu Pro Ile Thr
    450                 455                 460
```

```
Glu Tyr Asn Lys Gly Ser Leu Arg Asn His Ile Ala Cys Val Leu Gln
465                 470                 475                 480
Asn Pro Phe Leu Phe Tyr Asp Thr Val Trp Asn Asn Leu Thr Cys Gly
                485                 490                 495
Lys Asp Met Glu Glu Glu Ala Val Leu Glu Ala Leu Lys Arg Ala Tyr
            500                 505                 510
Ala Asp Glu Phe Ile Leu Lys Leu Pro Lys Gly Val His Ser Val Leu
        515                 520                 525
Glu Glu Ser Gly Lys Asn Leu Ser Gly Gly Gln Gln Gln Arg Leu Ala
    530                 535                 540
Ile Ala Arg Ala Leu Leu Lys Asn Ala Ser Ile Leu Ile Leu Asp Glu
545                 550                 555                 560
Ala Thr Ser Ala Leu Asp Ala Ile Ser Glu Asn Tyr Ile Lys Asn Ile
                565                 570                 575
Ile Gly Glu Leu Lys Gly Gln Cys Thr Gln Ile Ile Ile Ala His Lys
            580                 585                 590
Leu Thr Thr Leu Glu His Val Asp Arg Val Leu Tyr Ile Glu Asn Gly
        595                 600                 605
Gln Lys Ile Ala Glu Gly Thr Lys Glu Glu Leu Leu Gln Thr Cys Pro
    610                 615                 620
Glu Phe Leu Lys Met Trp Glu Leu Ser Gly Thr Lys Glu Tyr Asn Arg
625                 630                 635                 640
Val Phe Val Pro Asp His Lys Leu Val Ala Asn Pro Thr Asp Met Ala
                645                 650                 655
Ile Thr Thr
```

<210> 498
<211> 411
<212> PRT
<213> Chlamydia pneumoniae

<400> 498

```
Met Ile Pro Thr Met Leu Met Phe Phe Ile Ile Cys Phe Thr Leu Cys
 1               5                  10                  15
Ser Gly Phe Ile Ser Leu Ser Gln Ile Ala Leu Phe Ser Leu Pro Thr
            20                  25                  30
Ser Leu Ile Ser His Tyr Lys Arg Ser Lys Ser Lys Lys Gln Gln Arg
        35                  40                  45
Val Ala Thr Leu Leu Leu His Pro His His Leu Leu Ile Thr Leu Ile
    50                  55                  60
Phe Cys Asp Ile Gly Leu Asn Ile Ala Ile Gln Asn Cys Phe Ala Ile
65                  70                  75                  80
Leu Phe Gly Asp Ala Ala Ser Trp Trp Phe Thr Val Gly Leu Pro Leu
                85                  90                  95
Ala Ile Thr Leu Ile Leu Gly Glu Ile Leu Pro Lys Ala Val Ala Leu
            100                 105                 110
Pro Phe Asn Thr Gln Ile Ala Ser Ser Val Ala Pro Leu Ile Leu Cys
        115                 120                 125
Val Thr Lys Ile Phe Lys Pro Leu Leu His Trp Gly Ile Val Gly Ile
    130                 135                 140
Asn Tyr Val Val Gln Trp Ile Leu Ser Lys Gln Gln Ile Asp Ile Ile
145                 150                 155                 160
Gln Pro Gln Glu Leu Lys Glu Val Leu Gln Ser Cys Lys Asp Phe Gly
                165                 170                 175
Val Val Asn Gln Glu Glu Ser Arg Leu Leu Tyr Gly Tyr Leu Ser Leu
            180                 185                 190
Ser Asp Cys Ser Val Lys Glu Arg Met Gln Pro Arg Gln Asp Ile Leu
        195                 200                 205
Phe Tyr Asp Ile Gln Thr Pro Leu Glu Asn Leu Tyr Leu Leu Phe Ser
    210                 215                 220
```

```
Lys Gln His Cys Ser Arg Val Pro Ile Cys Asn Asp Asn Leu Gln Asn
225                 230                 235                 240
Leu Leu Gly Ile Cys Thr Ala Arg Ser Leu Leu Leu His Asp Lys Pro
                245                 250                 255
Leu Gln Ser Ser Asp Asp Leu Leu Pro Leu Leu Lys Lys Pro Tyr Tyr
            260                 265                 270
Met Pro Glu Thr Ile Ser Ala Lys Met Ala Leu Cys Gln Met Ala Ala
        275                 280                 285
Glu Asp Glu Thr Leu Gly Met Ile Ile Asp Glu Tyr Gly Ser Ile Glu
    290                 295                 300
Gly Leu Ile Thr Gln Glu Asp Leu Phe Glu Ile Val Ala Gly Glu Ile
305                 310                 315                 320
Val Asp Gln Arg Asp Asn Lys Ile Leu Tyr Thr Thr Ser Gly Ala Asp
                325                 330                 335
Val Ile Ile Ala Ser Gly Thr Leu Glu Leu Arg Glu Phe Ser Glu Ile
            340                 345                 350
Phe Asp Ile Asn Leu Pro Thr Asn Asn Asn Ile Ala Thr Ile Gly Gly
        355                 360                 365
Trp Leu Ile Glu Gln Ile Gly Thr Ile Pro Thr Thr Gly Met Lys Leu
    370                 375                 380
Ser Trp Asn Asn Leu Leu Phe Gln Val Leu Asp Ala Ala Pro Asn Arg
385                 390                 395                 400
Ile Arg Arg Val Tyr Ile Arg Lys Leu Tyr Asp
                405                 410

&lt;210&gt; 499
&lt;211&gt; 404
&lt;212&gt; PRT
&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 499
Met Thr Asn Ser Ala Leu Phe Trp Ile Gly Val Asn Ile Ile Cys Ile
 1               5                  10                  15
Val Leu Gln Gly Phe Tyr Ser Met Met Glu Met Ala Cys Val Ser Phe
            20                  25                  30
Asn Arg Val Arg Leu Gln Tyr Tyr Leu Thr Lys Asp His Lys Lys Ala
        35                  40                  45
Arg Tyr Ile Asn Phe Leu Ile Arg Arg Pro Tyr Arg Leu Phe Gly Thr
    50                  55                  60
Val Met Leu Gly Val Asn Ile Ala Leu Gln Val Gly Ser Glu Ser Ser
65                  70                  75                  80
Arg Asn Cys Tyr Arg Ala Leu Gly Ile Thr Pro Asp Tyr Ala Pro Phe
                85                  90                  95
Thr Gln Ile Phe Ile Val Val Ile Phe Ala Glu Leu Leu Pro Leu Thr
            100                 105                 110
Ile Ser Arg Lys Ile Pro Glu Lys Leu Ala Leu Trp Gly Ala Pro Ile
        115                 120                 125
Leu Tyr Tyr Ser His Tyr Ile Phe Tyr Pro Leu Ile Gln Leu Ile Gly
    130                 135                 140
Ser Leu Thr Glu Gly Leu Tyr Tyr Leu Leu Asn Ile Arg Lys Glu Lys
145                 150                 155                 160
Leu Asn Ser Thr Leu Ser Arg Asp Glu Phe Gln Lys Ala Leu Glu Thr
                165                 170                 175
His His Glu Glu Gln Asp Phe Asn Thr Ile Ala Thr Asn Ile Phe Ser
            180                 185                 190
Leu Ser Ala Thr Cys Ala Asp Gln Val Cys Gln Pro Leu Glu Gln Val
        195                 200                 205
Thr Met Leu Pro Ser Ser Ala Asn Val Lys Asp Phe Cys Arg Thr Ile
    210                 215                 220
Lys Asn Thr Asp Ile Asn Phe Ile Pro Val Tyr His Lys Ala Arg Lys
225                 230                 235                 240
```

Asn Val Ile Gly Ile Ala His Pro Lys Asp Phe Val Asn Lys Ala Leu
245 250 255
Asp Glu Pro Leu Ile Asn Asn Leu His Ser Pro Trp Phe Ile Thr Ala
260 265 270
Lys Ser Lys Leu Ile Arg Ile Leu Lys Glu Phe Arg Asp Asn Arg Ser
275 280 285
Ser Val Ala Val Val Leu Asn Ala Ser Gly Glu Pro Ile Gly Ile Leu
290 295 300
Ser Leu Asn Ala Ile Phe Lys Ile Leu Phe Asn Thr Thr Asn Ile Ala
305 310 315 320
His Leu Lys Pro Lys Thr Ile Ser Val Ile Glu Arg Thr Phe Pro Gly
325 330 335
Asn Ser Arg Ile Lys Asp Leu Gln Lys Glu Leu Asp Ile Gln Phe Pro
340 345 350
Gln Tyr Pro Val Glu Thr Leu Ala Gln Leu Val Leu Gln Leu Leu Asp
355 360 365
Ser Pro Ala Glu Val Gly Thr Ser Val Ile Ile Asn Asn Leu Leu Leu
370 375 380
Glu Val Lys Glu Met Ser Leu Ser Gly Ile Lys Thr Val Ser Ile Lys
385 390 395 400
Asn Leu Leu Ser

<210> 500
<211> 543
<212> PRT
<213> Chlamydia pneumoniae

<400> 500
Met Phe Gly Ser Glu Ser Leu Arg Tyr Gln Leu Leu Ile Gln Asp Phe
1 5 10 15
Ala Lys Val Ser Glu Glu Gly Ile Gly Leu Leu Glu Ser Lys Glu Tyr
20 25 30
Ser Leu Leu Gln Ala Lys Leu Val Leu Arg Ala Leu Ala Gln Asn Ser
35 40 45
Ser Phe Asp Asp Trp Phe Arg Ser Phe Lys Lys Cys Gln Ile Ser Tyr
50 55 60
Pro Glu Leu Ala His Asp Arg Asp Val Leu Glu Glu Phe Gly Ile Gln
65 70 75 80
Val Leu Arg Glu Gly Ile Glu Asn Pro Ser Val Thr Val Arg Ala Val
85 90 95
Ser Val Leu Ala Ile Gly Leu Ala Arg Asp Phe Arg Leu Val Pro Leu
100 105 110
Leu Leu Gln Ser Cys Asn Asp Asp Ser Ala Ile Val Arg Ser Leu Ala
115 120 125
Leu Gln Val Ala Val Asn Tyr Gly Ser Glu Ser Leu Lys Lys Ala Ile
130 135 140
Val Glu Leu Ala Arg Asn Asp Asp Ser Ile His Val Arg Ile Thr Ala
145 150 155 160
Tyr Gln Val Val Ala Leu Leu Gln Ile Glu Glu Leu Leu Pro Phe Leu
165 170 175
Arg Glu Arg Ala Glu Asn Lys Leu Val Asp Ser Val Glu Arg Arg Glu
180 185 190
Ala Trp Lys Ala Cys Leu Glu Leu Ser Ser Gln Phe Leu Glu Thr Gly
195 200 205
Val Ala Lys Asp Asp Ile Asp Gln Ala Leu Phe Thr Cys Glu Val Leu
210 215 220
Arg Asn Gly Met Leu Pro Glu Thr Thr Glu Ile Phe Thr Glu Leu Leu
225 230 235 240
Ser Val Glu His Pro Glu Val Gln Glu Ser Leu Leu Leu Ser Ala Leu
245 250 255

Ala Trp Ser His Gln Leu Gln Asn His Lys Glu Phe Leu Ser Lys Val
260 265 270
Arg His Val Met Cys Thr Ser Pro Phe Ala Lys Val Arg Phe Gln Ala
275 280 285
Ala Ala Leu Leu His Leu His Gly Asp Pro Leu Gly Arg Asp Ser Leu
290 295 300
Val Glu Gly Leu Arg Ser Pro Gln Pro Leu Val Cys Glu Ala Ala Ser
305 310 315 320
Ala Ala Leu Cys Ser Leu Gly Ile His Gly Val Pro Leu Ala Lys Glu
325 330 335
His Leu Glu Ser Leu Ser Ser Arg Lys Ala Ala Ala Asn Leu Ser Ile
340 345 350
Leu Leu Leu Val Ser Arg Glu Asp Ile Glu Arg Ala Gly Asp Val Ile
355 360 365
Ala Arg Tyr Leu Ser Asn Pro Glu Met Cys Trp Ala Ile Glu Tyr Phe
370 375 380
Leu Trp Asp Ala Gln Trp Asn Leu Arg Gly Asp Thr Phe Pro Leu Tyr
385 390 395 400
Ser Asp Met Ile Lys Arg Glu Ile Gly Arg Lys Leu Ile Arg Leu Leu
405 410 415
Ala Val Ala Arg Tyr Ser Gln Ala Lys Ala Val Thr Ala Thr Phe Leu
420 425 430
Ser Gly Gln Gln Ala Gln Gly Trp Ser Phe Phe Ser Gly Met Phe Trp
435 440 445
Glu Glu Gly Asp Val Lys Thr Ser Glu Asp Leu Val Thr Asp Ala Cys
450 455 460
Phe Ala Ala Lys Leu Glu Gly Ala Leu Ala Ser Leu Cys Gln Lys Lys
465 470 475 480
Asp Gln Ala Ser Leu Gln Arg Val Ser Gln Leu Tyr Asn Asp Ser Arg
485 490 495
Trp Gln Asp Lys Leu Ala Ile Leu Glu Ser Val Ala Phe Ser Glu Asn
500 505 510
Leu Asp Ala Val Pro Phe Leu Leu Asp Cys Cys His His Glu Ala Pro
515 520 525
Ser Leu Arg Ser Ala Ala Ala Gly Ala Leu Phe Ser Ile Phe Lys
530 535 540

<210> 501
<211> 103
<212> PRT
<213> Chlamydia pneumoniae

<400> 501
Met Ser Phe Lys Arg Phe Leu Gln Gln Ile Pro Val Arg Ile Cys Leu
1 5 10 15
Leu Ile Ile Tyr Leu Tyr Gln Trp Leu Ile Ser Pro Leu Leu Gly Ser
20 25 30
Cys Cys Arg Phe Phe Pro Ser Cys Ser His Tyr Ala Glu Gln Ala Leu
35 40 45
Lys Ser His Gly Phe Leu Met Gly Cys Trp Leu Ser Ile Lys Arg Ile
50 55 60
Gly Lys Cys Gly Pro Trp His Pro Gly Gly Ile Asp Met Val Pro Lys
65 70 75 80
Thr Ala Leu Gln Glu Val Leu Glu Pro Tyr Gln Glu Ile Asp Gly Gly
85 90 95
Asp Ser Ser His Phe Ser Glu
100

<210> 502
<211> 362
<212> PRT

<213> Chlamydia pneumoniae

<400> 502

Met Ala Phe Lys Arg Lys Thr Arg Trp Leu Trp Gln Val Leu Ile Leu
1   5   10   15
Ser Val Gly Leu Asn Met Leu Phe Leu Leu Leu Phe Tyr Ser Ala Ile
            20   25   30
Phe Arg Lys Asp Ile Tyr Lys Leu His Leu Phe Ser Gly Pro Leu Ile
        35   40   45
Ala Lys Ser Ser Arg Lys Val Tyr Leu Ser Glu Asp Phe Leu Asn Glu
    50   55   60
Ile Ser Gln Ala Ser Leu Asp Asp Leu Ile Ser Leu Phe Lys Asp Glu
65   70   75   80
Arg Tyr Met Tyr Gly Arg Pro Ile Lys Leu Trp Ala Leu Ser Val Ala
                85   90   95
Ile Ala Ser His His Ile Asp Ile Thr Pro Val Leu Ser Lys Pro Leu
            100   105   110
Thr Tyr Thr Glu Leu Lys Gly Ser Ser Val Arg Trp Leu Leu Pro Asn
        115   120   125
Ile Asp Leu Lys Asp Phe Pro Val Ile Leu Asp Tyr Leu Arg Cys His
    130   135   140
Lys Tyr Pro Tyr Thr Ser Lys Gly Leu Phe Leu Leu Ile Glu Lys Met
145   150   155   160
Val Gln Glu Gly Trp Val Asp Glu Asp Cys Leu Tyr His Phe Cys Ser
                165   170   175
Thr Pro Glu Phe Leu Tyr Leu Arg Thr Leu Leu Val Gly Ala Asp Val
            180   185   190
Gln Ala Ser Ser Val Ala Ser Leu Ala Arg Met Val Ile Arg Cys Gly
        195   200   205
Ser Glu Arg Phe Phe His Phe Cys Asn Glu Glu Ser Arg Thr Ser Met
    210   215   220
Ile Ser Ala Thr Gln Arg Gln Lys Val Leu Lys Ser Tyr Leu Asp Cys
225   230   235   240
Glu Glu Ser Leu Ala Ala Leu Leu Leu Leu Val His Asp Ser Asp Val
                245   250   255
Val Leu His Glu Phe Cys Asp Glu Asp Leu Glu Lys Val Ile Arg Leu
            260   265   270
Met Pro Gln Glu Ser Pro Tyr Ser Gln Asn Phe Phe Ser Arg Leu Gln
        275   280   285
His Ser Pro Arg Arg Glu Leu Ala Cys Met Ser Thr Gln Arg Val Glu
    290   295   300
Ala Pro Arg Val Gln Glu Asp Gln Asp Glu Glu Tyr Val Val Gln Asp
305   310   315   320
Gly Asp Ser Leu Trp Leu Ile Ala Lys Arg Phe Gly Ile Pro Met Asp
                325   330   335
Lys Ile Ile Gln Lys Asn Gly Leu Asn His His Arg Leu Phe Pro Gly
            340   345   350
Lys Val Leu Lys Leu Pro Ala Lys Gln Ser
        355   360

<210> 503
<211> 582
<212> PRT
<213> Chlamydia pneumoniae

<400> 503

Met Ser Gly Lys Lys Asp Gly Val Arg Gly Met Ile Phe Val Pro Leu
1   5   10   15
Ser Ile Leu Val Leu Ile Phe Leu Pro Leu Pro Gln Ile Leu Leu Asp
            20   25   30
Phe Gly Leu Cys Ile Ser Phe Ala Leu Ser Leu Leu Thr Val Cys Trp

```
        35                  40                  45
Val Phe Thr Leu Asn Ser Ser Asn Ser Ala Lys Leu Phe Pro Pro Phe
    50                  55                  60
Phe Leu Tyr Leu Cys Leu Leu Arg Leu Gly Leu Asn Leu Ala Ser Thr
65                  70                  75                  80
Arg Trp Ile Val Ser Ser Gly Thr Ala Ser Ser Leu Ile Val Ser Leu
                85                  90                  95
Gly Ser Phe Phe Ser Leu Gly Ser Leu Trp Ala Ala Thr Phe Ala Cys
            100                 105                 110
Leu Leu Leu Phe Phe Val Asn Phe Leu Met Val Ser Lys Gly Ser Glu
        115                 120                 125
Arg Ile Ala Glu Val Arg Ser Arg Phe Phe Leu Glu Ala Leu Pro Ala
    130                 135                 140
Lys Gln Met Ala Leu Asp Ser Asp Leu Val Ser Gly Arg Ala Ser Tyr
145                 150                 155                 160
Lys Ala Val Lys Lys Gln Lys Asn Ala Leu Ile Glu Glu Gly Asp Phe
                165                 170                 175
Phe Ser Ala Met Glu Gly Val Phe Arg Phe Val Lys Gly Asp Ala Ile
            180                 185                 190
Ile Ser Cys Ile Leu Leu Leu Val Asn Val Val Ser Val Thr Cys Leu
        195                 200                 205
Tyr Tyr Thr Ser Gly Tyr Ala Leu Glu Gln Met Trp Phe Thr Val Leu
    210                 215                 220
Gly Asp Ala Leu Val Ser Gln Val Pro Ala Leu Leu Thr Ser Cys Ala
225                 230                 235                 240
Ala Ala Thr Leu Ile Ser Lys Ile Asp Lys Glu Glu Ser Leu Leu Asn
                245                 250                 255
Tyr Leu Phe Glu Tyr Tyr Lys Gln Leu Arg Gln His Phe Arg Val Val
            260                 265                 270
Ser Leu Leu Ile Phe Ser Leu Cys Cys Ile Pro Ser Ser Pro Lys Phe
        275                 280                 285
Pro Ile Val Leu Leu Ala Ser Leu Leu Trp Leu Ala Tyr Arg Lys Glu
    290                 295                 300
Glu Pro Ala Ser Glu Asp Ser Cys Ile Glu Arg Ala Phe Ser Tyr Val
305                 310                 315                 320
Glu Gly Ala Cys Pro Lys Glu Gln Glu Ser Gln Phe Tyr Gln Val Tyr
                325                 330                 335
Arg Ala Ala Ser Glu Glu Val Phe Glu Asp Leu Gly Val Arg Leu Pro
            340                 345                 350
Val Leu Thr Ser Leu Arg Ile Glu Glu Arg Pro Trp Leu Arg Val Phe
        355                 360                 365
Gly Gln Asn Val Tyr Leu Asp Glu Met Thr Pro Glu Ala Val Leu Pro
    370                 375                 380
Phe Leu Arg Asn Ile Ala His Glu Ala Leu Asn Ala Glu Val Val Gln
385                 390                 395                 400
Lys Tyr Leu Glu Glu Ser Glu Arg Val Phe Gly Ile Ala Val Glu Asp
                405                 410                 415
Ile Val Pro Lys Lys Ile Ser Leu Ser Ser Leu Val Val Leu Ser Arg
            420                 425                 430
Leu Leu Val Arg Glu Arg Val Ser Leu Lys Leu Phe Pro Lys Ile Leu
        435                 440                 445
Glu Ala Val Ala Val Tyr Gln Asn Ser Gly Asp Ser Leu Glu Ile Leu
    450                 455                 460
Ala Glu Lys Val Arg Lys Ser Leu Gly Tyr Trp Ile Gly Arg Ser Leu
465                 470                 475                 480
Trp Asp Gln Lys Gln Thr Leu Glu Val Ile Thr Ile Asp Phe His Val
                485                 490                 495
Glu Glu Leu Ile Asn Ser Ser Tyr Ser Lys Ser Asn Pro Val Met Gln
            500                 505                 510
Glu Asn Val Ile Arg Arg Val Asp Ser Leu Leu Glu Arg Ser Val Phe
        515                 520                 525
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```
Lys Asp Phe Arg Ala Ile Val Thr Ser Cys Glu Thr Arg Phe Glu Met
    530                 535                 540
Lys Lys Met Leu Asp Pro His Phe Pro Asp Leu Leu Val Leu Ser His
545                 550                 555                 560
Asp Glu Leu Pro Lys Glu Ile Pro Ile Ser Phe Leu Gly Ile Val Ser
                565                 570                 575
Asp Glu Val Leu Val Pro
            580

<210> 504
<211> 435
<212> PRT
<213> Chlamydia pneumoniae

<400> 504
Met Phe Ser Arg Trp Ile Thr Leu Phe Leu Leu Phe Ile Ser Leu Thr
 1               5                  10                  15
Gly Cys Ser Ser Tyr Ser Ser Lys His Lys Gln Ser Leu Ile Ile Pro
            20                  25                  30
Ile His Asp Asp Pro Val Ala Phe Ser Pro Glu Gln Ala Lys Arg Ala
        35                  40                  45
Met Asp Leu Ser Ile Ala Gln Leu Leu Phe Asp Gly Leu Thr Arg Glu
    50                  55                  60
Thr His Arg Glu Ser Asn Asp Leu Glu Leu Ala Ile Ala Ser Arg Tyr
65                  70                  75                  80
Thr Val Ser Glu Asp Phe Cys Ser Tyr Thr Phe Phe Ile Lys Asp Ser
                85                  90                  95
Ala Leu Trp Ser Asp Gly Thr Pro Ile Thr Ser Glu Asp Ile Arg Asn
            100                 105                 110
Ala Trp Glu Tyr Ala Gln Glu Asn Ser Pro His Ile Gln Ile Phe Gln
        115                 120                 125
Gly Leu Asn Phe Ser Thr Pro Ser Ser Asn Ala Ile Thr Ile His Leu
    130                 135                 140
Asp Ser Pro Asn Pro Asp Phe Pro Lys Leu Leu Ala Phe Pro Ala Phe
145                 150                 155                 160
Ala Ile Phe Lys Pro Glu Asn Pro Lys Leu Phe Ser Gly Pro Tyr Thr
                165                 170                 175
Leu Val Glu Tyr Phe Pro Gly His Asn Ile His Leu Lys Lys Asn Pro
            180                 185                 190
Asn Tyr Tyr Asp Tyr His Cys Val Ser Ile Asn Ser Ile Lys Leu Leu
        195                 200                 205
Ile Ile Pro Asp Ile Tyr Thr Ala Ile His Leu Leu Asn Arg Gly Lys
    210                 215                 220
Val Asp Trp Val Gly Gln Pro Trp His Gln Gly Ile Pro Trp Glu Leu
225                 230                 235                 240
His Lys Gln Ser Gln Tyr His Tyr Tyr Thr Tyr Pro Val Glu Gly Ala
                245                 250                 255
Phe Trp Leu Cys Leu Asn Thr Lys Ser Pro His Leu Asn Asp Leu Gln
            260                 265                 270
Asn Arg His Arg Leu Ala Thr Cys Ile Asp Lys Arg Ser Ile Ile Glu
        275                 280                 285
Glu Ala Leu Gln Gly Thr Gln Gln Pro Ala Glu Thr Leu Ser Arg Gly
    290                 295                 300
Ala Pro Gln Pro Asn Gln Tyr Lys Lys Gln Lys Pro Leu Thr Pro Gln
305                 310                 315                 320
Glu Lys Leu Val Leu Thr Tyr Pro Ser Asp Ile Leu Arg Cys Gln Arg
                325                 330                 335
Ile Ala Glu Ile Leu Lys Glu Gln Trp Lys Ala Ala Gly Ile Asp Leu
            340                 345                 350
Ile Leu Glu Gly Leu Glu Tyr His Leu Phe Val Asn Lys Arg Lys Val
        355                 360                 365
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```
Gln Asp Tyr Ala Ile Ala Thr Gln Thr Gly Val Ala Tyr Tyr Pro Gly
    370                 375                 380
Ala Asn Leu Ile Ser Glu Glu Asp Lys Leu Leu Gln Asn Phe Glu Ile
385                 390                 395                     400
Ile Pro Ile Tyr Tyr Leu Ser Tyr Asp Tyr Leu Thr Gln Asp Phe Ile
                405                 410                     415
Glu Gly Val Ile Tyr Asn Ala Ser Gly Ala Val Asp Leu Lys Tyr Thr
            420                 425                 430
Tyr Phe Pro
        435

<210> 505
<211> 171
<212> PRT
<213> Chlamydia pneumoniae

<400> 505
Met Lys Lys Leu Leu Phe Ser Thr Phe Leu Leu Val Leu Gly Ser Thr
 1               5                  10                  15
Ser Ala Ala His Ala Asn Leu Gly Tyr Val Asn Leu Lys Arg Cys Leu
            20                  25                  30
Glu Glu Ser Asp Leu Gly Lys Lys Glu Thr Glu Glu Leu Glu Ala Met
        35                  40                  45
Lys Gln Gln Phe Val Lys Asn Ala Glu Lys Ile Glu Glu Glu Leu Thr
    50                  55                  60
Ser Ile Tyr Asn Lys Leu Gln Asp Glu Asp Tyr Met Glu Ser Leu Ser
65                  70                  75                  80
Asp Ser Ala Ser Glu Glu Leu Arg Lys Lys Phe Glu Asp Leu Ser Gly
                85                  90                  95
Glu Tyr Asn Ala Tyr Gln Ser Gln Tyr Tyr Gln Ser Ile Asn Gln Ser
            100                 105                 110
Asn Val Lys Arg Ile Gln Lys Leu Ile Gln Glu Val Lys Ile Ala Ala
        115                 120                 125
Glu Ser Val Arg Ser Lys Glu Lys Leu Glu Ala Ile Leu Asn Glu Glu
    130                 135                 140
Ala Val Leu Ala Ile Ala Pro Gly Thr Asp Lys Thr Thr Glu Ile Ile
145                 150                 155                 160
Ala Ile Leu Asn Glu Ser Phe Lys Lys Gln Asn
                165                 170

<210> 506
<211> 360
<212> PRT
<213> Chlamydia pneumoniae

<400> 506
Met Ser Glu Ala Pro Val Tyr Thr Leu Lys Gln Leu Ala Glu Leu Leu
 1               5                  10                  15
Gln Val Glu Val Gln Gly Asn Ile Glu Thr Pro Ile Ser Gly Val Glu
            20                  25                  30
Asp Ile Ser Gln Ala Gln Pro His His Ile Ala Phe Leu Asp Asn Glu
        35                  40                  45
Lys Tyr Ser Ser Phe Leu Lys Asn Thr Lys Ala Gly Ala Ile Ile Leu
    50                  55                  60
Ser Arg Ser Gln Ala Met Gln His Ala His Leu Lys Lys Asn Phe Leu
65                  70                  75                  80
Ile Thr Asn Glu Ser Pro Ser Leu Thr Phe Gln Lys Cys Ile Glu Leu
                85                  90                  95
Phe Ile Glu Pro Val Thr Ser Gly Phe Pro Gly Ile His Pro Thr Ala
            100                 105                 110
Val Ile His Pro Thr Ala Arg Ile Glu Lys Asn Val Thr Ile Glu Pro
```

115 120 125
Tyr Val Val Ile Ser Gln His Ala His Ile Gly Ser Asp Thr Tyr Ile
130 135 140
Gly Ala Gly Ser Val Ile Gly Ala His Ser Val Leu Gly Ala Asn Cys
145 150 155 160
Leu Ile His Pro Lys Val Val Ile Arg Glu Arg Val Leu Met Gly Asn
165 170 175
Arg Val Val Val Gln Pro Gly Ala Val Leu Gly Ser Cys Gly Phe Gly
180 185 190
Tyr Ile Thr Asn Ala Phe Gly His His Lys Pro Leu Lys His Leu Gly
195 200 205
Tyr Val Ile Val Gly Asp Asp Val Glu Ile Gly Ala Asn Thr Thr Ile
210 215 220
Asp Arg Gly Arg Phe Lys Asn Thr Val Ile His Glu Gly Thr Lys Ile
225 230 235 240
Asp Asn Gln Val Gln Val Ala His His Val Glu Ile Gly Lys His Ser
245 250 255
Ile Ile Val Ala Gln Ala Gly Ile Ala Gly Ser Thr Lys Ile Gly Glu
260 265 270
His Val Ile Ile Gly Gly Gln Thr Gly Ile Thr Gly His Ile Ser Ile
275 280 285
Ala Asp His Val Ile Met Ile Ala Gln Thr Gly Val Thr Lys Ser Ile
290 295 300
Thr Ser Pro Gly Ile Tyr Gly Gly Ala Pro Ala Arg Pro Tyr Gln Glu
305 310 315 320
Thr His Arg Leu Ile Ala Lys Ile Arg Asn Leu Pro Lys Thr Glu Glu
325 330 335
Arg Leu Ser Lys Leu Glu Lys Gln Val Arg Asp Leu Ser Thr Pro Ser
340 345 350
Leu Ala Glu Ile Pro Ser Glu Ile
355 360

<210> 507
<211> 399
<212> PRT
<213> Chlamydia pneumoniae

<400> 507
Met Ala Ala Ser Gly Gly Thr Gly Gly Leu Gly Gly Thr Gln Gly Val
1 5 10 15
Asn Leu Ala Ala Val Glu Ala Ala Ala Ala Lys Ala Asp Ala Ala Glu
20 25 30
Val Val Ala Ser Gln Glu Gly Ser Glu Met Asn Met Ile Gln Gln Ser
35 40 45
Gln Asp Leu Thr Asn Pro Ala Ala Ala Thr Arg Thr Lys Lys Lys Glu
50 55 60
Glu Lys Phe Gln Thr Leu Glu Ser Arg Lys Lys Gly Glu Ala Gly Lys
65 70 75 80
Ala Glu Lys Lys Ser Glu Ser Thr Glu Glu Lys Pro Asp Thr Asp Leu
85 90 95
Ala Asp Lys Tyr Ala Ser Gly Asn Ser Glu Ile Ser Gly Gln Glu Leu
100 105 110
Arg Gly Leu Arg Asp Ala Ile Gly Asp Asp Ala Ser Pro Glu Asp Ile
115 120 125
Leu Ala Leu Val Gln Glu Lys Ile Lys Asp Pro Ala Leu Gln Ser Thr
130 135 140
Ala Leu Asp Tyr Leu Val Gln Thr Thr Pro Pro Ser Gln Gly Lys Leu
145 150 155 160
Lys Glu Ala Leu Ile Gln Ala Arg Asn Thr His Thr Glu Gln Phe Gly
165 170 175
Arg Thr Ala Ile Gly Ala Lys Asn Ile Leu Phe Ala Ser Gln Glu Tyr

```
                180                     185                     190
Ala Asp Gln Leu Asn Val Ser Pro Ser Gly Leu Arg Ser Leu Tyr Leu
            195                     200                     205
Glu Val Thr Gly Asp Thr His Thr Cys Asp Gln Leu Leu Ser Met Leu
    210                     215                     220
Gln Asp Arg Tyr Thr Tyr Gln Asp Met Ala Ile Val Ser Ser Phe Leu
225                     230                     235                     240
Met Lys Gly Met Ala Thr Glu Leu Lys Arg Gln Gly Pro Tyr Val Pro
                    245                     250                     255
Ser Ala Gln Leu Gln Val Leu Met Thr Glu Thr Arg Asn Leu Gln Ala
                260                     265                     270
Val Leu Thr Ser Tyr Asp Tyr Phe Glu Ser Arg Val Pro Ile Leu Leu
            275                     280                     285
Asp Ser Leu Lys Ala Glu Gly Ile Gln Thr Pro Ser Asp Leu Asn Phe
    290                     295                     300
Val Lys Val Ala Glu Ser Tyr His Lys Ile Ile Asn Asp Lys Phe Pro
305                     310                     315                     320
Thr Ala Ser Lys Val Glu Arg Glu Val Arg Asn Leu Ile Gly Asp Asp
                    325                     330                     335
Val Asp Ser Val Thr Gly Val Leu Asn Leu Phe Phe Ser Ala Leu Arg
                340                     345                     350
Gln Thr Ser Ser Arg Leu Phe Ser Ser Ala Asp Lys Arg Gln Gln Leu
            355                     360                     365
Gly Ala Met Ile Ala Asn Ala Leu Asp Ala Val Asn Ile Asn Asn Glu
    370                     375                     380
Asp Tyr Pro Lys Ala Ser Asp Phe Pro Lys Pro Tyr Pro Trp Ser
385                     390                     395

<210> 508
<211> 224
<212> PRT
<213> Chlamydia pneumoniae

<400> 508
Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp Gln His
 1               5                  10                  15
Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys Leu Glu
                20                  25                  30
Lys Gln Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys
            35                  40                  45
Ala Phe Pro Cys Tyr Leu Ser Ala Leu His Ala Arg Cys Asp Asp Leu
    50                  55                  60
Gln Ile Arg Arg Gln Ile Leu Glu Asn Leu Met Asp Glu Glu Ala Gly
65                  70                  75                  80
Asn Pro Asn His Ile Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly
                85                  90                  95
Val Ser Glu Glu Glu Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln
                100                 105                 110
Asp Met Val Ala Thr Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala
            115                 120                 125
Val Gly Leu Gly Ala Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val
    130                 135                 140
Cys Val Glu Lys Ile Arg Gly Leu Lys Glu Tyr Phe Gly Val Ser Ala
145                 150                 155                 160
Arg Gly Tyr Ala Tyr Phe Thr Val His Gln Glu Ala Asp Ile Lys His
                165                 170                 175
Ala Ser Glu Glu Lys Glu Met Leu Gln Thr Leu Val Gly Arg Glu Asn
                180                 185                 190
Pro Asp Ala Val Leu Gln Gly Ser Gln Glu Val Leu Asp Thr Leu Trp
            195                 200                 205
Asn Phe Leu Ser Ser Phe Ile Asn Ser Thr Glu Pro Cys Ser Cys Lys
```

210 215 220

<210> 509
<211> 246
<212> PRT
<213> Chlamydia pneumoniae

<400> 509
Met Lys Ile Thr Thr Val Lys Thr Pro Lys Ile Tyr Pro Tyr Asp Asp
1 5 10 15
Leu Tyr Ser Ile Leu Glu Ser Ser Leu Pro Lys Leu Asn Glu Arg Ser
20 25 30
Ile Val Val Ile Thr Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val
35 40 45
Val Glu Leu Glu Lys Val Ser Lys Asp Glu Leu Ile Lys Gln Glu Ala
50 55 60
Asp Ala Tyr Val Phe Val Glu Lys Tyr Gly Ile Tyr Leu Thr Lys Lys
65 70 75 80
Trp Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn Val Glu
85 90 95
Gly Tyr Phe Val Leu Tyr Pro Arg Asp Phe Leu Leu Ser Val Asn Thr
100 105 110
Leu Gly Asp Trp Leu Arg Asn Phe Tyr His Leu Glu His Cys Gly Ile
115 120 125
Ile Ile Ser Asp Ser His Thr Thr Pro Leu Arg Arg Gly Thr Met Gly
130 135 140
Leu Gly Leu Cys Trp Asn Gly Phe Phe Pro Leu Tyr Asn Tyr Val Gly
145 150 155 160
Lys Pro Asp Cys Phe Gly Arg Ala Leu Lys Met Thr Tyr Ser Asn Leu
165 170 175
Leu Asp Gly Leu Ser Ala Ala Ala Val Leu Cys Met Gly Glu Gly Asp
180 185 190
Glu Gln Thr Pro Ile Ala Ile Ile Glu Glu Ala Pro Lys Ile Thr Phe
195 200 205
His Ser Ser Pro Thr Thr Leu Gln Asp Met Ser Thr Leu Ala Ile Ala
210 215 220
Glu Asp Glu Asp Leu Tyr Gly Pro Leu Leu Gln Ser Met Ala Trp Glu
225 230 235 240
Thr Pro Ala Pro Thr Ser
245

<210> 510
<211> 353
<212> PRT
<213> Chlamydia pneumoniae

<400> 510
Met Asn Lys Arg Gln Lys Asp Lys Leu Lys Ile Cys Val Ile Ile Ser
1 5 10 15
Thr Leu Ile Leu Val Gly Ile Phe Ala Arg Ala Pro Arg Gly Asp Thr
20 25 30
Phe Lys Thr Phe Leu Lys Ser Glu Glu Ala Ile Ile Tyr Ser Asn Gln
35 40 45
Cys Asn Glu Asp Met Arg Lys Ile Leu Cys Asp Ala Ile Glu His Ala
50 55 60
Asp Glu Glu Ile Phe Leu Arg Ile Tyr Asn Leu Ser Glu Pro Lys Ile
65 70 75 80
Gln Gln Ser Leu Thr Arg Gln Ala Gln Ala Lys Asn Lys Val Thr Ile
85 90 95
Tyr Tyr Gln Lys Phe Lys Ile Pro Gln Ile Leu Lys Gln Ala Ser Asn
100 105 110

```
Val Thr Leu Val Glu Gln Pro Pro Ala Gly Arg Lys Leu Met His Gln
        115                 120                 125
Lys Ala Leu Ser Ile Asp Lys Lys Asp Ala Trp Leu Gly Ser Ala Asn
    130                 135                 140
Tyr Thr Asn Leu Ser Leu Arg Leu Asp Asn Asn Leu Ile Leu Gly Met
145                 150                 155                 160
His Ser Ser Glu Leu Cys Asp Leu Ile Ile Thr Asn Thr Ser Gly Asp
                165                 170                 175
Phe Ser Ile Lys Asp Gln Thr Gly Lys Tyr Phe Val Leu Pro Gln Asp
            180                 185                 190
Arg Lys Ile Ala Ile Gln Ala Val Leu Glu Lys Ile Gln Thr Ala Gln
        195                 200                 205
Lys Thr Ile Gln Val Ala Met Phe Ala Leu Thr His Ser Glu Ile Ile
    210                 215                 220
Gln Ala Leu His Gln Ala Lys Gln Arg Gly Ile His Val Asp Ile Ile
225                 230                 235                 240
Ile Asp Arg Ser His Ser Lys Leu Thr Phe Lys Gln Leu Arg Gln Leu
                245                 250                 255
Asn Ile Asn Lys Asp Phe Val Ser Ile Asn Thr Ala Pro Cys Thr Leu
            260                 265                 270
His His Lys Phe Ala Val Ile Asp Asn Lys Thr Leu Leu Ala Gly Ser
        275                 280                 285
Ile Asn Trp Ser Lys Gly Arg Phe Ser Leu Asn Asp Glu Ser Leu Ile
    290                 295                 300
Ile Leu Glu Asn Leu Thr Lys Gln Gln Asn Gln Lys Leu Arg Met Ile
305                 310                 315                 320
Trp Lys Asp Leu Ala Lys His Ser Glu His Pro Thr Val Asp Asp Glu
                325                 330                 335
Glu Lys Glu Ile Ile Glu Lys Ser Leu Pro Val Glu Glu Gln Glu Ala
            340                 345                 350
Ala


<210> 511
<211> 186
<212> PRT
<213> Chlamydia pneumoniae

<400> 511
Met Ala Leu Asn Phe Lys Ile Asn Arg Gln Ile Arg Ala Pro Lys Val
 1               5                  10                  15
Arg Leu Ile Gly Ser Ala Gly Glu Gln Leu Gly Ile Leu Ala Ile Lys
            20                  25                  30
Asp Ala Leu Asp Leu Ala Arg Glu Ala Gly Leu Asp Leu Val Glu Val
        35                  40                  45
Ala Ser Asn Ser Glu Pro Pro Val Cys Lys Ile Met Asp Tyr Gly Lys
    50                  55                  60
Tyr Arg Tyr Gly Leu Thr Lys Lys Glu Lys Asp Ser Lys Lys Ala Gln
65                  70                  75                  80
His Gln Val Arg Ile Lys Glu Val Lys Leu Lys Pro Asn Ile Asp Glu
                85                  90                  95
Asn Asp Phe Ser Thr Lys Leu Lys Gln Ala Arg Thr Phe Val Glu Lys
            100                 105                 110
Gly Asn Lys Val Lys Ile Thr Cys Met Phe Arg Gly Arg Glu Leu Ala
        115                 120                 125
Tyr Pro Glu His Gly Phe Lys Val Val Gln Lys Met Ser Gln Gly Leu
    130                 135                 140
Glu Asp Ile Gly Phe Val Glu Ala Glu Pro Lys Leu Ala Gly Arg Ser
145                 150                 155                 160
Leu Ile Cys Val Val Ala Pro Gly Thr Val Lys Thr Lys Lys Lys Gln
                165                 170                 175
```

Glu Lys Ser His Ala Gln Asp Glu Asn Gln
180 185

<210> 512
<211> 276
<212> PRT
<213> Chlamydia pneumoniae

<220>
<221> VARIANT
<222> 269,270,271,272,274,275,276
<223> Xaa = Any Amino Acid

<400> 512
Met Gly Asn Ser Gly Phe Tyr Leu Gln Asp Thr Gln Asn Thr Ile Phe
1 5 10 15
Ala Asp Asn Ile Arg Leu Gly Gln Met Thr Thr Val Leu Lys Lys Asp
20 25 30
Glu Val Ile Ile Gly Thr Asp Thr Thr Pro Thr Val Thr Lys Phe Ser
35 40 45
Gly Asp Lys Gly Ile Val Ile Thr Thr Asp Ser Thr Ile Thr Pro Ser
50 55 60
Ser Thr Thr Phe Ser Leu Asp Met Glu Ala Val Ile Lys Glu Val Thr
65 70 75 80
Asp Lys Ile Leu Thr Gln Ile Glu Asp Glu Leu Val Lys Asp Ile Ile
85 90 95
Lys Asn Ile Thr Gln Ser Leu Ile Glu Glu Val Ile Lys Lys Ile His
100 105 110
Ile Asp Pro Ser Phe Ser Tyr Ser Arg Ala Phe Lys Asp Val Asn Ile
115 120 125
Thr Asn Lys Ile Gln Cys Asn Gly Leu Phe Thr Lys Glu Asn Ile Gly
130 135 140
Asn Leu Asp Gly Gly Thr Glu Ile Ala Ser Ser Ser Val Thr Pro Asp
145 150 155 160
Asn Ala Asn Ser Met Phe Leu Ile Cys Ala Asp Ile Ile Ala Thr Arg
165 170 175
Met Glu Gly Thr Val Ala Leu Ala Leu Val Lys Glu Gly Asp Leu Ser
180 185 190
Pro Cys Ser Ile Ser Tyr Gly Tyr Ser Ala Gly Tyr Pro Asn Ile Ile
195 200 205
Ser Leu Arg Ala Thr Val Gly Asn Lys Thr Thr Ala Pro Val Lys Phe
210 215 220
Ser Leu Arg Ala Gly Gly Met Asp Ser Gly Val Val Trp Val Asn Ala
225 230 235 240
Met Pro Asn Gly Glu Lys Ile Leu Gly Val Asp Ala Val Ser Lys Ile
245 250 255
Thr Ile Leu Glu Val Lys Pro Gln Thr Asn Gly Thr Xaa Xaa Xaa Xaa
260 265 270
Phe Xaa Xaa Xaa
275

<210> 513
<211> 1044
<212> PRT
<213> Chlamydia pneumoniae

<400> 513
Met Val Glu Val Glu Glu Lys His Tyr Thr Ile Val Lys Arg Asn Gly
1 5 10 15
Met Phe Val Pro Phe Asn Gln Asp Arg Ile Phe Gln Ala Leu Glu Ala
20 25 30

```
Ala Phe Arg Asp Thr Arg Ser Leu Glu Thr Ser Ser Pro Leu Pro Lys
        35                  40                  45
Asp Leu Glu Glu Ser Ile Ala Gln Ile Thr His Lys Val Val Lys Glu
    50                  55                  60
Val Leu Ala Lys Ile Ser Glu Gly Gln Val Val Thr Val Glu Arg Ile
65                  70                  75                  80
Gln Asp Leu Val Glu Ser Gln Leu Tyr Ile Ser Gly Leu Gln Asp Val
                85                  90                  95
Ala Arg Asp Tyr Ile Val Tyr Arg Asp Gln Arg Lys Ala Glu Arg Gly
            100                 105                 110
Asn Ser Ser Ser Ile Ile Ala Ile Ile Arg Arg Asp Gly Gly Ser Ala
        115                 120                 125
Lys Phe Asn Pro Met Lys Ile Ser Ala Ala Leu Glu Lys Ala Phe Arg
    130                 135                 140
Ala Thr Leu Gln Ile Asn Gly Met Thr Pro Pro Ala Thr Leu Ser Glu
145                 150                 155                 160
Ile Asn Asp Leu Thr Leu Arg Ile Val Glu Asp Val Leu Ser Leu His
                165                 170                 175
Gly Glu Glu Ala Ile Asn Leu Glu Glu Ile Gln Asp Ile Val Glu Lys
            180                 185                 190
Gln Leu Met Val Ala Gly Tyr Tyr Asp Val Ala Lys Asn Tyr Ile Leu
        195                 200                 205
Tyr Arg Glu Ala Arg Ala Arg Ala Arg Ala Asn Lys Asp Gln Asp Gly
    210                 215                 220
Gln Glu Glu Phe Val Pro Gln Glu Glu Thr Tyr Val Val Gln Lys Glu
225                 230                 235                 240
Asp Gly Thr Thr Tyr Leu Leu Arg Lys Thr Asp Leu Glu Lys Arg Phe
                245                 250                 255
Ser Trp Ala Cys Lys Arg Phe Pro Lys Thr Thr Asp Ser Gln Leu Leu
            260                 265                 270
Ala Asp Met Ala Phe Met Asn Leu Tyr Ser Gly Ile Lys Glu Asp Glu
        275                 280                 285
Val Thr Thr Ala Cys Ile Met Ala Ala Arg Ala Asn Ile Glu Arg Glu
    290                 295                 300
Pro Asp Tyr Ala Phe Ile Ala Ala Glu Leu Leu Thr Ser Ser Leu Tyr
305                 310                 315                 320
Glu Glu Thr Leu Gly Cys Ser Ser Gln Asp Pro Asn Leu Ser Glu Ile
                325                 330                 335
His Lys Lys His Phe Lys Glu Tyr Ile Leu Asn Gly Glu Glu Tyr Arg
            340                 345                 350
Leu Asn Pro Gln Leu Lys Asp Tyr Asp Leu Asp Ala Leu Ser Glu Val
        355                 360                 365
Leu Asp Leu Ser Arg Asp Gln Gln Phe Ser Tyr Met Gly Val Gln Asn
    370                 375                 380
Leu Tyr Asp Arg Tyr Phe Asn Leu His Glu Gly Arg Arg Leu Glu Thr
385                 390                 395                 400
Ala Gln Ile Phe Trp Met Arg Val Ser Met Gly Leu Ala Leu Asn Glu
                405                 410                 415
Gly Glu Gln Lys Asn Phe Trp Ala Ile Thr Phe Tyr Asn Leu Leu Ser
            420                 425                 430
Thr Phe Arg Tyr Thr Pro Ala Thr Pro Thr Leu Phe Asn Ser Gly Met
        435                 440                 445
Arg His Ser Gln Leu Ser Ser Cys Tyr Leu Ser Thr Val Lys Asp Asp
    450                 455                 460
Leu Ser His Ile Tyr Lys Val Ile Ser Asp Asn Ala Leu Leu Ser Lys
465                 470                 475                 480
Trp Ala Gly Gly Ile Gly Asn Asp Trp Thr Asp Val Arg Ala Thr Gly
                485                 490                 495
Ala Val Ile Lys Gly Thr Asn Gly Lys Ser Gln Gly Val Ile Pro Phe
            500                 505                 510
Ile Lys Val Ala Asn Asp Thr Ala Ile Ala Val Asn Gln Gly Gly Lys
```

```
        515                 520                 525
Arg Lys Gly Ala Met Cys Val Tyr Leu Glu Asn Trp His Leu Asp Tyr
    530                 535                 540
Glu Asp Phe Leu Glu Leu Arg Lys Asn Thr Gly Asp Glu Arg Arg Arg
545                 550                 555                 560
Thr His Asp Ile Asn Thr Ala Ser Trp Ile Pro Asp Leu Phe Phe Lys
                565                 570                 575
Arg Leu Glu Lys Lys Gly Met Trp Thr Leu Phe Ser Pro Asp Asp Val
            580                 585                 590
Pro Gly Leu His Glu Ala Tyr Gly Leu Glu Phe Glu Lys Leu Tyr Glu
        595                 600                 605
Glu Tyr Glu Arg Lys Val Glu Ser Gly Glu Ile Arg Leu Tyr Lys Lys
    610                 615                 620
Val Glu Ala Glu Val Leu Trp Arg Lys Met Leu Ser Met Leu Tyr Glu
625                 630                 635                 640
Thr Gly His Pro Trp Ile Thr Phe Lys Asp Pro Ser Asn Ile Arg Ser
                645                 650                 655
Asn Gln Asp His Val Gly Val Val Arg Cys Ser Asn Leu Cys Thr Glu
            660                 665                 670
Ile Leu Leu Asn Cys Ser Glu Ser Glu Thr Ala Val Cys Asn Leu Gly
        675                 680                 685
Ser Ile Asn Leu Val Glu His Ile Arg Asn Asp Lys Leu Asp Glu Glu
    690                 695                 700
Lys Leu Lys Glu Thr Ile Ser Ile Ala Ile Arg Ile Leu Asp Asn Val
705                 710                 715                 720
Ile Asp Leu Asn Phe Tyr Pro Thr Pro Glu Ala Lys Gln Ala Asn Leu
                725                 730                 735
Thr His Arg Ala Val Gly Leu Gly Val Met Gly Phe Gln Asp Val Leu
            740                 745                 750
Tyr Glu Leu Asn Ile Ser Tyr Ala Ser Gln Glu Ala Val Glu Phe Ser
        755                 760                 765
Asp Glu Cys Ser Glu Ile Ile Ala Tyr Tyr Ala Ile Leu Ala Ser Ser
    770                 775                 780
Leu Leu Ala Lys Glu Arg Gly Thr Tyr Ala Ser Tyr Ser Gly Ser Lys
785                 790                 795                 800
Trp Asp Arg Gly Tyr Leu Pro Leu Asp Thr Ile Glu Leu Leu Lys Glu
                805                 810                 815
Thr Arg Gly Glu His Asn Val Leu Val Asp Thr Ser Ser Lys Lys Asp
            820                 825                 830
Trp Thr Pro Val Arg Asp Thr Ile Gln Lys Tyr Gly Met Arg Asn Ser
        835                 840                 845
Gln Val Met Ala Ile Ala Pro Thr Ala Thr Ile Ser Asn Ile Ile Gly
    850                 855                 860
Val Thr Gln Ser Ile Glu Pro Met Tyr Lys His Leu Phe Val Lys Ser
865                 870                 875                 880
Asn Leu Ser Gly Glu Phe Thr Ile Pro Asn Thr Tyr Leu Ile Lys Lys
                885                 890                 895
Leu Lys Glu Leu Gly Leu Trp Asp Ala Glu Met Leu Asp Asp Leu Lys
            900                 905                 910
Tyr Phe Asp Gly Ser Leu Leu Glu Ile Glu Arg Ile Pro Asn His Leu
        915                 920                 925
Lys Lys Leu Phe Leu Thr Ala Phe Glu Ile Glu Pro Glu Trp Ile Ile
    930                 935                 940
Glu Cys Thr Ser Arg Arg Gln Lys Trp Ile Asp Met Gly Val Ser Leu
945                 950                 955                 960
Asn Leu Tyr Leu Ala Glu Pro Asp Gly Lys Lys Leu Ser Asn Met Tyr
                965                 970                 975
Leu Thr Ala Trp Lys Lys Gly Leu Lys Thr Thr Tyr Tyr Leu Arg Ser
            980                 985                 990
Gln Ala Ala Thr Ser Val Glu Lys Ser Phe Ile Asp Ile Asn Lys Arg
        995                 1000                1005
```

```
Gly Ile Gln Pro Arg Trp Met Lys Asn Lys Ser Ala Ser Thr Ser Ile
    1010                1015                1020
Val Val Glu Arg Lys Thr Thr Pro Val Cys Ser Met Glu Glu Gly Cys
1025                1030                1035                1040
Glu Ser Cys Gln


<210> 514
<211> 346
<212> PRT
<213> Chlamydia pneumoniae

<400> 514
Met Glu Ala Asp Ile Leu Asp Gly Lys Leu Lys Arg Val Glu Val Ser
 1               5                  10                  15
Lys Lys Gly Leu Val Asn Cys Asn Gln Val Asp Val Asn Gln Leu Val
            20                  25                  30
Pro Ile Lys Tyr Lys Trp Ala Trp Glu His Tyr Leu Asn Gly Cys Ala
        35                  40                  45
Asn Asn Trp Leu Pro Thr Glu Val Pro Met Ala Arg Asp Ile Glu Leu
    50                  55                  60
Trp Lys Ser Asp Glu Leu Ser Glu Asp Glu Arg Arg Val Ile Leu Leu
65                  70                  75                  80
Asn Leu Gly Phe Phe Ser Thr Ala Glu Ser Leu Val Gly Asn Asn Ile
                85                  90                  95
Val Leu Ala Ile Phe Lys His Ile Thr Asn Pro Glu Ala Arg Gln Tyr
            100                 105                 110
Leu Leu Arg Gln Ala Phe Glu Glu Ala Val His Thr His Thr Phe Leu
        115                 120                 125
Tyr Ile Cys Glu Ser Leu Gly Leu Asp Glu Gly Glu Val Phe Asn Ala
    130                 135                 140
Tyr Asn Glu Arg Ala Ser Ile Arg Ala Lys Asp Asp Phe Gln Met Thr
145                 150                 155                 160
Leu Thr Val Asp Val Leu Asp Pro Asn Phe Ser Val Gln Ser Ser Glu
                165                 170                 175
Gly Leu Gly Gln Phe Ile Lys Asn Leu Val Gly Tyr Tyr Ile Ile Met
            180                 185                 190
Glu Gly Ile Phe Phe Tyr Ser Gly Phe Val Met Ile Leu Ser Phe His
        195                 200                 205
Arg Gln Asn Lys Met Thr Gly Ile Gly Glu Gln Tyr Gln Tyr Ile Leu
    210                 215                 220
Arg Asp Glu Thr Ile His Leu Asn Phe Gly Ile Asp Leu Ile Asn Gly
225                 230                 235                 240
Ile Lys Glu Glu Asn Pro Glu Val Trp Thr Thr Glu Leu Gln Glu Glu
                245                 250                 255
Ile Val Ala Leu Ile Glu Lys Ala Val Glu Leu Glu Ile Glu Tyr Ala
            260                 265                 270
Lys Asp Cys Leu Pro Arg Gly Ile Leu Gly Leu Arg Ser Ser Met Phe
        275                 280                 285
Ile Asp Tyr Val Arg His Ile Ala Asp Arg Arg Leu Glu Arg Ile Gly
    290                 295                 300
Leu Lys Pro Ile Tyr His Ser Arg Asn Pro Phe Pro Trp Met Ser Glu
305                 310                 315                 320
Thr Met Asp Leu Asn Lys Glu Lys Asn Phe Phe Glu Thr Arg Val Thr
                325                 330                 335
Glu Tyr Gln Thr Ala Gly Asn Leu Ser Trp
            340                 345

<210> 515
<211> 327
<212> PRT
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<213> Chlamydia pneumoniae

<400> 515
Met Asp Ala Lys Met Gly Tyr Ile Phe Lys Val Met Arg Trp Ile Phe
1 5 10 15
Cys Phe Val Ala Cys Gly Ile Thr Phe Gly Cys Thr Asn Ser Gly Phe
20 25 30
Gln Asn Ala Asn Ser Arg Pro Cys Ile Leu Ser Met Asn Arg Met Ile
35 40 45
His Asp Cys Val Glu Arg Val Val Gly Asn Arg Leu Ala Thr Ala Val
50 55 60
Leu Ile Lys Gly Ser Leu Asp Pro His Ala Tyr Glu Met Val Lys Gly
65 70 75 80
Asp Lys Asp Lys Ile Ala Gly Ser Ala Val Ile Phe Cys Asn Gly Leu
85 90 95
Gly Leu Glu His Thr Leu Ser Leu Arg Lys His Leu Glu Asn Asn Pro
100 105 110
Asn Ser Val Lys Leu Gly Glu Arg Leu Ile Ala Arg Gly Ala Phe Val
115 120 125
Pro Leu Glu Glu Asp Gly Ile Cys Asp Pro His Ile Trp Met Asp Leu
130 135 140
Ser Ile Trp Lys Glu Ala Val Ile Glu Ile Thr Glu Val Leu Ile Glu
145 150 155 160
Lys Phe Pro Glu Trp Ser Ala Glu Phe Lys Ala Asn Ser Glu Glu Leu
165 170 175
Val Cys Glu Met Ser Ile Leu Asp Ser Trp Ala Lys Gln Cys Leu Ser
180 185 190
Thr Ile Pro Glu Asn Leu Arg Tyr Leu Val Ser Gly His Asn Ala Phe
195 200 205
Ser Tyr Phe Thr Arg Arg Tyr Leu Ala Thr Pro Glu Glu Val Ala Ser
210 215 220
Gly Ala Trp Arg Ser Arg Cys Ile Ser Pro Glu Gly Leu Ser Pro Glu
225 230 235 240
Ala Gln Ile Ser Val Arg Asp Ile Met Ala Val Val Asp Tyr Ile Asn
245 250 255
Glu His Asp Val Ser Val Val Phe Pro Glu Asp Thr Leu Asn Gln Asp
260 265 270
Ala Leu Lys Lys Ile Val Ser Ser Leu Lys Lys Ser His Leu Val Arg
275 280 285
Leu Ala Gln Lys Pro Leu Tyr Ser Asp Asn Val Asp Asp Asn Tyr Phe
290 295 300
Ser Thr Phe Lys His Asn Val Cys Leu Ile Thr Glu Glu Leu Gly Gly
305 310 315 320
Val Ala Leu Glu Cys Gln Arg
325

<210> 516
<211> 101
<212> PRT
<213> Chlamydia pneumoniae

<400> 516
Met Asn Asn Arg Gln Asn Thr Asn Asp Phe Ile Arg Ile Val Lys Asp
1 5 10 15
Val Glu Lys Ala Phe Pro Glu Leu Asp Ile Lys Val Lys Ile Asp Lys
20 25 30
Glu Lys Val Thr Phe Leu Thr Ser Pro Thr Glu Leu Tyr His Lys Ser
35 40 45
Ile Ser Val Ile Leu Asn Leu Leu Asn Ser Ile Glu Ser Ser Leu Asp
50 55 60
Leu Phe Pro Asp Ser Pro Val Val Glu Glu Leu Glu Lys Asn Asn Leu

65 70 75 80
Lys Leu Lys Lys Ala Leu Ile Met Leu Ile Leu Ser Arg Lys Asp Met
85 90 95
Phe Ser Lys Thr Glu
100

<210> 517
<211> 261
<212> PRT
<213> Chlamydia pneumoniae

<400> 517
Met Lys Thr Ile Ala Phe Cys Ser Phe Lys Gly Gly Thr Gly Lys Thr
1 5 10 15
Thr Leu Ser Leu Asn Val Gly Cys Asn Leu Ala Gln Tyr Ser Asn Lys
20 25 30
Lys Val Leu Leu Val Asp Leu Asp Pro Gln Ala Asn Leu Thr Thr Gly
35 40 45
Leu Gly Val Gln Ser Cys Tyr Glu Ser Asn Leu Asn Asp Ile Phe Arg
50 55 60
Ser Ser Gly Asn Val Arg Asp Ile Ile Gln Asp Thr Lys Ile Glu Asn
65 70 75 80
Leu His Ile Val Pro Ser Ser Ile Leu Ile Glu Glu Phe Arg Glu Phe
85 90 95
Asn Arg Asn Ser Val Leu Asp Thr Ser His Leu Arg Ser Ser Leu Gln
100 105 110
Leu Ile Glu Ser Asn Tyr Asp Leu Cys Ile Leu Asp Thr Pro Pro Ser
115 120 125
Leu Gly Thr Leu Thr Glu Glu Ala Phe Ile Ala Ser Asp His Leu Ile
130 135 140
Val Cys Leu Thr Pro Glu Pro Phe Ser Ile Leu Gly Leu Gln Lys Ile
145 150 155 160
Lys Glu Phe Cys Ser Val Leu Pro Lys Lys Lys Asp Leu Ser Val Leu
165 170 175
Gly Ile Val Phe Ser Phe Trp Asp Gly Arg Asn Ser Thr Asn Ser Thr
180 185 190
Tyr Leu Asn Ile Ile Glu Ser Ile Tyr Glu Gly Lys Val Leu Ser Ser
195 200 205
Lys Val Arg Arg Asp Ile Thr Leu Ser Arg Ser Leu Leu Lys Glu Thr
210 215 220
Ser Ile Ala Asn Ala Tyr Pro Asn Ser Arg Ala Ser His Asp Ile Leu
225 230 235 240
Arg Leu Thr Lys Glu Ile Glu Asp Lys Leu Phe Asn Lys Glu Met Ser
245 250 255
Ala Gln Glu Val Leu
260

<210> 518
<211> 526
<212> PRT
<213> Chlamydia pneumoniae

<400> 518
Met Asn Val Leu Lys Tyr Thr Lys His Ser Pro Ser Ala His Ala Trp
1 5 10 15
Lys Leu Ile Gly Thr Ser Pro Lys His Gly Ile Tyr Leu Pro Leu Phe
20 25 30
Ser Ile His Thr Lys Asn Ser Cys Gly Ile Gly Glu Phe Leu Asp Leu
35 40 45
Ile Pro Leu Ile Ser Trp Cys Gln Lys Gln Gly Phe Ser Val Ile Gln
50 55 60

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Leu Leu Pro Leu Asn Asp Thr Gly Glu Asp Thr Ser Pro Tyr Asn Ser
65                  70                  75                  80
Ile Ser Ser Val Ala Leu Asn Pro Leu Phe Leu Ser Leu Ser Ser Leu
                85                  90                  95
Pro Asn Ile Asp Thr Ile Pro Glu Val Ala Lys Lys Leu Gln Asp Met
            100                 105                 110
His Glu Leu Cys Ser Thr Pro Ser Val Ser Tyr Thr Gln Val Lys Glu
        115                 120                 125
Lys Lys Trp Ala Phe Leu Arg Glu Tyr Tyr Gln Lys Cys Cys Lys Ser
    130                 135                 140
Ser Leu Glu Gly Asn Ser Asn Phe Ser Glu Phe Leu Glu Ser Glu Arg
145                 150                 155                 160
Tyr Trp Leu Tyr Pro Tyr Gly Thr Phe Arg Ala Ile Lys His His Met
                165                 170                 175
His Gly Glu Pro Ile Asn Asn Trp Pro Lys Ser Leu Thr Asp Gln Glu
            180                 185                 190
Asn Phe Pro Asp Leu Thr Lys Lys Phe His Asp Glu Val Leu Phe Phe
        195                 200                 205
Ser Tyr Leu Gln Phe Leu Cys Tyr Gln Gln Leu Cys Glu Val Lys Ala
    210                 215                 220
Tyr Ala Asp Gln His His Val Leu Leu Lys Gly Asp Leu Pro Ile Leu
225                 230                 235                 240
Ile Ser Lys Asp Ser Cys Asp Val Trp Tyr Phe Arg Asp Tyr Phe Ser
                245                 250                 255
Ser Ser Arg Ser Val Gly Ala Pro Pro Asp Leu Tyr Asn Ser Glu Gly
            260                 265                 270
Gln Asn Trp His Leu Pro Ile Tyr Asn Phe Ser Gln Leu Ala Lys Asp
        275                 280                 285
Asp Tyr Ile Trp Trp Lys Glu Arg Leu Arg Tyr Ala Gln Asn Phe Tyr
    290                 295                 300
Ser Val Tyr Arg Leu Asp His Ile Ile Gly Phe Phe Arg Leu Trp Ile
305                 310                 315                 320
Trp Asp Ser Ser Gly Arg Gly Arg Phe Ile Pro Asp Asn Pro Lys Asp
                325                 330                 335
Tyr Ile Lys Gln Gly Thr Glu Ile Leu Ser Thr Met Leu Gly Ala Ser
            340                 345                 350
Ser Met Leu Pro Ile Gly Glu Asp Leu Gly Ile Ile Pro Gln Asp Val
        355                 360                 365
Lys Thr Thr Leu Thr His Leu Gly Ile Cys Gly Thr Arg Ile Pro Arg
    370                 375                 380
Trp Glu Arg Asn Trp Glu Ser Asp Ser Ala Phe Ile Pro Leu Lys Asp
385                 390                 395                 400
Tyr Asn Pro Leu Ser Val Thr Thr Leu Ser Thr His Asp Ser Asp Thr
                405                 410                 415
Phe Ala Gln Trp Trp Leu Asn Ser Pro Lys Glu Ala Lys Gln Phe Ala
            420                 425                 430
Lys Phe Leu His Leu Pro Phe Gln Lys Thr Leu Thr Thr Glu Thr Gln
        435                 440                 445
Ile Asp Ile Leu Lys Leu Ser His Glu Ser Ala Ser Ile Phe His Ile
    450                 455                 460
Asn Leu Phe Asn Asp Tyr Leu Ala Leu Cys Pro Asp Leu Val Ser Lys
465                 470                 475                 480
Asn Leu Gln Arg Glu Arg Ile Asn Thr Pro Gly Thr Ile Ser Lys Lys
                485                 490                 495
Asn Trp Ser Tyr Arg Val Arg Pro Ser Leu Glu Glu Leu Ala Ile His
            500                 505                 510
Lys Lys Phe Asn Gly Tyr Ile Glu Lys Ile Leu Thr Gly Leu
        515                 520                 525
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<210> 519
<211> 147

<212> PRT
<213> Chlamydia pneumoniae

<400> 519
Met Gln Asn Gln Tyr Glu Gln Leu Leu Glu Ser Leu Ala Pro Leu Leu
1 5 10 15
Asn Thr Thr Leu Ala Pro Asp Lys Asn Asn Ser Cys Leu Ile Arg Phe
20 25 30
Ser Asp Thr His Val Pro Val Gln Ile Glu Glu Asp Gly Asn Ser Gly
35 40 45
Asp Leu Ala Val Ser Thr Leu Leu Gly Thr Leu Pro Glu Asn Val Phe
50 55 60
Arg Glu Arg Ile Phe Lys Ala Ala Leu Ser Val Asn Gly Ser Phe Gln
65 70 75 80
Ser Ser Ile Lys Gly Ile Leu Gly Tyr Gly Glu Val Thr Gln Gln Leu
85 90 95
Tyr Leu Ser Asp Ile Leu Ser Met Asn Tyr Leu Asn Gly Glu Lys Leu
100 105 110
Phe Glu Tyr Leu Lys Leu Phe Ser Leu His Ala Lys Ile Trp Met Glu
115 120 125
Ser Leu Arg Thr Gly Asn Leu Pro Asp Leu His Val Leu Gly Ile Tyr
130 135 140
Tyr Val Ala
145

<210> 520
<211> 635
<212> PRT
<213> Chlamydia pneumoniae

<400> 520
Met Ile Pro Phe Thr Lys Thr Ile Gly Phe Arg Leu Trp Leu Ala Cys
1 5 10 15
Ala Val Ala Ile Ile Ala Pro Leu Gly Ile Asn Ile Val Trp Leu Asn
20 25 30
Leu Asp Gln Tyr Arg Thr Ile Val Ser Ala Ile Ser Thr Ala Leu Lys
35 40 45
Glu Asn Ala Ala Phe Lys Ala Asn Thr Leu Thr Gln Ile Val Pro Leu
50 55 60
Asn Val Asp Val Leu Ser Leu Phe Ser Asp Val Leu Asp Leu Asp Ala
65 70 75 80
Gly Ile Pro Glu Thr Pro Asn Val Leu Leu Ser Asn Glu Met Gln Lys
85 90 95
Val Phe Gln Gly Ile Tyr Asn Glu Ile Ser Leu Ile Lys Val Phe Pro
100 105 110
Asn Gly Asp Lys Ile Val Val Ala Ser Ser Ile Pro Glu His Leu Gly
115 120 125
Glu Asn Tyr Asn His Lys Ile Asp Ile Pro Lys Asn Thr Pro Phe Leu
130 135 140
Ala Ala Leu Lys Gln Ser Pro Lys Asn Gln Glu Val Phe Ser Val Met
145 150 155 160
Gln Ala Asn Val Phe Asp Ala Lys Thr Gln Glu Leu Gln Gly Ile Leu
165 170 175
Tyr Thr Thr Phe Ser Ala Glu Ser Leu Leu Lys Asp Leu Leu Ile Asn
180 185 190
Lys Gln Ser Tyr Leu Thr Val Lys Thr Ala Ile Leu Ser Lys Tyr Gly
195 200 205
Val Ile Leu Lys Ala Ser Asp Pro Ala Leu His Leu His Thr Val Tyr
210 215 220
Pro Asp Met Thr Lys Glu Lys Phe Cys Gln Val Phe Leu Asn Asp Asp
225 230 235 240

Pro Cys Pro Ile Asp Ser Glu Leu Gly Pro Leu Thr Leu Ser Pro Leu
245 250 255
Asp Ile Gly Glu Asn Phe Tyr Ser Phe Lys Ile Lys Asp Thr Glu Ile
260 265 270
Trp Gly Cys Ile Glu Asn Val Pro Ser Ile Asp Ile Ala Val Leu Ser
275 280 285
Tyr Ala Lys Lys Glu Glu Ser Phe Ala Pro Leu Trp Arg Arg Ala Arg
290 295 300
Met Tyr Thr Ala Tyr Phe Phe Cys Ile Leu Leu Gly Ser Leu Ile Ala
305 310 315 320
Phe Ile Val Ala Arg Arg Leu Ser Leu Pro Ile Arg Lys Leu Ala Thr
325 330 335
Ala Met Ile Glu Ser Arg Lys Asn Lys Asn Cys Leu Tyr Thr Asp Asp
340 345 350
Ser Leu Gly Phe Glu Ile Asn Arg Leu Gly His Ile Phe Asn Ala Met
355 360 365
Val Glu Asn Leu His Lys Gln Gln His Leu Ala Lys Thr Asn Phe Glu
370 375 380
Met Lys Glu Asn Ala Gln Asn Ala Leu His Leu Gly Glu Gln Ala Gln
385 390 395 400
Gln Arg Leu Leu Pro Asn Thr Leu Pro Ser Tyr Pro His Ile Glu Leu
405 410 415
Ala Lys Ala Tyr Ile Pro Ala Ile Thr Val Gly Gly Asp Phe Phe Asp
420 425 430
Val Phe Val Val Gly Glu Gly Ser Lys Ala Arg Leu Phe Leu Ile Val
435 440 445
Ala Asp Ala Ser Gly Lys Gly Val Asn Ala Cys Gly Tyr Ser Leu Phe
450 455 460
Leu Lys Asn Met Leu Arg Thr Phe Leu Ser Arg Ser Ser Ser Leu Gln
465 470 475 480
Gln Ala Ile Gln Glu Thr Ser Arg Leu Phe Tyr Asn Asn Thr Lys Asn
485 490 495
Ser Gly Met Phe Val Thr Leu Cys Val Tyr Cys Tyr His Gln Thr Ser
500 505 510
Asn Thr Met Glu Tyr Tyr Ser Cys Gly His Pro Pro Ala Cys Tyr Leu
515 520 525
Asp Pro Asp Gly Glu Thr Ser Trp Leu Phe His Pro Gly Met Ala Leu
530 535 540
Gly Phe Leu Pro Glu Val Ala Asn Ile Thr Ser Lys Leu Phe His Pro
545 550 555 560
Lys Pro Gly Ser Leu Phe Val Leu Tyr Ser Asp Gly Ile Thr Glu Ala
565 570 575
His Asn Asn Asn Asn Asp Met Phe Gly Glu Glu Arg Leu Gln Ala Ala
580 585 590
Ile Gln Gly Leu Thr Gly Lys Ser Ala Ala Asp Ala Val His Arg Leu
595 600 605
Met Leu Ser Val Lys Thr Phe Val Gly Asn Ser His Gln His Asp Asp
610 615 620
Ile Thr Leu Leu Ile Leu Lys Val Leu Glu Ser
625 630 635

<210> 521
<211> 314
<212> PRT
<213> Chlamydia pneumoniae

<400> 521
Met Phe Ser Tyr Ile Lys Asn Arg Ile Leu Phe Asn Leu Leu Ser Leu
1 5 10 15
Trp Ile Val Leu Thr Leu Thr Phe Leu Val Met Lys Thr Ile Pro Gly
20 25 30

Asp Pro Phe Asn Asp Glu Gly Cys Asn Val Leu Ser Glu Glu Val Leu
35 40 45
Gln Thr Leu Lys Ser Arg Tyr Gly Leu Asp Lys Pro Leu Tyr Gln Gln
50 55 60
Tyr Thr Gln Tyr Leu His Ser Ile Ala Lys Leu Asp Phe Gly Asn Ser
65 70 75 80
Leu Val Tyr Lys Asp Arg Lys Val Thr Asn Ile Ile Ser Thr Ala Phe
85 90 95
Pro Ile Ser Ala Ile Leu Gly Leu Gln Ser Leu Phe Leu Ser Ile Gly
100 105 110
Gly Gly Ile Ala Leu Gly Thr Ile Ala Ala Leu Lys Lys Lys Lys Gln
115 120 125
Arg Arg Tyr Ile Leu Gly Ala Ser Ile Leu Gln Ile Ser Ile Pro Ala
130 135 140
Phe Ile Phe Ala Thr Leu Leu Gln Tyr Val Phe Ala Val Lys Ile Pro
145 150 155 160
Leu Leu Pro Ile Ala Cys Trp Gly Ser Phe Thr His Thr Ile Leu Pro
165 170 175
Thr Leu Ala Leu Ala Val Thr Pro Met Ala Phe Ile Ile Gln Leu Thr
180 185 190
Tyr Ser Ser Val Ser Ala Ala Leu Asn Lys Asp Tyr Val Leu Leu Ala
195 200 205
Tyr Ala Lys Gly Leu Ser Pro Leu Lys Val Val Ile Lys His Ile Leu
210 215 220
Pro Tyr Ala Ile Phe Pro Thr Ile Ser Tyr Ser Ala Phe Leu Thr Thr
225 230 235 240
Thr Val Ile Thr Gly Thr Phe Ala Ile Glu Asn Ile Phe Cys Ile Pro
245 250 255
Gly Leu Gly Lys Trp Phe Ile Cys Ser Ile Lys Gln Arg Asp Tyr Pro
260 265 270
Val Ala Leu Gly Leu Ser Val Phe Tyr Gly Thr Leu Phe Met Leu Ser
275 280 285
Ser Leu Leu Ser Asp Leu Ile Gln Ser Ile Ile Asp Pro Gln Ile Arg
290 295 300
Tyr Ala His Gly Lys Glu Lys Lys Arg Lys
305 310

<210> 522
<211> 1240
<212> PRT
<213> Chlamydia pneumoniae

<400> 522
Met Thr Trp Ile Pro Leu His Cys His Ser Gln Tyr Ser Val Leu Asp
1 5 10 15
Ala Met Ser Ser Ile Lys Asp Phe Val Ala Lys Gly Gln Glu Phe Gly
20 25 30
Ile Pro Ala Leu Ala Leu Thr Asp His Gly Asn Leu Tyr Gly Ala Val
35 40 45
Asp Phe Tyr Lys Glu Cys Thr Gln Lys Gly Ile Gln Pro Ile Ile Gly
50 55 60
Cys Glu Cys Tyr Ile Ala Pro Gly Ser Arg Phe Asp Lys Lys Lys Glu
65 70 75 80
Lys Arg Ser Arg Ala Ala His His Leu Ile Leu Leu Cys Lys Asn Glu
85 90 95
Gln Gly Tyr Arg Asn Leu Cys Ile Leu Thr Ser Leu Ala Phe Thr Glu
100 105 110
Gly Phe Tyr Tyr Phe Pro Arg Ile Asp Lys Asp Leu Leu Arg Gln Tyr
115 120 125
Ser Glu Gly Leu Ile Cys Leu Ser Gly Cys Leu Ser Ser Ser Val Ser
130 135 140

Asp Ala Ala Leu Lys Ser Pro Glu Ala Leu Leu Leu Glu Leu Gln Trp
145 150 155 160
Phe Gln Asp Leu Phe Lys Asp Asp Tyr Phe Thr Glu Val Gln Leu His
165 170 175
Lys Met Ser Glu Glu Ser Ile Ala Gly Phe Lys Glu Glu Trp Leu Lys
180 185 190
Gln Glu Tyr Tyr Ser Leu Ile Glu Lys Gln Ile Lys Val Asn Thr Ala
195 200 205
Val Leu Glu Ala Ser Lys Arg Leu Gly Ile Pro Thr Val Ala Thr Asn
210 215 220
Asp Ile His Tyr Ile Asn Ala Asn Asp Trp Gln Ala His Glu Ile Leu
225 230 235 240
Leu Asn Val Gln Ser Gly Glu Thr Val Arg Ile Ala Lys Gln Asn Thr
245 250 255
His Ile Pro Asn Pro Lys Arg Lys Val Tyr Arg Ser Arg Glu Tyr Tyr
260 265 270
Phe Lys Ser Pro Ala Gln Met Ala Glu Leu Phe Lys Asp Ile Pro Glu
275 280 285
Val Ile Ser Asn Thr Leu Glu Val Ala Lys Arg Cys Asp Phe Thr Phe
290 295 300
Asp Phe Ser Lys Lys His Tyr Pro Ile Tyr Val Pro Glu Ser Leu Lys
305 310 315 320
Thr Leu Asn Ser Tyr Thr Glu Glu Asp Arg Tyr Gln Ala Ser Ala Val
325 330 335
Phe Leu Lys Gln Leu Ala Glu Glu Ala Leu Pro Lys Lys Tyr Ser Ser
340 345 350
Glu Val Leu Ala His Ile Ala Lys Lys Phe Pro His Arg Asp Pro Ile
355 360 365
Asp Ile Val Lys Glu Arg Met Asp Met Glu Met Ala Ile Ile Ile Pro
370 375 380
Lys Gly Met Cys Asp Tyr Leu Leu Ile Val Trp Asp Ile Ile His Trp
385 390 395 400
Ala Lys Ala Asn Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Gly Ala
405 410 415
Gly Ser Val Leu Leu Phe Leu Leu Gly Ile Thr Glu Ile Glu Pro Ile
420 425 430
Arg Phe Asp Leu Phe Phe Glu Arg Phe Ile Asn Pro Glu Arg Leu Ser
435 440 445
Tyr Pro Asp Ile Asp Ile Asp Ile Cys Met Ala Gly Arg Glu Arg Val
450 455 460
Ile Asn Tyr Ala Ile Glu Arg His Gly Lys Asp Asn Val Ala Gln Ile
465 470 475 480
Ile Thr Phe Gly Thr Met Lys Ala Lys Met Ala Val Lys Asp Val Gly
485 490 495
Arg Thr Leu Asp Met Ala Leu Ser Lys Val Asn His Ile Ala Lys His
500 505 510
Ile Pro Asp Leu Asn Thr Thr Leu Ser Lys Ala Leu Glu Thr Asp Pro
515 520 525
Asp Leu His Gln Leu Tyr Ile Asn Asp Ala Glu Ser Ala Gln Val Ile
530 535 540
Asp Met Ala Leu Cys Leu Glu Gly Ser Ile Arg Asn Thr Gly Val His
545 550 555 560
Ala Ala Gly Val Ile Ile Cys Gly Asp Gln Leu Thr Asn His Ile Pro
565 570 575
Ile Cys Ile Ser Lys Asp Ser Thr Met Ile Thr Thr Gln Tyr Ser Met
580 585 590
Lys Pro Val Glu Ser Val Gly Met Leu Lys Val Asp Leu Leu Gly Leu
595 600 605
Lys Thr Leu Thr Ser Ile Asn Ile Ala Met Ser Ala Ile Glu Lys Lys
610 615 620
Thr Gly Gln Ser Leu Ala Met Ala Thr Leu Pro Leu Asp Asp Ala Thr

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625                 630                 635                 640
Thr Phe Ser Leu Leu His Gln Gly Lys Thr Met Gly Ile Phe Gln Met
                645                 650                 655
Glu Ser Lys Gly Met Gln Glu Leu Ala Lys Asn Leu Arg Pro Asp Leu
            660                 665                 670
Phe Glu Glu Ile Ile Ala Met Gly Ala Leu Tyr Arg Pro Gly Pro Met
        675                 680                 685
Asp Met Ile Pro Ser Phe Ile Asn Arg Lys His Gly Lys Glu Ile Ile
    690                 695                 700
Glu Tyr Asp His Pro Leu Met Glu Ser Ile Leu Lys Glu Thr Tyr Gly
705                 710                 715                 720
Ile Met Val Tyr Gln Glu Gln Val Met Gln Ile Ala Gly Ala Leu Ala
                725                 730                 735
Ser Tyr Ser Leu Gly Glu Gly Asp Val Leu Arg Arg Ala Met Gly Lys
            740                 745                 750
Lys Asp Phe Gln Gln Met Glu Gln Glu Arg Glu Lys Phe Cys Lys Arg
        755                 760                 765
Ala Cys Asn Asn Gly Ile Asp Pro Glu Leu Ala Thr Val Ile Phe Asp
    770                 775                 780
Lys Met Glu Lys Phe Ala Ala Tyr Gly Phe Asn Lys Ser His Ala Ala
785                 790                 795                 800
Ala Tyr Gly Leu Ile Thr Tyr Thr Thr Ala Tyr Leu Lys Ala Asn Tyr
                805                 810                 815
Pro Lys Glu Trp Leu Ala Ala Leu Leu Thr Cys Asp Ser Asp Asp Ile
            820                 825                 830
Glu Lys Ile Gly Lys Leu Ile Arg Glu Ala Gln Ser Met Gly Ile Pro
        835                 840                 845
Ile Leu Pro Pro His Ile Asn Val Ser Ser Asn His Phe Val Ala Thr
    850                 855                 860
Asp Glu Gly Ile Arg Phe Ala Met Gly Ala Ile Lys Gly Ile Gly Arg
865                 870                 875                 880
Gly Leu Ile Glu Ser Ile Val Glu Glu Arg Asp His His Gly Pro Tyr
                885                 890                 895
Glu Ser Ile Arg Asp Phe Ile Gln Arg Ser Asp Leu Lys Lys Val Ser
            900                 905                 910
Lys Lys Ser Ile Glu Ser Leu Ile Asp Ala Gly Cys Phe Asp Cys Phe
        915                 920                 925
Asp Ser Asn Arg Asp Leu Leu Leu Ala Ser Val Glu Pro Leu Tyr Glu
    930                 935                 940
Ala Ile Ala Lys Asp Lys Lys Glu Ala Ala Ser Gly Val Met Thr Phe
945                 950                 955                 960
Phe Thr Leu Gly Ala Met Asp Arg Lys Asn Glu Val Pro Ile Cys Leu
                965                 970                 975
Pro Lys Asp Ile Pro Thr Arg Ser Lys Lys Glu Leu Leu Lys Lys Glu
            980                 985                 990
Lys Glu Leu Leu Gly Ile Tyr Leu Thr Glu His Pro Met Asp Thr Val
        995                 1000                1005
Arg Asp His Leu Ser Arg Leu Ser Val Val Leu Ala Gly Glu Phe Glu
    1010                1015                1020
Asn Leu Pro His Gly Ser Val Val Arg Thr Val Phe Ile Ile Asp Lys
1025                1030                1035                1040
Val Thr Thr Lys Ile Ser Ser Lys Ala Gln Lys Lys Phe Ala Val Leu
                1045                1050                1055
Arg Val Ser Asp Gly Ile Asp Ser Tyr Glu Leu Pro Ile Trp Pro Asp
            1060                1065                1070
Met Tyr Glu Glu Gln Gln Glu Leu Leu Glu Glu Asp Arg Leu Ile Tyr
        1075                1080                1085
Ala Ile Leu Val Leu Asp Lys Arg Ser Asp Ser Leu Arg Ile Ser Cys
    1090                1095                1100
Arg Trp Met Lys Asp Leu Ser Ile Val Asn Glu Asn Ile Ile Tyr Glu
1105                1110                1115                1120
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Cys Asp Gln Ala Phe Asp Arg Ile Lys Asn Gln Val Gln Lys Met Ser
                1125                1130                1135
Phe Thr Met Ser Thr Ser Gly Lys Glu Thr Lys Ala Lys Gly Asn Lys
            1140                1145                1150
Pro Asn Glu Asn Gly His Thr Gln Ala Leu Ala Pro Val Thr Leu Ser
        1155                1160                1165
Leu Asp Leu Asn Glu Leu Arg His Ser His Leu Cys Ile Leu Lys Lys
    1170                1175                1180
Ile Val Gln Lys His Pro Gly Ser Arg Thr Leu Val Leu Val Phe Thr
1185                1190                1195                1200
Gln Asp Asn Glu Arg Val Ala Ser Met Ser Pro Asp Asp Ala Tyr Phe
                1205                1210                1215
Val Cys Glu Asp Ile Glu Glu Leu Arg Gln Glu Leu Val Thr Ala Asp
            1220                1225                1230
Leu Pro Val Arg Val Ile Thr Val
        1235                1240

<210> 523
<211> 576
<212> PRT
<213> Chlamydia pneumoniae

<400> 523
Met Thr Asp Phe Pro Thr His Phe Lys Gly Pro Lys Leu Asn Pro Ile
 1               5                  10                  15
Lys Val Asn Pro Asn Phe Phe Glu Arg Asn Pro Lys Val Ala Arg Val
            20                  25                  30
Leu Gln Ile Thr Ala Val Val Leu Gly Ile Ile Ala Leu Leu Ser Gly
        35                  40                  45
Ile Val Leu Ile Ile Gly Thr Pro Leu Gly Ala Pro Ile Ser Met Ile
    50                  55                  60
Leu Gly Gly Cys Leu Leu Ala Ser Gly Gly Ala Leu Phe Val Gly Gly
65                  70                  75                  80
Thr Ile Ala Thr Ile Leu Gln Ala Arg Asn Ser Tyr Lys Lys Ala Val
                85                  90                  95
Asn Gln Lys Lys Leu Ser Glu Pro Leu Met Glu Arg Pro Glu Leu Lys
            100                 105                 110
Ala Leu Asp Tyr Ser Leu Asp Leu Lys Glu Val Trp Asp Leu His His
        115                 120                 125
Ser Val Val Lys His Leu Lys Lys Leu Asp Leu Asn Leu Ser Lys Thr
    130                 135                 140
Gln Arg Glu Val Leu Asn Gln Ile Lys Ile Asp Asp Glu Gly Pro Ser
145                 150                 155                 160
Leu Gly Glu Cys Ala Ala Met Ile Ser Glu Asn Tyr Asp Ala Cys Leu
                165                 170                 175
Lys Met Leu Ala Tyr Arg Glu Glu Leu Leu Lys Glu Gln Thr Gln Tyr
            180                 185                 190
Gln Glu Thr Arg Phe Asn Gln Asn Leu Thr His Arg Asn Lys Val Leu
        195                 200                 205
Leu Ser Ile Leu Ser Arg Ile Thr Asp Asn Ile Ser Lys Ala Gly Gly
    210                 215                 220
Val Phe Ser Leu Lys Phe Ser Thr Leu Ser Ser Arg Met Ser Arg Ile
225                 230                 235                 240
His Thr Thr Thr Thr Val Ile Leu Ala Leu Ser Ala Val Val Ser Val
                245                 250                 255
Met Val Val Ala Ala Leu Ile Pro Gly Gly Ile Leu Ala Leu Pro Ile
            260                 265                 270
Leu Leu Ala Val Ala Ile Ser Ala Gly Val Ile Val Thr Gly Leu Ser
        275                 280                 285
Tyr Leu Val Arg Gln Ile Leu Ser Asn Thr Lys Arg Asn Arg Gln Asp
    290                 295                 300
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Phe Tyr Lys Asp Phe Val Lys Asn Val Asp Ile Glu Leu Leu Asn Gln
305 310 315 320
Thr Val Thr Leu Gln Arg Phe Leu Phe Glu Met Leu Lys Gly Val Leu
325 330 335
Lys Glu Glu Glu Glu Val Ser Leu Glu Gly Gln Asp Trp Tyr Thr Gln
340 345 350
Tyr Ile Thr Asn Ala Pro Ile Glu Lys Arg Leu Ile Glu Glu Ile Arg
355 360 365
Val Thr Tyr Lys Glu Ile Asp Ala Gln Thr Lys Lys Met Lys Thr Asp
370 375 380
Leu Glu Phe Leu Glu Asn Glu Val Arg Ser Gly Arg Leu Ser Val Ala
385 390 395 400
Ser Pro Ser Glu Asp Pro Ser Glu Thr Pro Ile Phe Thr Gln Gly Lys
405 410 415
Glu Phe Ala Lys Leu Arg Arg Gln Thr Ser Gln Asn Ile Ser Thr Ile
420 425 430
Tyr Gly Pro Asp Asn Glu Asn Ile Asp Pro Glu Phe Ser Leu Pro Trp
435 440 445
Met Pro Lys Lys Glu Glu Glu Ile Asp His Ser Leu Glu Pro Val Thr
450 455 460
Lys Leu Glu Pro Gly Ser Arg Glu Glu Leu Leu Leu Val Glu Gly Val
465 470 475 480
Asn Pro Thr Leu Arg Glu Leu Asn Met Arg Ile Ala Leu Leu Gln Gln
485 490 495
Gln Leu Ser Ser Val Arg Lys Trp Arg His Pro Arg Gly Glu His Tyr
500 505 510
Gly Asn Val Ile Tyr Ser Asp Thr Glu Leu Asp Arg Ile Gln Met Leu
515 520 525
Glu Gly Ala Phe Tyr Asn His Leu Arg Glu Ala Gln Glu Glu Ile Thr
530 535 540
Gln Ser Leu Gly Asp Leu Val Asp Ile Gln Asn Arg Ile Leu Gly Ile
545 550 555 560
Ile Val Glu Gly Asp Ser Asp Ser Arg Thr Glu Glu Glu Pro Gln Glu
565 570 575

<210> 524
<211> 439
<212> PRT
<213> Chlamydia pneumoniae

<220>
<221> VARIANT
<222> 428,429,430,431,432,433,434,435,437,438,439
<223> Xaa = Any Amino Acid

<400> 524
Ile Thr Ile Ala Val Asn Ser Thr Ser Gly Gly Leu Lys Ile Ser Gly
1 5 10 15
Asp Leu Lys Phe His Asn Asn Glu Gly Ser Phe Tyr Asp Asn Pro Gly
20 25 30
Leu Lys Ala Asn Leu Asn Leu Pro Phe Leu Asp Leu Ser Ser Thr Ser
35 40 45
Gly Thr Val Asn Leu Asp Asp Phe Asn Pro Ile Pro Ser Ser Met Ala
50 55 60
Ala Pro Asp Tyr Gly Tyr Gln Gly Ser Trp Thr Leu Val Pro Lys Val
65 70 75 80
Gly Ala Gly Gly Lys Val Thr Leu Val Ala Glu Trp Gln Ala Leu Gly
85 90 95
Tyr Thr Pro Lys Pro Glu Leu Arg Ala Thr Leu Val Pro Asn Ser Leu
100 105 110
Trp Asn Ala Tyr Val Asn Ile His Ser Ile Gln Gln Glu Ile Ala Thr

115 120 125
Ala Met Ser Asp Ala Pro Ser His Pro Gly Ile Trp Ile Gly Gly Ile
130 135 140
Gly Asn Ala Phe His Gln Asp Lys Gln Lys Glu Asn Ala Gly Phe Arg
145 150 155 160
Leu Ile Ser Arg Gly Tyr Ile Val Gly Gly Ser Met Thr Thr Pro Gln
165 170 175
Glu Tyr Thr Phe Ala Val Ala Phe Ser Gln Leu Phe Gly Lys Ser Lys
180 185 190
Asp Tyr Val Val Ser Asp Ile Lys Ser Gln Val Tyr Ala Gly Ser Leu
195 200 205
Cys Ala Gln Ser Ser Tyr Val Ile Pro Leu His Ser Ser Leu Arg Arg
210 215 220
His Val Leu Ser Lys Val Leu Pro Glu Leu Pro Gly Glu Thr Pro Leu
225 230 235 240
Val Leu His Gly Gln Val Ser Tyr Gly Arg Asn His His Asn Met Thr
245 250 255
Thr Lys Leu Ala Asn Asn Thr Gln Gly Lys Ser Asp Trp Asp Ser His
260 265 270
Ser Phe Ala Val Glu Val Gly Gly Ser Leu Pro Val Asp Leu Asn Tyr
275 280 285
Arg Tyr Leu Thr Ser Tyr Ser Pro Tyr Val Lys Leu Gln Val Val Ser
290 295 300
Val Asn Gln Lys Gly Phe Gln Glu Val Ala Ala Asp Pro Arg Ile Phe
305 310 315 320
Asp Ala Ser His Leu Val Asn Val Ser Ile Pro Met Gly Leu Thr Phe
325 330 335
Lys His Glu Ser Ala Lys Pro Pro Ser Ala Leu Leu Leu Thr Leu Gly
340 345 350
Tyr Ala Val Asp Ala Tyr Arg Asp His Pro His Cys Leu Thr Ser Leu
355 360 365
Thr Asn Gly Thr Ser Trp Ser Thr Phe Ala Thr Asn Leu Ser Arg Gln
370 375 380
Ala Phe Phe Ala Glu Ala Ser Gly His Leu Lys Leu Leu His Gly Leu
385 390 395 400
Asp Cys Phe Ala Ser Gly Ser Cys Glu Leu Arg Ser Ser Ser Arg Ser
405 410 415
Tyr Asn Ala Asn Cys Gly Thr Arg Tyr Ser Phe Xaa Xaa Xaa Xaa Xaa
420 425 430
Xaa Xaa Xaa Phe Xaa Xaa Xaa
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<213> C. Trachomatis D serovar

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<213> C. Trachomatis D serovar

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<211> 615
<212> DNA
<213> C. Trachomatis D serovar

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<213> C. Trachomatis D serovar

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<213> C. Trachomatis D serovar

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<212> DNA
<213> C. Trachomatis D serovar

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<213> C. Trachomatis D serovar

<400> 536

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<212> DNA
<213> C. Trachomatis D serovar

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<211> 1278
<212> DNA
<213> C. Trachomatis D serovar

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<210> 541
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<212> DNA
<213> C. Trachomatis D serovar

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<210> 542
<211> 1263
<212> DNA
<213> C. Trachomatis D serovar

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<210> 544
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<212> DNA
<213> C. Trachomatis D serovar

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<210> 545
<211> 1149
<212> DNA
<213> C. Trachomatis D serovar

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<212> DNA
<213> C. Trachomatis D serovar

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<213> C. Trachomatis D serovar

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<210> 548
<211> 1038
<212> DNA
<213> C. Trachomatis D serovar

<400> 548

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<210> 549
<211> 978
<212> DNA
<213> C. Trachomatis D serovar

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<210> 550
<211> 438
<212> DNA
<213> C. Trachomatis D serovar

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<210> 551
<211> 1581
<212> DNA

<213> C. Trachomatis D serovar

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<210> 552
<211> 1950
<212> DNA
<213> C. Trachomatis D serovar

<400> 552
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<210> 553
<211> 939
<212> DNA
<213> C. Trachomatis D serovar

<400> 553

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<210> 554
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<212> DNA
<213> C. Trachomatis D serovar

<400> 554

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<212> DNA
<213> C. Trachomatis D serovar

<400> 555

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gacgaaaatg ctaaaactaa agaatcgcag cttctagact cagaaaatga ttcaaattct    1260
gaatttcagg agattataaa taaaggacta gaagctgcca ataaacgacg agctgacgct    1320
aagtcaaaat tctatacgga agacgaaacc tctgacaaaa tattctctat atggaaaccc    1380
acaaagaact tggcattaga agatttgtgg agagtgcatg aagcttgcaa tgaagagcaa    1440
caagctctcc tcttagaaga ttatatgagt tataaaacct cagaatgtca agctgcactc    1500
caaaaagtga gtcaagaact gaaggcggca caaaaatcat tcgcagtcct agaaaagcat    1560
gctctagaca gatcttatga atccagtgta gccacgatgg atttagctag agcgaatcaa    1620
gaaacacacc ggcttctgaa catcctctct gaattacaac aactagcaca atacctgtta    1680
gataatcac                                                            1689
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<210> 556
<211> 5253
<212> DNA
<213> C. Trachomatis D serovar

<400> 556

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tttactgaaa cagttggaga agctggggca gaatatatcg tctctggtaa cgcatctttc     180
acaaaattta ccaacattcc tactaccgat acaacaactc ccacgaactc aaactcctct     240
agctctaacg gagagactgc ttccgtttct gaggatagtg actctacaac aacgactcct     300
gatcctaaag gtggcggcgc cttttataac gcgcactccg gagttttatc ctttatgaca     360
cgatcaggaa cagaaggttc cttaactctg tctgagataa aaataactgg tgaaggcggt     420
gctatcttct ctcaaggaga gctgctattt acagatctga caggtctaac catccaaaat     480
aacttatccc agctatccgg aggagcgatt tttggagaat ctacaatctc cctatcaggg     540
attactaaag cgactttctc ctccaactct gcagaagttc ctgctcctgt taagaaacct     600
acagaaccta aagctcaaac agcaagcgaa acgtcgggtt ctagtagttc tagcggaaat     660
gattcggtgt cttcccccag ttccagtaga gctgaacccg cagcagctaa tcttcaaagt     720
cactttattt gtgctacagc tactcctgct gctcaaaccg atacagaaac atcaactccc     780
tctcataagc caggatctgg gggagctatc tatgctaaag gcgaccttac tatcgcagac     840
tctcaagagg tactattctc aataaataaa gctactaaag atggaggagc gatctttgct     900
gagaaagatg tttctttcga gaatattaca tcattaaaag tacaaactaa cggtgctgaa     960
gaaaagggag gagctatcta tgctaaaggt gacctctcaa ttcaatcttc taaacagagt    1020
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aacttccaag atcttgaaga aattcgcatt aagtacaata aagctggaac gttcgaaaca    1140
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gcgacagatg ttggaggtgg tgcttacgta aaaggaaccc ttacttgtga aaactctcac    1440
cgtctacaat ttttgaaaaa ctcttccgat aaacaaggtg gaggaatcta cggagaagac    1500
aacatcaccc tatctaattt gacagggaag actctattcc aagagaatac tgccaaagaa    1560
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gaaatctctc agacttacac ctctgatgtg gaaacaattc caggaatcac gcctgtacat    1740
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cccgcagcag cttctgccgc gacgtctact cccgagtctg ccccagtggt ctcaactgct    1980
ctaagcacac cttcatcttc taccgtctct tcattaacct tactagcagc ctcttcacaa    2040
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acagagatag gtggaggtat ctgctgtaaa gaatctttag aactagatgc cctagtctcc    2280
ttatctgtaa cagagaacct tgttgggaaa gaaggtggag gcttacatgc taaaactgta    2340
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aatatttcta atctgaaatc aggcttctct ttctcgaaca acaaagcaaa ctcctcatcc 2400
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gcagcagccg taccatcatc tccagcaaca ccaacttatt caggtgtagt aggaggagct 2520
atctatggag aaaaggttac attctctcaa tgtagcggga cttgtcagtt ctctgggaac 2580
caagctatcg ataacaatcc ctcccaatca tcgttgaacg tacaaggagg agccatctat 2640
gccaaaacct ctttgtctat tggatcttcc gatgctggaa cctcctatat tttctcgggg 2700
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tcccctactg ttacattgaa ttgtcctgcg acattctcta acaatacagc ctctatggct 2820
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gatgctacga ttgagtcttt aggatctgtt ctttttacag gaaataacgt tacagctaca 3240
caagctagtt ctgcaacatc tggacaaaat acaaatactg ccaactatgg ggcagccatc 3300
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actttatctg gggatctttt ccctcagaaa gggtacatgg gaacctggac attagattct 4200
aatccacaaa cagggaaact tcaagccaga tggacattcg atacctatcg tcgctgggta 4260
tacataccta gggataatca tttttatgcg aactctatct taggctccca aaactcaatg 4320
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caaatgacta gctgcggtgc tcgcatgatc ttc 5253

<210> 557
<211> 792
<212> DNA
<213> C. Trachomatis D serovar

<400> 557
atgggaaatt ctggttttta tttgtataac actgaaaact gcgtctttgc tgataatatc 60
aaagttgggc aaatgacaga gccgctcaag gaccagcaaa taatccttgg gacaaaatca 120
acacctgtcg cagccaaaat gacagcttct gatggaatat ctttaacagt ctccaataat 180

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tcatcaacca atgcttctat tacaattggt ttggatgcgg aaaaagctta ccagcttatt      240
ctagaaaagt tgggaaatca aattcttgat ggaattgctg atactattgt tgatagtaca      300
gtccaagata ttttagacaa aatcacaaca gacccttctc taggtttgtt gaaagctttt      360
aacaactttc caatcactaa taaaattcaa tgcaacgggt tattcactcc cagtaacatt      420
gaaactttat taggaggaac tgaaatagga aaattcacag tcacacccaa aagctctggg      480
agcatgttct tagtctcagc agatattatt gcatcaagaa tggaaggcgg cgttgttcta      540
gctttggtac gagaaggtga ttctaagccc tgcgcgatta gttatggata ctcatcaggc      600
gttcctaatt tatgtagtct aagaaccagc attactaata caggattgac accaacaacg      660
tattcattac gtgtaggcgg tttagaaagc ggtgtggtat gggttaatgc cctttctaat      720
ggcaatgata ttttaggaat aacaaatact tctaatgtat ctttttgga agtaataccT      780
caaacaaacg ct                                                          792
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<210> 558
<211> 306
<212> DNA
<213> C. Trachomatis D serovar

<400> 558
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gatttccccg aattagacct aaaaatacga gtaaacaagg aaaaagtaac tttcttaaat      120
tctcccttag aactctacca taaaagtgtc tcactaattc taggactgct tcaacaaata      180
gaaaactctt taggattatt cccagactct cctgttcttg aaaaattaga ggataacagt      240
ttaaagctaa aaaaggcttt gattatgctt atcttgtcta gaaaagacat gttttccaag      300
gctgaa                                                                 306

<210> 559
<211> 729
<212> DNA
<213> C. Trachomatis D serovar

<400> 559
gtgggatgca acttggccca atttttaggg aaaaaagtgt tacttgctga cctagacccg       60
caatccaatt tatcttctgg attgggggct agtgtcagaa ataaccaaaa aggcttgcac      120
gacatagtat acaaatcaaa cgatttaaaa tcaatcattt gcgaaacaaa aaaagatagt      180
gtggacctaa ttcctgcatc atttttatcc gaacagttta gagaattgga tattcataga      240
ggacctagta acaacttaaa gttatttctg aatgagtact gcgctccttt ttatgacatc      300
tgcataatag acactccacc tagcctagga gggttaacga aagaagcttt tgttgcagga      360
gacaaattaa ttgcttgttt aactccagaa cctttttcta ttctagggtt acaaaagata      420
cgtgaattct taagttcggt cggaaaacct gaagaagaac acattcttgg aatagctttg      480
tctttttggg atgatcgtaa ctcgactaac caaatgtata tagacattat cgagtctatt      540
tacaaaaaca agctttttc aacaaaaatt cgtcgagata tttctctcag ccgttctctt      600
cttaaagaag attctgtagc taatgtctat ccaaattcta gggccgcaga agatattctg      660
aagttaacgc atgaaatagc aaatattttg catatcgaat atgaacgaga ttactctcag      720
aggacaacg                                                              729

<210> 560
<211> 289
<212> PRT
<213> C. Trachomatis D serovar

<400> 560
Met Thr His Gln His Lys Lys Ile Ser Glu Glu Thr Ile Ala Cys Asp
 1               5                  10                  15
Met Leu Glu Arg Tyr Thr Gly Ser Thr Val Gln Glu Phe Gln Pro Tyr
            20                  25                  30
Leu Leu Leu Thr Asn Phe Ala Tyr Tyr Val Asp Val Phe Ala Glu Ile
        35                  40                  45
Tyr Gln Val Pro Val Ser Arg Gly Ser Met Phe Ser Ala Ala His Ala
    50                  55                  60
Pro Gln Ile His Thr Ser Ile Ile Asp Phe Lys Leu Gly Ser Pro Gly
65                  70                  75                  80
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Ala Ala Leu Thr Val Asp Leu Cys Ser Phe Leu Pro Asn Ala Thr Ala
                85                  90                  95
Ala Ile Met Leu Gly Met Cys Gly Gly Leu Arg Ser His Tyr Gln Ile
            100                 105                 110
Gly Asp Tyr Phe Val Pro Val Ala Ser Ile Arg Lys Asp Gly Thr Ser
        115                 120                 125
Asp Ala Tyr Phe Pro Pro Glu Val Pro Ala Leu Ala Asn Phe Val Val
    130                 135                 140
Gln Lys Met Ile Thr Asn Ile Leu Glu Ala Lys Asn Leu Pro Tyr His
145                 150                 155                 160
Ile Gly Ile Thr His Thr Thr Asn Ile Arg Phe Trp Glu Phe Asn Lys
                165                 170                 175
Glu Phe Arg Arg Lys Leu Tyr Glu Asn Lys Ala Gln Thr Val Glu Met
            180                 185                 190
Glu Cys Ala Thr Leu Phe Ala Ala Gly Tyr Arg Arg Asn Leu Pro Leu
        195                 200                 205
Gly Ala Leu Leu Leu Ile Ser Asp Leu Pro Leu Arg Lys Asp Gly Ile
    210                 215                 220
Lys Thr Lys Glu Ser Ser Ser Ala Val Leu Asn Ser His Thr Lys Glu
225                 230                 235                 240
His Ile Leu Thr Gly Val Glu Val Phe Ala Ser Leu Gln Glu Lys Ser
                245                 250                 255
Gly Pro Gly Ile Lys Lys Thr Lys Gly Leu Pro His Met Glu Phe Gly
            260                 265                 270
Gln Ala Asp Asp Ser Leu Ser Glu Gln Thr Glu Val Ser Gly Gly Asp
        275                 280                 285
Phe


<210> 561
<211> 394
<212> PRT
<213> C. Trachomatis D serovar

<400> 561
Met Ser Lys Glu Thr Phe Gln Arg Asn Lys Pro His Ile Asn Ile Gly
 1               5                  10                  15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
            20                  25                  30
Thr Arg Ala Leu Ser Gly Asp Gly Leu Ala Asp Phe Arg Asp Tyr Ser
        35                  40                  45
Ser Ile Asp Asn Thr Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
    50                  55                  60
Ala Ser His Val Glu Tyr Glu Thr Ala Asn Arg His Tyr Ala His Val
65                  70                  75                  80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
                85                  90                  95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Thr Asp Gly Ala
            100                 105                 110
Met Pro Gln Thr Lys Glu His Ile Leu Leu Ala Arg Gln Val Gly Val
        115                 120                 125
Pro Tyr Ile Val Val Phe Leu Asn Lys Ile Asp Met Ile Ser Glu Glu
    130                 135                 140
Asp Ala Glu Leu Val Asp Leu Val Glu Met Glu Leu Val Glu Leu Leu
145                 150                 155                 160
Glu Glu Lys Gly Tyr Lys Gly Cys Pro Ile Ile Arg Gly Ser Ala Leu
                165                 170                 175
Lys Ala Leu Glu Gly Asp Ala Ala Tyr Ile Glu Lys Val Arg Glu Leu
            180                 185                 190
Met Gln Ala Val Asp Asp Asn Ile Pro Thr Pro Glu Arg Glu Ile Asp
        195                 200                 205
```

Lys Pro Phe Leu Met Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
210 215 220
Gly Thr Val Val Thr Gly Arg Ile Glu Arg Gly Ile Val Lys Val Ser
225 230 235 240
Asp Lys Val Gln Leu Val Gly Leu Arg Asp Thr Lys Glu Thr Ile Val
245 250 255
Thr Gly Val Glu Met Phe Arg Lys Glu Leu Pro Glu Gly Arg Ala Gly
260 265 270
Glu Asn Val Gly Leu Leu Leu Arg Gly Ile Gly Lys Asn Asp Val Glu
275 280 285
Arg Gly Met Val Val Cys Leu Pro Asn Ser Val Lys Pro His Thr Gln
290 295 300
Phe Lys Cys Ala Val Tyr Val Leu Gln Lys Glu Glu Gly Gly Arg His
305 310 315 320
Lys Pro Phe Phe Thr Gly Tyr Arg Pro Gln Phe Phe Phe Arg Thr Thr
325 330 335
Asp Val Thr Gly Val Val Thr Leu Pro Glu Gly Ile Glu Met Val Met
340 345 350
Pro Gly Asp Asn Val Glu Phe Glu Val Gln Leu Ile Ser Pro Val Ala
355 360 365
Leu Glu Glu Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile
370 375 380
Gly Ala Gly Thr Ile Ser Lys Ile Ile Ala
385 390

<210> 562
<211> 550
<212> PRT
<213> C. Trachomatis D serovar

<400> 562
Met Glu Ser Ser Arg Ile Leu Ile Thr Ser Ala Leu Pro Tyr Ala Asn
1 5 10 15
Gly Pro Leu His Phe Gly His Ile Thr Gly Ala Tyr Leu Pro Ala Asp
20 25 30
Val Tyr Ala Arg Phe Gln Arg Leu Gln Gly Lys Glu Val Leu Tyr Ile
35 40 45
Cys Gly Ser Asp Glu Tyr Gly Ile Ala Ile Thr Leu Asn Ala Glu Leu
50 55 60
Ala Gly Met Gly Tyr Gln Glu Tyr Val Asp Met Tyr His Lys Leu His
65 70 75 80
Lys Asp Thr Phe Lys Lys Leu Gly Ile Ser Val Asp Phe Phe Ser Arg
85 90 95
Thr Thr Asn Thr Tyr His Pro Ala Ile Val Gln Asp Phe Tyr Arg Asn
100 105 110
Leu Gln Glu Arg Gly Leu Val Glu Asn Gln Val Thr Glu Gln Leu Tyr
115 120 125
Ser Glu Glu Glu Gly Lys Phe Leu Ala Asp Arg Tyr Val Val Gly Thr
130 135 140
Cys Pro Lys Cys Gly Phe Asp Arg Ala Arg Gly Asp Glu Cys Gln Gln
145 150 155 160
Cys Gly Ala Asp Tyr Glu Ala Arg Asp Leu Lys Glu Pro Arg Ser Lys
165 170 175
Leu Thr Gly Ala Ala Leu Ser Leu Arg Asp Thr Glu His Ala Tyr Leu
180 185 190
His Leu Glu Arg Met Lys Glu Asp Leu Leu Ala Phe Val Gln Gly Ile
195 200 205
Tyr Leu Arg Pro His Met Arg Asn Phe Val Thr Asp Tyr Ile Glu His
210 215 220
Leu Arg Pro Arg Ala Val Thr Arg Asp Leu Ser Trp Gly Ile Pro Val
225 230 235 240

Pro Asp Leu Glu Asn Lys Val Phe Tyr Val Trp Phe Asp Ala Pro Ile
245 250 255
Gly Tyr Ile Ser Gly Thr Met Asp Trp Ala Ala Ser Ile Gly Asp Pro
260 265 270
Glu Ala Trp Lys Lys Phe Trp Leu Asp Asp Thr Val Thr Tyr Ala Gln
275 280 285
Phe Ile Gly Lys Asp Asn Thr Ser Phe His Ala Ala Ile Phe Pro Ala
290 295 300
Met Glu Ile Gly Gln Ser Leu Pro Tyr Lys Lys Val Asp Ala Leu Val
305 310 315 320
Thr Ser Glu Phe Leu Leu Leu Glu Gly Phe Gln Phe Ser Lys Ser Asp
325 330 335
Gly Asn Phe Ile Asp Met Asp Ala Phe Leu Glu Thr Tyr Ser Leu Asp
340 345 350
Lys Leu Arg Tyr Val Leu Ala Ala Ile Ala Pro Glu Thr Ser Asp Ser
355 360 365
Glu Phe Ser Phe Gln Glu Phe Lys Thr Arg Cys Asn Ser Glu Leu Val
370 375 380
Gly Lys Tyr Gly Asn Phe Val Asn Arg Val Leu Ala Phe Ala Val Lys
385 390 395 400
Asn Gly Cys Thr Glu Leu Ser Ser Pro Gln Leu Glu Gln Lys Asp Leu
405 410 415
Asp Phe Ile Ser Lys Ser Gln Lys Leu Ala Lys Asp Ala Ala Glu His
420 425 430
Tyr Ala Gln Tyr Ser Leu Arg Lys Ala Cys Ser Thr Ile Met Glu Leu
435 440 445
Ala Ala Leu Gly Asn Gly Tyr Phe Asn Asp Glu Ala Pro Trp Lys Leu
450 455 460
Ala Lys Glu Gly Asn Trp Asn Arg Val Arg Ala Ile Leu Phe Cys Ala
465 470 475 480
Cys Tyr Cys Gln Lys Leu Leu Ala Leu Ile Ser Tyr Pro Ile Met Pro
485 490 495
Glu Thr Ala Leu Lys Ile Leu Glu Met Ile Ala Pro His Ser Leu Asp
500 505 510
Leu Gly Ser Gln Asp Pro Asp Arg Leu Gln Ser Leu Trp Thr Asp Ser
515 520 525
Phe Phe Asp Tyr Ser Glu Glu Lys Phe Ser Leu Lys Glu Pro Glu Leu
530 535 540
Leu Phe Thr Met Val Glu
545 550

<210> 563
<211> 100
<212> PRT
<213> C. Trachomatis D serovar

<400> 563
Met Ala Arg Lys Asp Arg Leu Thr Asn Glu Arg Leu Asn Lys Leu Phe
1 5 10 15
Asp Ser Pro Phe Ser Leu Val Asn Tyr Val Ile Lys Gln Ala Lys Asn
20 25 30
Lys Ile Ala Arg Gly Asp Val Arg Ser Ser Asn Val Ala Ile Glu Ala
35 40 45
Leu Asn Phe Leu Asp Leu Tyr Gly Ile Gln Ser Glu Tyr Ala Glu Arg
50 55 60
Asp Asp Arg Glu Arg His Leu Ser Ala Thr Gly Glu Arg Arg Arg Glu
65 70 75 80
Gln Gly Phe Gly Thr Ser Arg Arg Lys Asp Pro Ser Leu Tyr Asn Trp
85 90 95
Ser Asp Val Lys
100

<210> 564
<211> 205
<212> PRT
<213> C. Trachomatis D serovar

<400> 564
Met Ser Val Lys Val Ile Ser Pro Phe Ser Gln Asp Gly Val Gln Cys
1 5 10 15
Phe Pro Lys Leu Phe Ile Ile Ser Ala Pro Ala Gly Ala Gly Lys Thr
20 25 30
Thr Leu Thr His Met Leu Gln Arg Glu Phe Pro Asp Ala Phe Glu Lys
35 40 45
Thr Val Ser Ser Thr Thr Arg Ser Ala Arg Pro Gly Glu Val His Gly
50 55 60
Val Asp Tyr Leu Phe Val Ser Glu Asp Asp Phe Lys Gln Ser Leu Asp
65 70 75 80
Arg Glu Asp Phe Leu Glu Trp Val Phe Leu Phe Gly Thr Tyr Tyr Gly
85 90 95
Thr Ser Lys Ala Glu Ile Ser Arg Val Leu Gln Lys Gly Lys His Cys
100 105 110
Ile Ala Val Ile Asp Val Gln Gly Ala Leu Ala Leu Lys Lys Gln Met
115 120 125
Pro Ala Val Thr Ile Phe Ile Gln Ala Pro Ser Gln Glu Glu Leu Glu
130 135 140
Arg Arg Leu Asn Ala Arg Asp Ser Glu Lys Asp Phe Gln Lys Lys Glu
145 150 155 160
Arg Leu Glu His Ser Ala Val Glu Ile Ala Ala Ala Ser Glu Phe Asp
165 170 175
Tyr Val Val Val Asn Asp Asp Leu Ile Thr Ala Tyr Gln Val Leu Arg
180 185 190
Ser Ile Phe Ile Ala Glu Glu His Arg Met Ser His Gly
195 200 205

<210> 565
<211> 602
<212> PRT
<213> C. Trachomatis D serovar

<400> 565
Met Lys Pro Tyr Lys Ile Glu Asn Ile Arg Asn Phe Ser Ile Ile Ala
1 5 10 15
His Ile Asp His Gly Lys Ser Thr Ile Ala Asp Arg Leu Leu Glu Ser
20 25 30
Thr Ser Thr Ile Glu Gln Arg Glu Met Arg Glu Gln Leu Leu Asp Ser
35 40 45
Met Asp Leu Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala His Pro Val
50 55 60
Thr Met Thr Tyr Glu Tyr Glu Gly Glu Thr Tyr Glu Leu Asn Leu Ile
65 70 75 80
Asp Thr Pro Gly His Val Asp Phe Ser Tyr Glu Val Ser Arg Ser Leu
85 90 95
Ala Ala Cys Glu Gly Ala Leu Leu Ile Val Asp Ala Ala Gln Gly Val
100 105 110
Gln Ala Gln Ser Leu Ala Asn Val Tyr Leu Ala Leu Glu Arg Asp Leu
115 120 125
Glu Ile Ile Pro Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Gln Pro
130 135 140
Glu Ala Ile Lys Lys Gln Ile Glu Glu Phe Ile Gly Leu Asp Thr Ser
145 150 155 160
Asn Thr Ile Ala Cys Ser Ala Lys Thr Gly Gln Gly Ile Pro Glu Ile

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                165                 170                 175
Leu Glu Ser Ile Ile Arg Leu Val Pro Pro Pro Lys Pro Pro Gln Glu
            180                 185                 190
Thr Glu Leu Lys Ala Leu Ile Phe Asp Ser His Tyr Asp Pro Tyr Val
        195                 200                 205
Gly Ile Met Val Tyr Val Arg Val Ile Ser Gly Glu Ile Lys Lys Gly
    210                 215                 220
Asp Arg Ile Thr Phe Met Ala Thr Lys Gly Ser Ser Phe Glu Val Leu
225                 230                 235                 240
Gly Ile Gly Ala Phe Leu Pro Glu Ala Thr Leu Met Glu Gly Ser Leu
                245                 250                 255
Arg Ala Gly Gln Val Gly Tyr Phe Ile Ala Asn Leu Lys Lys Val Lys
            260                 265                 270
Asp Val Lys Ile Gly Asp Thr Val Thr Thr Val Lys His Pro Ala Lys
        275                 280                 285
Glu Pro Leu Glu Gly Phe Lys Glu Ile Lys Pro Val Val Phe Ala Gly
    290                 295                 300
Ile Tyr Pro Ile Asp Ser Ser Asp Phe Asp Thr Leu Lys Asp Ala Leu
305                 310                 315                 320
Gly Arg Leu Gln Leu Asn Asp Ser Ala Leu Thr Ile Glu Gln Glu Asn
                325                 330                 335
Ser His Ser Leu Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu
            340                 345                 350
His Leu Glu Ile Ile Phe Glu Arg Ile Ser Arg Glu Phe Asp Leu Asp
        355                 360                 365
Ile Ile Ala Thr Ala Pro Ser Val Ile Tyr Lys Val Val Leu Lys Asn
    370                 375                 380
Gly Lys Thr Leu Phe Ile Asp Asn Pro Thr Ala Tyr Pro Asp Pro Ala
385                 390                 395                 400
Leu Ile Glu His Met Glu Glu Pro Trp Val His Val Asn Ile Ile Thr
                405                 410                 415
Pro Gln Glu Tyr Leu Ser Asn Ile Met Ser Leu Cys Met Asp Lys Arg
            420                 425                 430
Gly Ile Cys Leu Lys Thr Asp Met Leu Asp Gln His Arg Leu Val Leu
        435                 440                 445
Ser Tyr Glu Leu Pro Leu Asn Glu Ile Val Ser Asp Phe Asn Asp Lys
    450                 455                 460
Leu Lys Ser Val Thr Lys Gly Tyr Gly Ser Phe Asp Tyr Arg Leu Gly
465                 470                 475                 480
Asp Tyr Lys Lys Gly Ala Ile Ile Lys Leu Glu Ile Leu Ile Asn Asp
                485                 490                 495
Glu Ala Val Asp Ala Phe Ser Cys Leu Val His Arg Asp Lys Ala Glu
            500                 505                 510
Ser Lys Gly Arg Ser Ile Cys Glu Lys Leu Val Asp Val Ile Pro Pro
        515                 520                 525
Gln Leu Phe Lys Ile Pro Ile Gln Ala Ala Ile Asn Lys Lys Ile Ile
    530                 535                 540
Ala Arg Glu Thr Ile Arg Ala Leu Ala Lys Asn Val Thr Ala Lys Cys
545                 550                 555                 560
Tyr Gly Gly Asp Ile Thr Arg Lys Arg Lys Leu Trp Asp Lys Gln Lys
                565                 570                 575
Lys Gly Lys Lys Arg Met Lys Glu Phe Gly Lys Val Ser Ile Pro Asn
            580                 585                 590
Thr Ala Phe Val Glu Val Leu Lys Met Glu
        595                 600
```

<210> 566
<211> 324
<212> PRT
<213> C. Trachomatis D serovar

<400> 566
Met Glu Leu Leu Pro His Glu Lys Gln Val Val Glu Tyr Glu Lys Thr
1   5   10   15
Ile Ala Glu Phe Lys Glu Lys Asn Lys Glu Asn Ser Leu Leu Ser Ser
            20   25   30
Ser Glu Ile Gln Lys Leu Asp Lys Arg Leu Asp Arg Leu Lys Glu Lys
        35   40   45
Ile Tyr Ser Asp Leu Thr Pro Trp Glu Arg Val Gln Ile Cys Arg His
    50   55   60
Pro Ser Arg Pro Arg Thr Val Asn Tyr Ile Glu Gly Met Cys Glu Glu
65   70   75   80
Phe Val Glu Leu Cys Gly Asp Arg Thr Phe Arg Asp Asp Pro Ala Val
                85   90   95
Val Gly Gly Phe Ala Lys Ile Gln Gly Gln Arg Phe Met Leu Ile Gly
            100   105   110
Gln Glu Lys Gly Cys Asp Thr Lys Ser Arg Met His Arg Asn Phe Gly
        115   120   125
Met Leu Cys Pro Glu Gly Phe Arg Lys Ala Leu Arg Leu Ala Lys Met
    130   135   140
Ala Glu Lys Phe Gly Leu Pro Ile Ile Phe Leu Val Asp Thr Pro Gly
145   150   155   160
Ala Phe Pro Gly Leu Thr Ala Glu Glu Arg Gly Gln Gly Trp Ala Ile
                165   170   175
Ala Thr Asn Leu Phe Glu Leu Ala Arg Leu Ala Thr Pro Ile Ile Val
            180   185   190
Ile Val Ile Gly Glu Gly Cys Ser Gly Gly Ala Leu Gly Met Ala Ile
        195   200   205
Gly Asp Val Val Ala Met Leu Glu His Ser Tyr Tyr Ser Val Ile Ser
    210   215   220
Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Asp Pro Lys Lys Asn Ser
225   230   235   240
Asp Ala Ala Ala Met Leu Lys Met His Gly Glu Asp Leu Lys Gly Phe
                245   250   255
Ala Ile Val Asp Ala Val Ile Lys Glu Pro Ile Gly Gly Ala His His
            260   265   270
Asn Pro Ala Ala Thr Tyr Arg Ser Val Gln Glu Tyr Val Leu Gln Glu
        275   280   285
Trp Leu Lys Leu Lys Asp Leu Pro Val Glu Glu Leu Leu Glu Lys Arg
    290   295   300
Tyr Gln Lys Phe Arg Thr Ile Gly Leu Tyr Glu Thr Ser Ser Glu Ser
305   310   315   320
Asp Ser Glu Ala

<210> 567
<211> 646
<212> PRT
<213> C. Trachomatis D serovar

<400> 567
Met Lys Leu Leu Leu Lys Ala Ile Leu Arg His Lys Lys His Leu Val
1   5   10   15
Leu Phe Gly Phe Ser Leu Leu Ser Ile Leu Gly Leu Thr Ile Thr Ser
            20   25   30
Gln Ala Glu Ile Phe Ser Leu Gly Leu Ile Ala Lys Thr Gly Pro Asp
        35   40   45
Thr Phe Leu Leu Phe Gly Lys Gln Glu Gly Ala Ser Leu Val Lys Arg
    50   55   60
Lys Glu Leu Ser Lys Asp Gln Leu Leu Glu Gln Trp Asp Asn Ile Val
65   70   75   80
Gly Glu Gly Asp Thr Leu Ser Leu Pro Gln Ala Asn Ala Tyr Ile Ala

```
                85                  90                  95
Lys His Ser Gly Gly Ser Gln Ser Ile Thr Lys Arg Leu Ser Ala Tyr
            100                 105                 110
Leu Ser Gly Cys Phe Asp Phe Ser Arg Leu Gln Cys Leu Ala Leu Phe
        115                 120                 125
Leu Val Val Val Ala Ile Leu Lys Ser Thr Thr Leu Phe Phe Gln Arg
    130                 135                 140
Phe Leu Ala Gln Leu Ile Ala Ile Arg Val Ser Cys Ser Leu Arg Lys
145                 150                 155                 160
Asp Tyr Phe Leu Ala Leu Gln Thr Leu Pro Met Thr Phe Phe His Ala
                165                 170                 175
His Asp Met Gly Asn Leu Ser Ser Arg Val Ile Ala Asp Ser Ser Met
            180                 185                 190
Ile Ala Leu Ala Ile Asn Ala Leu Met Val Asn Tyr Ile Gln Ala Pro
        195                 200                 205
Ile Thr Met Thr Leu Ala Leu Val Val Cys Leu Ser Ile Ser Trp Lys
    210                 215                 220
Phe Cys Ala Cys Val Cys Leu Ala Phe Pro Ile Phe Ile Leu Pro Ile
225                 230                 235                 240
Val Ile Ile Ala Lys Lys Val Lys Ala Leu Ala Lys Arg Ile Gln Lys
                245                 250                 255
Ser Gln Asp His Ser Ala Ala Ala Leu Leu Asp Phe Leu Leu Gly Ile
            260                 265                 270
Leu Thr Val Lys Val Phe Arg Thr Glu Gln Phe Ser Phe Ser Lys Tyr
        275                 280                 285
Cys Gln Lys Asn Asp Glu Ile Ala Arg Leu Glu Glu Arg Ser Ala Ala
    290                 295                 300
Tyr Ser Leu Ile Pro Arg Pro Leu Leu His Thr Ile Ala Ser Leu Phe
305                 310                 315                 320
Phe Ala Leu Val Ile Met Ile Gly Leu Tyr His Phe His Ile Pro Pro
                325                 330                 335
Glu Glu Leu Val Val Phe Cys Gly Leu Leu Tyr Leu Ile Tyr Asp Pro
            340                 345                 350
Ile Lys Lys Phe Ala Asp Glu Asn Ala Asn Ile Met Trp Gly Cys Ala
        355                 360                 365
Ala Ala Glu Arg Phe Tyr Glu Val Leu Asp Leu Ala Lys Gln Gln Ser
    370                 375                 380
Asn Val Ser Glu Lys Leu Asn Glu Phe Gln Gly Leu Gln His Ser Ile
385                 390                 395                 400
Gln Phe Cys Asn Val Ser Phe Gly Tyr Val Glu Asp Ser Pro Val Leu
                405                 410                 415
Ser Asp Phe Asn Leu Val Leu Lys Lys Gly Glu Ala Ile Gly Ile Val
            420                 425                 430
Gly Pro Thr Gly Ser Gly Lys Ser Thr Ile Ala Lys Leu Leu Pro Arg
        435                 440                 445
Leu Tyr Glu Val Ser His Gly Glu Leu Leu Ile Asp Ser Leu Pro Ile
    450                 455                 460
Arg Ser Tyr Cys Lys Asn Ser Leu Arg Lys His Ile Gly Cys Val Leu
465                 470                 475                 480
Gln His Pro Phe Leu Phe Tyr Asp Thr Val Trp Asn Asn Leu Thr Cys
                485                 490                 495
Gly Arg Thr Phe Ser Glu Glu Glu Val Phe His Ala Leu Lys Gln Ala
            500                 505                 510
His Ala Tyr Glu Phe Val Ser Lys Met Pro Gln Gly Val His Ser Leu
        515                 520                 525
Leu Glu Glu Ser Ser Lys Asn Leu Ser Gly Gly Gln Gln Gln Arg Leu
    530                 535                 540
Thr Ile Ala Arg Ala Leu Leu His Asn Thr Ser Ile Leu Leu Leu Asp
545                 550                 555                 560
Glu Ala Thr Ser Ala Leu Asp Ala Ile Ser Glu Asn Tyr Val Lys Glu
                565                 570                 575
```

```
Ile Val Gly Gln Leu Lys Gly Arg Cys Thr Gln Ile Ile Ile Ala His
            580                 585                 590
Lys Leu Ser Thr Leu Glu Tyr Val Asp Arg Ile Val Tyr Leu Glu Gln
        595                 600                 605
Gly Lys Lys Ile Ala Glu Gly Thr Lys Glu Glu Leu Leu Asp Ser Cys
    610                 615                 620
Pro Ala Phe Gln Arg Met Trp Val Leu Ser Gly Ala Lys Asp Trp Glu
625                 630                 635                 640
Leu Asn Ala Val Val Lys
                645

<210> 568
<211> 414
<212> PRT
<213> C. Trachomatis D serovar

<400> 568
Met Phe Ser Ser Ala Ile Val Ile Leu Thr Ala Ile Phe Val Leu Cys
 1               5                  10                  15
Ser Gly Phe Val Ser Leu Ser His Ile Ala Leu Phe Ser Leu Pro Ser
            20                  25                  30
Ser Leu Ile Ala His Tyr Ser His Ser Lys Asn Arg Gln Leu Arg Gln
        35                  40                  45
Ile Ala Asn Leu Met Ala Tyr Pro Asn His Leu Leu Met Thr Leu Val
    50                  55                  60
Phe Phe Asp Ile Gly Ile Asn Ile Gly Val Gln Asn Cys Ile Ala Thr
65                  70                  75                  80
Leu Val Gly Asp Ser Ala Ser Leu Leu Leu Thr Val Gly Val Pro Leu
                85                  90                  95
Ala Leu Thr Leu Val Leu Gly Glu Ile Val Pro Lys Val Ile Ala Ile
            100                 105                 110
Pro Tyr Asn Ala Arg Ile Ala Lys Ile Val Thr Pro Ile Ile Phe Ala
        115                 120                 125
Ser Thr Lys Ser Phe Arg Pro Ile Phe Asp Trp Ala Ile Ser Gly Ile
    130                 135                 140
Asn Phe Ile Val Gln Lys Met Leu Ala Arg Gln Glu Ser Asp Phe Ile
145                 150                 155                 160
Gln Pro Gln Glu Leu Lys Glu Val Leu Arg Ser Cys Lys Asp Phe Gly
                165                 170                 175
Val Val Asn His Glu Glu Ser Arg Leu Leu Phe Gly Tyr Leu Ser Met
            180                 185                 190
Glu Glu Gly Ser Ile Lys Glu Arg Met Thr Pro Lys Gln Glu Ile Ile
        195                 200                 205
Phe Tyr Asp Val Leu Thr Pro Ile Glu Asn Leu Tyr Lys Leu Phe Ser
    210                 215                 220
Gly Pro Lys Gln Ser Tyr Ser Lys Val Leu Val Cys Lys Gly Gly Leu
225                 230                 235                 240
Gln Asn Leu Leu Gly Val Cys Ser Ala Lys Leu Leu Leu Tyr Lys
                245                 250                 255
Glu Lys Leu Gln Ser Ala Glu Glu Leu Leu Pro Leu Leu Arg Lys Pro
            260                 265                 270
His Tyr Ile Pro Glu Thr Val Ser Ala Lys Thr Ala Leu Tyr His Leu
        275                 280                 285
Ala Gly Glu Asp Cys Gly Leu Gly Ile Ile Ile Asp Glu Tyr Gly Ser
    290                 295                 300
Ile Glu Gly Leu Ile Thr Gln Asn Asp Leu Phe Lys Ile Val Ser Asp
305                 310                 315                 320
Gly Val Ala His Asn Arg Pro Ser Phe Lys Gln Phe Ala His Ser Asp
                325                 330                 335
Lys Asn Val Val Ile Ala Ala Gly Thr Tyr Glu Leu Ser Asp Phe Tyr
            340                 345                 350
```

```
Asp Leu Phe Gly Val Asp Leu Pro Thr Thr Ala Asn Cys Val Thr Ile
        355                 360                 365
Gly Gly Trp Leu Thr Glu Gln Leu Gly Glu Ile Pro Glu Thr Gly Thr
    370                 375                 380
Lys Phe Ala Trp Gly Gln Phe Val Phe Gln Ile Leu Asp Ala Ala Pro
385                 390                 395                 400
Asn Cys Val Lys Arg Val Tyr Ile Arg Lys Thr His Gly Asn
                405                 410
```

<210> 569
<211> 404
<212> PRT
<213> C. Trachomatis D serovar

<400> 569

```
Met Glu Thr Asn Ser Pro Phe Phe Trp Leu Gly Val Asn Leu Leu Cys
 1               5                  10                  15
Ile Phe Val Gln Gly Phe Phe Ser Met Met Glu Met Ala Cys Ile Ser
            20                  25                  30
Phe Asn Arg Val Arg Leu Gln Tyr Tyr Leu Thr Lys Ser Asn Lys Lys
        35                  40                  45
Ala Ser Tyr Ile Asn Phe Leu Val Arg Arg Pro Tyr Arg Leu Phe Gly
    50                  55                  60
Thr Val Met Leu Gly Val Asn Ile Ala Leu Gln Ile Gly Ser Glu Ser
65                  70                  75                  80
Ser Arg Thr Cys Tyr Lys Leu Leu Gly Ile Ser Pro Glu Tyr Ala Pro
                85                  90                  95
Ala Thr Gln Ile Ile Leu Val Val Ile Phe Ala Glu Leu Ile Pro Leu
            100                 105                 110
Ala Ile Ser Arg Lys Ile Pro Glu Lys Ile Ala Leu Lys Gly Ala Pro
        115                 120                 125
Ile Leu Tyr Phe Ala His Tyr Leu Phe Tyr Pro Leu Ile Gln Cys Val
    130                 135                 140
Gly Gly Ile Thr Asn Met Ile Tyr Phe Ile Leu Asn Ile Lys Glu Glu
145                 150                 155                 160
Thr Leu His Ser Thr Leu Ser Arg Asp Glu Leu Gln Lys Thr Leu Glu
                165                 170                 175
Thr His His Glu Glu His Asp Phe Asn Val Ile Ala Thr Asn Ile Phe
            180                 185                 190
Ser Leu Ser Ala Thr Ser Val Glu Gln Val Cys Gln Tyr Leu Asp Gln
        195                 200                 205
Ile Pro Ile Leu Ser Ala Thr Ala Ser Val Arg Asp Val Cys Gln Leu
    210                 215                 220
Val Arg Arg His Arg Leu Asp Phe Val Pro Val Tyr His Lys Val Lys
225                 230                 235                 240
Lys Asn Val Val Gly Ile Ala Phe Pro Lys Asn Leu Ile Asn Arg Asn
                245                 250                 255
Pro Ser Asp Pro Val Val Pro Tyr Leu Ser Ser Pro Trp Phe Ile Thr
            260                 265                 270
Ala Lys Ser Lys Leu Ile His Ala Ile Gln Glu Phe Arg Lys Asn Ser
        275                 280                 285
Ser Asn Val Ala Ile Val Leu Asn Asn Asn Gly Glu Pro Met Gly Val
    290                 295                 300
Leu Gly Leu His Thr Val Phe Lys Thr Leu Phe Asn Thr Arg Asn Ile
305                 310                 315                 320
Ala Gln Leu Lys Pro Lys Pro Thr Ser Leu Ile Glu Arg Thr Phe Ser
                325                 330                 335
Gly Asn Thr Pro Leu Ser Glu Ile Glu Asn Glu Leu Asp Ile Ile Phe
            340                 345                 350
Met Asp Asn Asp Cys Thr Thr Ile Glu Gln Leu Met Leu Lys Leu Leu
        355                 360                 365
```

```
Asp Thr Pro Pro Glu Val Gly Ala Ser Ile Ile Ile Asn Asp Leu Leu
    370                 375                 380
Leu Glu Val Lys Glu Ile Ser Leu Tyr Gly Ile Lys Thr Val Ala Ile
385                 390                 395                 400
Lys Asp Thr Leu


<210> 570
<211> 539
<212> PRT
<213> C. Trachomatis D serovar

<400> 570
Met Cys Cys Val Asp Gly Ser Asn Ser Ile Gln Gln Arg Met Arg Phe
 1               5                  10                  15
Cys Glu Tyr Arg Thr Ala Ala Gln Glu Ala Lys Thr Ser Leu Ser Ser
            20                  25                  30
Asp Cys Ser Leu Leu Glu Ala Arg Leu Ala Leu Arg Ala Leu Ala Lys
        35                  40                  45
His His Glu Tyr Ser Ala Trp Arg Glu Ala Phe Leu Arg Ser Gln Glu
    50                  55                  60
Arg Phe Pro Ser Leu Glu Ala Asp Arg Asp Ile His Glu Asp Leu Ala
65                  70                  75                  80
Ala Ser Leu Leu Gln Lys Asn Ile Arg His Ser Ser Leu Thr Val Arg
                85                  90                  95
Val Ile Thr Ile Leu Ala Val Gly Met Ala Arg Asp Tyr Arg Leu Val
            100                 105                 110
Pro Ile Val Leu Gln Ala Leu Ser Asp Asp Ser Asp Thr Val Arg Glu
        115                 120                 125
Ile Ala Val Gln Val Ala Val Met Tyr Gly Ser Ser Cys Leu Leu Arg
    130                 135                 140
Ala Val Gly Asp Leu Ala Lys Asn Asp Ser Ser Ile Gln Val Arg Ile
145                 150                 155                 160
Thr Ala Tyr Arg Ala Ala Ala Val Leu Glu Ile Gln Asp Leu Val Pro
                165                 170                 175
His Leu Arg Val Val Val Gln Asn Thr Gln Leu Asp Gly Thr Glu Arg
            180                 185                 190
Arg Glu Ala Trp Arg Ser Leu Cys Val Leu Thr Arg Pro His Ser Gly
        195                 200                 205
Val Leu Thr Gly Ile Asp Gln Ala Leu Met Thr Cys Glu Met Leu Lys
    210                 215                 220
Glu Tyr Pro Glu Lys Cys Thr Glu Glu Gln Ile Arg Thr Leu Leu Ala
225                 230                 235                 240
Ala Asp His Pro Glu Val Gln Val Ala Thr Leu Gln Ile Ile Leu Arg
                245                 250                 255
Gly Gly Arg Val Phe Arg Ser Ser Ser Ile Met Glu Ser Val Gln Lys
            260                 265                 270
Leu Ala Cys Asn Ser Leu Ser Ala Arg Val Gln Met Gln Ala Ala Ala
        275                 280                 285
Ile Leu Tyr Leu Glu Gly Asp Pro Phe Gly Glu Asp Lys Leu Thr Glu
    290                 295                 300
Gly Leu Ser Ala Thr Ser Ser Ile Leu Cys Glu Ala Ala Ser Glu Ala
305                 310                 315                 320
Val Cys Ser Leu Gly Ile His Gly Val His Leu Ala Gly Arg Phe Leu
                325                 330                 335
Ser Lys Val Gln Gly Met Arg Ser Arg Val Asn Leu Ala Phe Ala Leu
            340                 345                 350
Leu Val Ser Arg Glu Lys Val Glu Glu Ala Gly Asp Val Val Ala Ser
        355                 360                 365
Phe Ile His Arg Ile Glu Pro Cys Arg Ala Ile Glu Gln Phe Leu Cys
    370                 375                 380
```

```
Glu Asp Gln Lys Ile Phe Val Ala Ser Ser Pro Leu Gln Val Glu Ile
385                 390                 395                 400
Met Lys Arg Asp Leu Ala Lys Lys Ile Ile Arg Leu Leu Val Ala Ala
                405                 410                 415
Gln Tyr Ser Lys Ala Lys Met Val Val Ala Gln Tyr Leu Ala Gly Gln
            420                 425                 430
Gln Val Gly Trp Ser Phe Cys Ser Glu Val Phe Trp Glu Glu Gly Asp
        435                 440                 445
Ser Glu Asp Phe Val Glu Pro Leu Gln Glu Glu Ser Phe Ala Phe Ala
    450                 455                 460
Leu Glu Lys Ala Leu Ser Phe Leu Gln Arg Glu Gly Gly Glu Ala Gly
465                 470                 475                 480
Leu His Ala Val Ile Ser Leu Tyr Pro His Ser Arg Trp Gln Asp Lys
                485                 490                 495
Leu Thr Ile Leu Glu Ala Ile Ala Tyr Ser Glu Asn Arg Ile Ala Thr
            500                 505                 510
Cys Phe Leu Arg Glu Arg Cys Leu Gln Glu Ala Ala Ser Leu Gln Ser
        515                 520                 525
Ala Ala Ala Gly Ala Val Phe Ala Leu Phe Lys
    530                 535

<210> 571
<211> 104
<212> PRT
<213> C. Trachomatis D serovar

<400> 571
Met Gln Thr Ser Arg Ile Ser Ser Phe Phe Arg Gly Leu Val His Leu
 1               5                  10                  15
Tyr Arg Trp Ala Ile Ser Pro Phe Leu Gly Ala Pro Cys Arg Phe Phe
            20                  25                  30
Pro Thr Cys Ser Glu Tyr Ala Leu Val Ala Leu Lys Lys His Pro Leu
        35                  40                  45
Arg Lys Ser Leu Phe Leu Ile Ala Lys Arg Leu Leu Lys Cys Gly Pro
    50                  55                  60
Trp Cys Ile Gly Gly Ile Asp Leu Val Pro Arg Thr Ser Val Glu Glu
65                  70                  75                  80
Tyr Leu Ser Ser Pro Thr Pro Leu Ala Glu Ser Pro Asp Asp Arg Thr
                85                  90                  95
Val Pro His Thr Gln Glu Thr Ser
            100

<210> 572
<211> 336
<212> PRT
<213> C. Trachomatis D serovar

<400> 572
Met Gln Leu Phe Phe Gly Arg Phe Tyr Glu Val Ala Cys Ile Val Ala
 1               5                  10                  15
Ser Ile Leu Arg Glu Arg Asp Val Gly Val Phe Met Gly Ile Glu Gly
            20                  25                  30
Arg Gly Ser Gly Ala Met Gln Ser Lys Lys Thr Ile Lys Trp Leu Lys
        35                  40                  45
Gln Ala Leu Val Leu Ser Ser Ile Val Asn Ile Leu Leu Leu Leu
    50                  55                  60
Ile Tyr Ser Thr Val Phe Arg Lys Asp Ile Tyr Lys Leu Arg Val Phe
65                  70                  75                  80
Pro Gly Asn Leu Ile Ala Lys Ser Ser Arg Ile Gly Lys Ile Pro Glu
                85                  90                  95
Asp Ile Leu Glu Arg Leu Glu Asn Ala Ser Phe Ala Asp Leu Leu Ala
```

```
                100                     105                     110
Leu Leu Gln Glu Glu Arg Met Val Phe Gly His Pro Leu Lys Ser Trp
            115                     120                     125
Ala Leu Gly Val Ser Ile Gln Lys Tyr Phe Val Asp Ile Ala Pro Met
        130                     135                     140
Leu Thr His Pro Leu Thr Phe Ile Arg Leu Lys Ser Pro Glu Arg Thr
145                     150                     155                     160
Trp Leu Leu Pro Asp Ile Asn Asp Gln Glu Phe Thr Arg Ile Cys Gln
                    165                     170                     175
Tyr Leu Leu Thr Glu Arg Phe Pro Phe Ser Ser Arg Gly Phe Phe Arg
                180                     185                     190
Ile Met Val Arg Asp Cys Glu Ala Gly Met Val Asp Glu Asp Val Leu
            195                     200                     205
Tyr Arg Phe Cys His Leu Pro Glu Phe Leu Tyr Val Arg Ser Leu Leu
        210                     215                     220
Phe Gly Ala Glu Ile Glu Ala Ala Ser Val Ala Ser Leu Ala Arg Met
225                     230                     235                     240
Ile Ile Gln Gly Gly Glu Asp Leu Phe Phe Ser Leu Cys Cys Leu Glu
                    245                     250                     255
Asn Arg Gln Thr Ala Ile Ser Asp His Gln Arg Arg Cys Phe Leu Lys
                260                     265                     270
Ala Tyr Val Asp Arg Gln Glu Pro Leu Ala Ala Leu Leu Leu Leu Val
            275                     280                     285
His Asp Ala Asp Trp Val Leu His Glu Phe Ser Asp Ser Asp Leu Gln
        290                     295                     300
Ser Phe Ile Gln Leu Leu Pro Arg Glu Ala His Tyr Thr Lys Lys Phe
305                     310                     315                     320
Leu Gly Cys Val Ala Gln Ser Cys Arg Leu Gly Ile Leu Leu Glu Gly
                    325                     330                     335
```

<210> 573
<211> 426
<212> PRT
<213> C. Trachomatis D serovar

<400> 573

```
Met Tyr Val Arg Ser Ile Phe Phe Ser Ile Ile Ala Phe Leu Thr Val
 1               5                  10                  15
Gly Cys Ser Phe Ser Pro Pro Glu Ser Gly Leu Ile Ile Ala Ile His
            20                  25                  30
Asp Asp Pro Arg Ser Leu Ser Pro Glu Lys Gly Glu Asn Ala Phe His
        35                  40                  45
Phe Ser Leu Ser Lys Ala Leu Phe Ala Thr Leu Phe Arg Glu Glu Leu
    50                  55                  60
Ser Gly Leu Thr Pro Ala Leu Val Ser Ser Tyr Gln Val Ser Glu Asp
65                  70                  75                  80
Gly Arg Phe Tyr Arg Phe Cys Ile Arg Lys Asp Ala Lys Trp Ser Asp
                85                  90                  95
Gly Ser Leu Leu Leu Ala Glu Asp Val Ile Ala Ala Trp Glu His Thr
            100                 105                 110
Lys Gln Ala Gly Arg Tyr Ser Leu Leu Phe Glu Lys Leu Ser Phe Arg
        115                 120                 125
Ala Ser Ser Ser Ser Glu Ile Leu Ile Glu Leu Lys Glu Pro Glu Pro
    130                 135                 140
Gln Leu Leu Ala Ile Leu Ala Ser Pro Phe Phe Ala Val Tyr Arg Pro
145                 150                 155                 160
Glu Asn Pro Phe Leu Ser Ser Gly Pro Phe Met Pro Lys Thr Tyr Val
                165                 170                 175
Gln Gly Gln Thr Leu Val Leu Gln Lys Asn Pro Tyr Tyr Tyr Asp His
            180                 185                 190
Ala His Val Glu Leu His Ser Ile Asp Phe Arg Ile Ile Pro Asn Ile
```

```
        195                 200                 205
Tyr Thr Ala Leu His Leu Leu Arg Arg Gly Asp Val Asp Trp Val Gly
    210                 215                 220
Gln Pro Trp His Gln Gly Ile Pro Phe Glu Leu Arg Thr Thr Ser Ala
225                 230                 235                 240
Leu Tyr Thr His Tyr Ser Val Asp Gly Thr Phe Trp Leu Ile Leu Asn
                245                 250                 255
Pro Lys Asp Pro Val Leu Ser Ser Leu Ser Asn Arg Gln Arg Leu Ile
            260                 265                 270
Ala Ala Val Gln Lys Glu Lys Leu Val Lys Gln Ala Leu Gly Thr Gln
        275                 280                 285
Tyr Arg Val Ala Glu Ser Ser Pro Ser Pro Glu Gly Ile Ile Ala His
    290                 295                 300
Gln Glu Ala Ser Thr Pro Phe Pro Gly Lys Ile Thr Leu Ile Tyr Pro
305                 310                 315                 320
Asn Asn Ile Thr Arg Cys Gln Arg Leu Ala Glu Val Leu Gln Glu Gln
                325                 330                 335
Cys Arg Asp Ala Gly Ile Gln Leu Thr Leu Glu Gly Leu Glu Tyr His
            340                 345                 350
Val Phe Val Gln Lys Arg Ala Thr Gln Asp Phe Ser Val Ser Thr Ala
        355                 360                 365
Thr Ser Ile Ala Phe His Pro Leu Ala Lys Ser Lys Phe Asp Gln Thr
    370                 375                 380
Ala Leu Asp Asn Phe Thr Cys Leu Pro Leu Tyr His Ile Glu Tyr Asp
385                 390                 395                 400
Tyr Ile Leu Ser Arg Pro Leu Asp Gln Ile Val His Tyr Pro Ser Gly
                405                 410                 415
Ser Val Asp Leu Thr Tyr Ala His Phe His
            420                 425
```

<210> 574
<211> 605
<212> PRT
<213> C. Trachomatis D serovar

<400> 574

```
Met Gln Asn Ile Leu Arg Thr Ser Ser Cys Arg Tyr Met Phe Leu Leu
 1               5                  10                  15
Gly Ile Arg Ser Val Trp Asn Arg Val Ala Val Val Asn Asn Phe Arg
            20                  25                  30
Gly Ser Ser Trp Lys Ile Val Ala Ile Pro Ser Cys Ile Leu Phe Thr
        35                  40                  45
Leu Ile Phe His Leu Pro Arg Trp Leu Ile Asp Phe Gly Val Cys Thr
    50                  55                  60
Asn Leu Ala Cys Ser Leu Ser Ile Ile Phe Trp Val Phe Ser Leu Arg
65                  70                  75                  80
Ser Ser Ala Ser Ala Arg Ile Phe Pro Ser Leu Leu Leu Tyr Leu Cys
                85                  90                  95
Leu Leu Arg Leu Gly Leu Asn Leu Ala Ser Thr Arg Trp Ile Leu Ser
            100                 105                 110
Ser Gly Trp Ala Ser Pro Leu Ile Phe Ala Leu Gly Asn Phe Phe Ser
        115                 120                 125
Leu Gly Ser Ile Pro Val Ala Leu Thr Val Cys Leu Leu Leu Phe Leu
    130                 135                 140
Val Asn Phe Leu Val Ile Thr Lys Gly Ala Glu Arg Ile Ala Glu Val
145                 150                 155                 160
Arg Ala Arg Phe Ser Leu Glu Ala Leu Pro Gly Lys Gln Met Ser Leu
                165                 170                 175
Asp Ala Asp Ile Ala Ala Gly Arg Ile Gly Tyr Ser Arg Ala Ser Val
            180                 185                 190
Lys Lys Ser Ser Leu Leu Glu Glu Ser Asp Tyr Phe Ser Ala Met Glu
```

```
        195                 200                 205
Gly Val Phe Arg Phe Val Lys Gly Asp Ala Ile Met Ser Trp Val Leu
    210                 215                 220
Leu Gly Val Asn Ile Leu Ala Ala Leu Phe Leu Gly Arg Ala Thr His
225                 230                 235                 240
Val Gly Asp Leu Trp Leu Thr Val Leu Gly Asp Ala Leu Val Ser Gln
                245                 250                 255
Ile Pro Ala Leu Leu Thr Ser Cys Ala Ala Ala Thr Leu Ile Ala Lys
            260                 265                 270
Val Gly Glu Lys Glu Ser Leu Ala Gln His Leu Leu Asp Tyr Tyr Glu
        275                 280                 285
Gln Ser Arg Gln Ser Phe Leu Phe Ile Ala Leu Ile Leu Cys Gly Met
    290                 295                 300
Ala Cys Ile Pro Gly Ala Pro Lys Ala Leu Ile Leu Gly Phe Ser Val
305                 310                 315                 320
Leu Leu Phe Leu Gly Tyr Lys Asn Pro Ser Ser Gly Glu Thr Leu Leu
                325                 330                 335
Phe Gln Lys Glu Arg Val Glu Phe Val Leu Pro Asp Glu Gly Val Gly
            340                 345                 350
Asn Pro Ala Asn Leu Tyr Lys Asp Ala Arg Asn Gln Ile Tyr Gln Glu
        355                 360                 365
Leu Gly Val Val Phe Pro Glu Ala Ile Val Val Arg His Val Thr Gly
    370                 375                 380
Ser Ser Pro Arg Leu Ile Phe Ser Gly Gln Glu Val Ala Leu Arg Glu
385                 390                 395                 400
Leu Ser Cys Pro Ala Ile Leu Glu Ser Ile Arg Gln Leu Ala Pro Glu
                405                 410                 415
Thr Ile Ser Glu Arg Phe Val Thr Arg Leu Val Asp Glu Phe Arg Glu
            420                 425                 430
His Ala Phe Leu Ser Ile Glu Glu Ile Leu Pro Leu Lys Ile Ser Glu
        435                 440                 445
Asn Ser Leu Ile Phe Leu Leu Arg Ala Leu Val Arg Glu Arg Val Ser
    450                 455                 460
Leu His Leu Phe Pro Lys Ile Leu Glu Ala Ile Asp Val Tyr Gly Ser
465                 470                 475                 480
Gln Pro Lys Asn Ser Gln Glu Leu Val Glu Cys Val Arg Lys Tyr Leu
                485                 490                 495
Gly Lys Gln Ile Gly Leu Ser Leu Trp Asn Arg Gln Asp Val Leu Glu
            500                 505                 510
Val Ile Thr Ile Asp Ser Leu Val Glu Gln Phe Val Arg Asp Ser Gln
        515                 520                 525
Glu Lys Val Val Leu Asp Leu Asn Glu Lys Val Val Ala Gln Val Lys
    530                 535                 540
His Leu Leu Arg Val Gly Glu Gly Asn Phe Arg Ala Ile Val Thr Gly
545                 550                 555                 560
Ser Glu Thr Arg Lys Glu Leu Lys Arg Ile Val Asp Pro Tyr Phe Pro
                565                 570                 575
Asp Leu Leu Val Leu Ala His Ser Glu Leu Pro Glu Glu Ile Pro Ile
            580                 585                 590
Thr Leu Leu Gly Ala Val Ser Asp Glu Val Leu Leu Ser
        595                 600                 605

<210> 575
<211> 173
<212> PRT
<213> C. Trachomatis D serovar

<400> 575
Met Lys Lys Phe Leu Leu Leu Ser Leu Met Ser Leu Ser Ser Leu Pro
 1               5                  10                  15
Thr Phe Ala Ala Asn Ser Thr Gly Thr Ile Gly Ile Val Asn Leu Arg
```

```
            20                  25                  30
Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe
        35                  40                  45
Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu
    50                  55                  60
Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu
65                  70                  75                  80
Gly Leu Ser Glu Thr Ala Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp
                85                  90                  95
Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu
            100                 105                 110
Asn Gln Ser Asn Leu Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys
        115                 120                 125
Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu
    130                 135                 140
Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp
145                 150                 155                 160
Ala Val Ile Lys Val Leu Asp Asp Ser Phe Gln Asn Asn
                165                 170
```

<210> 576
<211> 354
<212> PRT
<213> C. Trachomatis D serovar

<400> 576

```
Met Ser Gln Ser Thr Tyr Ser Leu Glu Gln Leu Ala Asp Phe Leu Lys
 1               5                  10                  15
Val Glu Phe Gln Gly Asn Gly Ala Thr Leu Leu Ser Gly Val Glu Glu
            20                  25                  30
Ile Glu Glu Ala Lys Thr Ala His Ile Thr Phe Leu Asp Asn Glu Lys
        35                  40                  45
Tyr Ala Lys His Leu Lys Ser Ser Glu Ala Gly Ala Ile Ile Ile Ser
    50                  55                  60
Arg Thr Gln Phe Gln Lys Tyr Arg Asp Leu Asn Lys Asn Phe Leu Ile
65                  70                  75                  80
Thr Ser Glu Ser Pro Ser Leu Val Phe Gln Lys Cys Leu Glu Leu Phe
                85                  90                  95
Ile Thr Pro Val Asp Ser Gly Phe Pro Gly Ile His Pro Thr Ala Val
            100                 105                 110
Ile His Pro Thr Ala Ile Ile Glu Asp His Val Cys Ile Glu Pro Tyr
        115                 120                 125
Ala Val Val Cys Gln His Ala His Val Gly Ser Ala Cys His Ile Gly
    130                 135                 140
Ser Gly Ser Val Ile Gly Ala Tyr Ser Thr Val Gly Glu His Ser Tyr
145                 150                 155                 160
Ile His Pro Arg Val Val Ile Arg Glu Arg Val Ser Ile Gly Lys Arg
                165                 170                 175
Val Ile Ile Gln Pro Gly Ala Val Ile Gly Ser Cys Gly Phe Gly Tyr
            180                 185                 190
Val Thr Ser Ala Phe Gly Gln His Lys His Leu Lys His Leu Gly Lys
        195                 200                 205
Val Ile Ile Glu Asp Asp Val Glu Ile Gly Ala Asn Thr Thr Ile Asp
    210                 215                 220
Arg Gly Arg Phe Lys His Ser Val Val Arg Glu Gly Ser Lys Ile Asp
225                 230                 235                 240
Asn Leu Val Gln Ile Ala His Gln Val Glu Val Gly Gln His Ser Met
                245                 250                 255
Ile Val Ala Gln Ala Gly Ile Ala Gly Ser Thr Lys Ile Gly Asn His
            260                 265                 270
Val Ile Ile Gly Gly Gln Ala Gly Ile Thr Gly His Ile Cys Ile Ala
```

```
        275                 280                 285
Asp His Val Ile Met Met Ala Gln Thr Gly Val Thr Lys Ser Ile Thr
    290                 295                 300
Ser Pro Gly Ile Tyr Gly Gly Ala Pro Ala Arg Pro Tyr Gln Glu Ile
305                 310                 315                 320
His Arg Gln Val Ala Lys Val Arg Asn Leu Pro Arg Leu Glu Glu Arg
                325                 330                 335
Ile Ala Ala Leu Glu Lys Leu Val Gln Lys Leu Glu Ala Leu Ser Glu
            340                 345                 350
Gln His


<210> 577
<211> 421
<212> PRT
<213> C. Trachomatis D serovar

<400> 577
Met Thr Ala Ser Gly Gly Ala Gly Gly Leu Gly Ser Thr Gln Thr Val
 1               5                  10                  15
Asp Val Ala Arg Ala Gln Ala Ala Ala Ala Thr Gln Asp Ala Gln Glu
            20                  25                  30
Val Ile Gly Ser Gln Glu Ala Ser Glu Ala Ser Met Leu Lys Gly Cys
        35                  40                  45
Glu Asp Leu Ile Asn Pro Ala Ala Ala Thr Arg Ile Lys Lys Lys Gly
    50                  55                  60
Glu Lys Phe Glu Ser Leu Glu Ala Arg Arg Lys Pro Thr Ala Asp Lys
65                  70                  75                  80
Ala Glu Lys Lys Ser Glu Ser Thr Glu Glu Lys Gly Asp Thr Pro Leu
                85                  90                  95
Glu Asp Arg Phe Thr Glu Asp Leu Ser Glu Val Ser Gly Glu Asp Phe
            100                 105                 110
Arg Gly Leu Lys Asn Ser Phe Asp Asp Asp Ser Ser Pro Asp Glu Ile
        115                 120                 125
Leu Asp Ala Leu Thr Ser Lys Phe Ser Asp Pro Thr Ile Lys Asp Leu
    130                 135                 140
Ala Leu Asp Tyr Leu Ile Gln Thr Ala Pro Ser Asp Gly Lys Leu Lys
145                 150                 155                 160
Ser Thr Leu Ile Gln Ala Lys His Gln Leu Met Ser Gln Asn Pro Gln
                165                 170                 175
Ala Ile Val Gly Gly Arg Asn Val Leu Leu Ala Ser Glu Thr Phe Ala
            180                 185                 190
Ser Arg Ala Asn Thr Ser Pro Ser Ser Leu Arg Ser Leu Tyr Phe Gln
        195                 200                 205
Val Thr Ser Ser Pro Ser Asn Cys Ala Asn Leu His Gln Met Leu Ala
    210                 215                 220
Ser Tyr Leu Pro Ser Glu Lys Thr Ala Val Met Glu Phe Leu Val Asn
225                 230                 235                 240
Gly Met Val Ala Asp Leu Lys Ser Glu Gly Pro Ser Ile Pro Pro Ala
                245                 250                 255
Lys Leu Gln Val Tyr Met Thr Glu Leu Ser Asn Leu Gln Ala Leu His
            260                 265                 270
Ser Val Asn Ser Phe Phe Asp Arg Asn Ile Gly Asn Leu Glu Asn Ser
        275                 280                 285
Leu Lys His Glu Gly His Ala Pro Ile Pro Ser Leu Thr Thr Gly Asn
    290                 295                 300
Leu Thr Lys Thr Phe Leu Gln Leu Val Glu Asp Lys Phe Pro Ser Ser
305                 310                 315                 320
Ser Lys Ala Gln Lys Ala Leu Asn Glu Leu Val Gly Pro Asp Thr Gly
                325                 330                 335
Pro Gln Thr Glu Val Leu Asn Leu Phe Phe Arg Ala Leu Asn Gly Cys
```

```
            340                 345                 350
Ser Pro Arg Ile Phe Ser Gly Ala Glu Lys Lys Gln Gln Leu Ala Ser
        355                 360                 365
Val Ile Thr Asn Thr Leu Asp Ala Ile Asn Ala Asp Asn Glu Asp Tyr
    370                 375                 380
Pro Lys Pro Gly Asp Phe Pro Arg Ser Ser Phe Ser Ser Thr Pro Pro
385                 390                 395                 400
His Ala Pro Val Pro Gln Ser Glu Ile Pro Thr Ser Pro Thr Ser Thr
                405                 410                 415
Gln Pro Pro Ser Pro
            420

<210> 578
<211> 231
<212> PRT
<213> C. Trachomatis D serovar

<400> 578
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
 1               5                  10                  15
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
            20                  25                  30
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
        35                  40                  45
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
    50                  55                  60
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
65                  70                  75                  80
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
                85                  90                  95
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
            100                 105                 110
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
        115                 120                 125
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
    130                 135                 140
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145                 150                 155                 160
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
                165                 170                 175
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
            180                 185                 190
Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
        195                 200                 205
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
    210                 215                 220
Cys Ser Cys His Gln Ser Tyr
225                 230

<210> 579
<211> 243
<212> PRT
<213> C. Trachomatis D serovar

<400> 579
Met Lys Ile Thr Pro Ile Lys Thr Arg Lys Val Phe Ala His Asp Ser
 1               5                  10                  15
Leu Gln Glu Ile Leu Gln Glu Ala Leu Pro Pro Leu Gln Glu Arg Ser
            20                  25                  30
Val Val Val Val Ser Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val
        35                  40                  45
```

```
Ala Asp Ala Arg Met Cys Lys Ala Glu Leu Ile Lys Lys Glu Ala Asp
    50                  55                  60
Ala Tyr Leu Phe Cys Glu Lys Ser Gly Ile Tyr Leu Thr Lys Lys Glu
65                  70                  75                  80
Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn Thr Asp Gln
                85                  90                  95
Pro Phe Val Leu Tyr Pro Lys Asp Ile Leu Gly Ser Cys Asn Arg Ile
            100                 105                 110
Gly Glu Trp Leu Arg Asn Tyr Phe Arg Val Lys Glu Leu Gly Val Ile
        115                 120                 125
Ile Thr Asp Ser His Thr Thr Pro Met Arg Arg Gly Val Leu Gly Ile
    130                 135                 140
Gly Leu Cys Trp Tyr Gly Phe Ser Pro Leu His Asn Tyr Ile Gly Ser
145                 150                 155                 160
Leu Asp Cys Phe Gly Arg Pro Leu Gln Met Thr Gln Ser Asn Leu Val
                165                 170                 175
Asp Ala Leu Ala Val Ala Ala Val Val Cys Met Gly Glu Gly Asn Glu
            180                 185                 190
Gln Thr Pro Leu Ala Val Ile Glu Gln Ala Pro Asn Met Val Tyr His
        195                 200                 205
Ser His Pro Thr Ser Arg Glu Glu Tyr Cys Ser Leu Arg Ile Asp Glu
    210                 215                 220
Thr Glu Asp Leu Tyr Gly Pro Phe Leu Gln Ala Val Thr Trp Ser Gln
225                 230                 235                 240
Glu Lys Lys
```

<210> 580
<211> 383
<212> PRT
<213> C. Trachomatis D serovar

<400> 580

```
Met Leu Pro His Gln Gln Asn Ser Ser Ser Glu Arg Ala Arg His His
1               5                   10                  15
Glu Ser Arg Ser His Arg His Ser Ser Ser Ser Arg His His Val Thr
            20                  25                  30
Arg Ser Gln Ser Ser Ala Leu Pro Gln Leu Gln Glu Arg Pro Val Pro
        35                  40                  45
His Pro Leu Ala Glu Arg Glu Leu Ile Ile Phe His Ser Val His Gln
    50                  55                  60
Gln Gln Asn Asn Asn Pro Leu Arg Met Ile Cys Asp Thr Ile Arg Gln
65                  70                  75                  80
Ala Gln Arg Gly Ile Phe Met Arg Ile Tyr Thr Ile Ser Ser Asp Asp
                85                  90                  95
Ile Ile Gln Ser Leu Ile Gln Thr Ser His His Val Pro Val Glu Val
            100                 105                 110
Lys Tyr His Cys Gly Glu Ser Leu Pro Val Ala Cys Gln Asn Ser Arg
        115                 120                 125
Val Val Leu Arg Leu Thr Asn Gly Arg Thr Leu Gln His Lys Lys Thr
    130                 135                 140
Met Leu Ala Asp Phe Gln Thr Val Val Thr Gly Ser Ala Asn Tyr Thr
145                 150                 155                 160
Asp Leu Ser Leu Asn His Asp Ala Asn Val Thr Ala Cys Ile Glu Ser
                165                 170                 175
Ser Glu Leu His Asp Ala Val Phe Ser Glu Arg Pro Gln Leu Val His
            180                 185                 190
Val Gly Pro Gln Leu Leu Asn Tyr Ile Pro Ile Gln Arg Leu Ile Pro
        195                 200                 205
Asn Ala Ala Ser Lys Met Ile Leu Asn Ala Ile Asn Gln Ala Thr Asp
    210                 215                 220
```

Ser Ile Phe Val Leu Met Tyr Ile Phe Leu Ser Pro Glu Phe Phe Leu
225 230 235 240
Ala Leu Ala Gln Ala Met Arg Arg Gly Val Arg Val Lys Val Ile Ile
245 250 255
Asp Asn His Ser Lys Gln Asp Thr Cys Lys Leu Leu Ser Lys Leu Gly
260 265 270
Ile Gln Leu Pro Ile Tyr Glu Arg Lys Thr Glu Gly Val Leu His Thr
275 280 285
Lys Ile Cys Cys Ile Asp Asn Lys Thr Leu Ile Phe Gly Ser Ala Asn
290 295 300
Trp Ser Gly Ala Gly Met Ile Lys Asn Phe Glu Asp Leu Phe Ile Leu
305 310 315 320
Arg Pro Ile Thr Glu Thr Gln Leu Gln Ala Phe Met Asp Val Trp Ser
325 330 335
Leu Leu Glu Thr Asn Ser Ser Tyr Leu Ser Pro Glu Ser Val Leu Thr
340 345 350
Ala Pro Thr Pro Ser Ser Arg Pro Thr Gln Gln Asp Thr Asp Ser Asp
355 360 365
Asp Glu Gln Pro Ser Thr Ser Gln Gln Asp Ile Arg Met Arg Lys
370 375 380

<210> 581
<211> 193
<212> PRT
<213> C. Trachomatis D serovar

<400> 581
Met Trp Phe Phe Leu Gly Ser Pro Ser Ala Ile Thr Asn Phe Ser Arg
1 5 10 15
Val Asp Val Ala Leu Asn Leu Arg Ile Asn Arg Gln Ile Arg Ala Pro
20 25 30
Arg Val Arg Val Ile Gly Ser Ala Gly Glu Gln Leu Gly Ile Leu Ser
35 40 45
Ile Lys Glu Ala Leu Asp Leu Ala Lys Glu Ala Asn Leu Asp Leu Val
50 55 60
Glu Val Ala Ser Asn Ser Glu Pro Pro Val Cys Lys Ile Met Asp Tyr
65 70 75 80
Gly Lys Tyr Arg Tyr Asp Val Thr Lys Lys Glu Lys Asp Ser Lys Lys
85 90 95
Ala Gln His Gln Val Arg Ile Lys Glu Val Lys Leu Lys Pro Asn Ile
100 105 110
Asp Asp Asn Asp Phe Leu Thr Lys Ala Lys Gln Ala Arg Ala Phe Ile
115 120 125
Glu Lys Gly Asn Lys Val Lys Val Ser Cys Met Phe Arg Gly Arg Glu
130 135 140
Leu Ala Tyr Pro Glu His Gly Tyr Lys Val Ile Gln Arg Met Cys Gln
145 150 155 160
Gly Leu Glu Asp Ile Gly Phe Val Glu Ser Glu Pro Lys Leu Asn Gly
165 170 175
Arg Ser Leu Ile Cys Val Ile Ala Pro Gly Thr Leu Lys Thr Lys Lys
180 185 190
Lys

<210> 582
<211> 264
<212> PRT
<213> C. Trachomatis D serovar

<400> 582
Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn Thr Glu Asn Cys Val Phe

1 5 10 15
Ala Asp Asn Ile Lys Val Gly Gln Met Thr Glu Pro Leu Lys Asp Gln
20 25 30
Gln Ile Ile Leu Gly Thr Lys Ser Thr Pro Val Ala Ala Lys Met Thr
35 40 45
Ala Ser Asp Gly Ile Ser Leu Thr Val Ser Asn Asn Ser Ser Thr Asn
50 55 60
Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu Lys Ala Tyr Gln Leu Ile
65 70 75 80
Leu Glu Lys Leu Gly Asn Gln Ile Leu Asp Gly Ile Ala Asp Thr Ile
85 90 95
Val Asp Ser Thr Val Gln Asp Ile Leu Asp Lys Ile Thr Thr Asp Pro
100 105 110
Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn Phe Pro Ile Thr Asn Lys
115 120 125
Ile Gln Cys Asn Gly Leu Phe Thr Pro Ser Asn Ile Glu Thr Leu Leu
130 135 140
Gly Gly Thr Glu Ile Gly Lys Phe Thr Val Thr Pro Lys Ser Ser Gly
145 150 155 160
Ser Met Phe Leu Val Ser Ala Asp Ile Ile Ala Ser Arg Met Glu Gly
165 170 175
Gly Val Val Leu Ala Leu Val Arg Glu Gly Asp Ser Lys Pro Cys Ala
180 185 190
Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro Asn Leu Cys Ser Leu Arg
195 200 205
Thr Ser Ile Thr Asn Thr Gly Leu Thr Pro Thr Thr Tyr Ser Leu Arg
210 215 220
Val Gly Gly Leu Glu Ser Gly Val Val Trp Val Asn Ala Leu Ser Asn
225 230 235 240
Gly Asn Asp Ile Leu Gly Ile Thr Asn Thr Ser Asn Val Ser Phe Leu
245 250 255
Glu Val Ile Pro Gln Thr Asn Ala
260

<210> 583
<211> 1053
<212> PRT
<213> C. Trachomatis D serovar

<400> 583
Met Phe Thr Arg Ile Val Met Val Asp Leu Gln Glu Lys Gln Cys Thr
1 5 10 15
Ile Val Lys Arg Asn Gly Met Phe Val Pro Phe Asp Arg Asn Arg Ile
20 25 30
Phe Gln Ala Leu Glu Ala Ala Phe Arg Asp Thr Arg Arg Ile Asp Asp
35 40 45
His Met Pro Leu Pro Glu Asp Leu Glu Ser Ser Ile Arg Ser Ile Thr
50 55 60
His Gln Val Val Lys Glu Val Val Gln Lys Ile Thr Asp Gly Gln Val
65 70 75 80
Val Thr Val Glu Arg Ile Gln Asp Met Val Glu Ser Gln Leu Tyr Val
85 90 95
Asn Gly Leu Gln Asp Val Ala Arg Asp Tyr Ile Val Tyr Arg Asp Asp
100 105 110
Arg Lys Ala His Arg Lys Lys Ser Trp Gln Ser Leu Ser Val Val Arg
115 120 125
Arg Cys Gly Thr Val Val His Phe Asn Pro Met Lys Ile Ser Ala Ala
130 135 140
Leu Glu Lys Ala Phe Arg Ala Thr Asp Lys Thr Glu Gly Met Thr Pro
145 150 155 160
Ser Ser Val Arg Glu Glu Ile Asn Ala Leu Thr Gln Asn Ile Val Ala

```
                165                 170                 175
Glu Ile Glu Glu Cys Cys Pro Gln Gln Asp Arg Arg Ile Asp Ile Glu
            180                 185                 190
Lys Ile Gln Asp Ile Val Glu Gln Gln Leu Met Val Val Gly His Tyr
        195                 200                 205
Ala Val Ala Lys Asn Tyr Ile Leu Tyr Arg Glu Ala Arg Ala Arg Val
    210                 215                 220
Arg Asp Asn Arg Glu Glu Asp Gly Ser Thr Glu Lys Thr Ile Ala Glu
225                 230                 235                 240
Glu Ala Val Glu Val Leu Ser Lys Asp Gly Ser Thr Tyr Thr Met Thr
                245                 250                 255
His Ser Gln Leu Leu Ala His Leu Ala Arg Ala Cys Ser Arg Phe Pro
            260                 265                 270
Glu Thr Thr Asp Ala Ala Leu Leu Thr Asp Met Ala Phe Ala Asn Phe
        275                 280                 285
Tyr Ser Gly Ile Lys Glu Ser Glu Val Val Leu Ala Cys Ile Met Ala
    290                 295                 300
Ala Arg Ala Asn Ile Glu Lys Glu Pro Asp Tyr Ala Phe Val Ala Ala
305                 310                 315                 320
Glu Leu Leu Leu Asp Val Val Tyr Lys Glu Ala Leu Gly Lys Ser Lys
                325                 330                 335
Tyr Ala Glu Asp Leu Glu Gln Ala His Arg Asp His Phe Lys Arg Tyr
            340                 345                 350
Ile Ala Glu Gly Asp Thr Tyr Arg Leu Asn Ala Glu Leu Lys His Leu
        355                 360                 365
Phe Asp Leu Asp Ala Leu Ala Asp Ala Met Asp Leu Ser Arg Asp Leu
    370                 375                 380
Gln Phe Ser Tyr Met Gly Ile Gln Asn Leu Tyr Asp Arg Tyr Phe Asn
385                 390                 395                 400
His His Glu Gly Cys Arg Leu Glu Thr Pro Gln Ile Phe Trp Met Arg
                405                 410                 415
Val Ala Met Gly Leu Ala Leu Asn Glu Gln Asp Lys Thr Ser Trp Ala
            420                 425                 430
Ile Thr Phe Tyr Asn Leu Leu Ser Thr Phe Arg Tyr Thr Pro Ala Thr
        435                 440                 445
Pro Thr Leu Phe Asn Ser Gly Met Arg His Ser Gln Leu Ser Ser Cys
    450                 455                 460
Tyr Leu Ser Thr Val Gln Asp Asn Leu Val Asn Ile Tyr Lys Val Ile
465                 470                 475                 480
Ala Asp Asn Ala Met Leu Ser Lys Trp Ala Gly Gly Ile Gly Asn Asp
                485                 490                 495
Trp Thr Ala Ile Arg Ala Thr Gly Ala Leu Ile Lys Gly Thr Asn Gly
            500                 505                 510
Arg Ser Gln Gly Val Ile Pro Phe Ile Lys Val Thr Asn Asp Thr Ala
        515                 520                 525
Val Ala Val Asn Gln Gly Gly Lys Arg Lys Gly Ala Val Cys Val Tyr
    530                 535                 540
Leu Glu Val Trp His Leu Asp Tyr Glu Asp Phe Leu Glu Leu Arg Lys
545                 550                 555                 560
Asn Thr Gly Asp Glu Arg Arg Arg Ala His Asp Val Asn Ile Ala Ser
                565                 570                 575
Trp Ile Pro Asp Leu Phe Phe Lys Arg Leu Gln Gln Lys Gly Thr Trp
            580                 585                 590
Thr Leu Phe Ser Pro Asp Asp Val Pro Gly Leu His Asp Ala Tyr Gly
        595                 600                 605
Glu Glu Phe Glu Arg Leu Tyr Glu Glu Tyr Glu Arg Lys Val Asp Thr
    610                 615                 620
Gly Glu Ile Arg Leu Phe Lys Lys Val Glu Ala Glu Asp Leu Trp Arg
625                 630                 635                 640
Lys Met Leu Ser Met Leu Phe Glu Thr Gly His Pro Trp Met Thr Phe
                645                 650                 655
```

```
Lys Asp Pro Ser Asn Ile Arg Ser Ala Gln Asp His Lys Gly Val Val
            660                 665                 670
Arg Cys Ser Asn Leu Cys Thr Glu Ile Leu Leu Asn Cys Ser Glu Thr
        675                 680                 685
Glu Thr Ala Val Cys Asn Leu Gly Ser Ile Asn Leu Val Gln His Ile
    690                 695                 700
Val Gly Asp Gly Leu Asp Glu Glu Lys Leu Ser Glu Thr Ile Ser Ile
705                 710                 715                 720
Ala Val Arg Met Leu Asp Asn Val Ile Asp Ile Asn Phe Tyr Pro Thr
                725                 730                 735
Lys Glu Ala Lys Glu Ala Asn Phe Ala His Arg Ala Ile Gly Leu Gly
            740                 745                 750
Val Met Gly Phe Gln Asp Ala Leu Tyr Lys Leu Asp Ile Ser Tyr Ala
        755                 760                 765
Ser Gln Glu Ala Val Glu Phe Ala Asp Tyr Ser Ser Glu Leu Ile Ser
    770                 775                 780
Tyr Tyr Ala Ile Gln Ala Ser Cys Leu Leu Ala Lys Glu Arg Gly Thr
785                 790                 795                 800
Tyr Ser Ser Tyr Lys Gly Ser Lys Trp Asp Arg Gly Leu Leu Pro Ile
                805                 810                 815
Asp Thr Ile Gln Leu Leu Ala Asn Tyr Arg Gly Glu Ala Asn Leu Gln
            820                 825                 830
Met Asp Thr Ser Ser Arg Lys Asp Trp Glu Pro Ile Arg Ser Leu Val
        835                 840                 845
Lys Glu His Gly Met Arg His Cys Gln Leu Met Ala Ile Ala Pro Thr
    850                 855                 860
Ala Thr Ile Ser Asn Ile Ile Gly Val Thr Gln Ser Ile Glu Pro Thr
865                 870                 875                 880
Tyr Lys His Leu Phe Val Lys Ser Asn Leu Ser Gly Glu Phe Thr Ile
                885                 890                 895
Pro Asn Val Tyr Leu Ile Glu Lys Leu Lys Lys Leu Gly Ile Trp Asp
            900                 905                 910
Ala Asp Met Leu Asp Asp Leu Lys Tyr Phe Asp Gly Ser Leu Leu Glu
        915                 920                 925
Ile Glu Arg Ile Pro Asp His Leu Lys His Ile Phe Leu Thr Ala Phe
    930                 935                 940
Glu Ile Glu Pro Glu Trp Ile Ile Glu Cys Ala Ser Arg Arg Gln Lys
945                 950                 955                 960
Trp Ile Asp Met Gly Gln Ser Leu Asn Leu Tyr Leu Ala Gln Pro Asp
                965                 970                 975
Gly Lys Lys Leu Ser Asn Met Tyr Leu Thr Ala Trp Lys Lys Gly Leu
            980                 985                 990
Lys Thr Thr Tyr Tyr Leu Arg Ser Ser Ser Ala Thr Thr Val Glu Lys
        995                 1000                1005
Ser Phe Val Asp Ile Asn Lys Arg Gly Ile Gln Pro Arg Trp Met Lys
    1010                1015                1020
Asn Lys Ser Ala Ser Ala Gly Ile Ile Val Glu Arg Ala Lys Lys Ala
1025                1030                1035                1040
Pro Val Cys Ser Leu Glu Glu Gly Cys Glu Ala Cys Gln
                1045                1050
```

<210> 584
<211> 346
<212> PRT
<213> C. Trachomatis D serovar

<400> 584

```
Met Gln Ala Asp Ile Leu Asp Gly Lys Gln Lys Arg Val Asn Leu Asn
 1               5                  10                  15
Ser Lys Arg Leu Val Asn Cys Asn Gln Val Asp Val Asn Gln Leu Val
            20                  25                  30
```

```
Pro Ile Lys Tyr Lys Trp Ala Trp Glu His Tyr Leu Asn Gly Cys Ala
        35                  40                  45
Asn Asn Trp Leu Pro Thr Glu Ile Pro Met Gly Lys Asp Ile Glu Leu
    50                  55                  60
Trp Lys Ser Asp Arg Leu Ser Glu Asp Glu Arg Arg Val Ile Leu Leu
65                  70                  75                  80
Asn Leu Gly Phe Phe Ser Thr Ala Glu Ser Leu Val Gly Asn Asn Ile
                85                  90                  95
Val Leu Ala Ile Phe Lys His Val Thr Asn Pro Glu Ala Arg Gln Tyr
            100                 105                 110
Leu Leu Arg Gln Ala Phe Glu Glu Ala Val His Thr His Thr Phe Leu
        115                 120                 125
Tyr Ile Cys Glu Ser Leu Gly Leu Asp Glu Lys Glu Ile Phe Asn Ala
    130                 135                 140
Tyr Asn Glu Arg Ala Ala Ile Lys Ala Lys Asp Asp Phe Gln Met Glu
145                 150                 155                 160
Ile Thr Gly Lys Val Leu Asp Pro Asn Phe Arg Thr Asp Ser Val Glu
                165                 170                 175
Gly Leu Gln Glu Phe Val Lys Asn Leu Val Gly Tyr Tyr Ile Ile Met
            180                 185                 190
Glu Gly Ile Phe Phe Tyr Ser Gly Phe Val Met Ile Leu Ser Phe His
        195                 200                 205
Arg Gln Asn Lys Met Ile Gly Ile Gly Glu Gln Tyr Gln Tyr Ile Leu
    210                 215                 220
Arg Asp Glu Thr Ile His Leu Asn Phe Gly Ile Asp Leu Ile Asn Gly
225                 230                 235                 240
Ile Lys Glu Glu Asn Pro Glu Ile Trp Thr Pro Glu Leu Gln Gln Glu
                245                 250                 255
Ile Val Glu Leu Ile Lys Arg Ala Val Asp Leu Glu Ile Glu Tyr Ala
            260                 265                 270
Gln Asp Cys Leu Pro Arg Gly Ile Leu Gly Leu Arg Ala Ser Met Phe
        275                 280                 285
Ile Asp Tyr Val Gln His Ile Ala Asp Arg Arg Leu Glu Arg Ile Gly
    290                 295                 300
Leu Lys Pro Ile Tyr His Thr Lys Asn Pro Phe Pro Trp Met Ser Glu
305                 310                 315                 320
Thr Ile Asp Leu Asn Lys Glu Lys Asn Phe Phe Glu Thr Arg Val Ile
                325                 330                 335
Glu Tyr Gln His Ala Ala Ser Leu Thr Trp
            340                 345
```

<210> 585
<211> 326
<212> PRT
<213> C. Trachomatis D serovar

<400> 585

```
Met Ser Phe Phe His Thr Arg Lys Tyr Lys Leu Ile Leu Arg Gly Leu
 1              5                   10                  15
Leu Cys Leu Ala Gly Cys Phe Leu Met Asn Ser Cys Ser Ser Ser Arg
            20                  25                  30
Gly Asn Gln Pro Ala Asp Glu Ser Ile Tyr Val Leu Ser Met Asn Arg
        35                  40                  45
Met Ile Cys Asp Cys Val Ser Arg Ile Thr Gly Asp Arg Val Lys Asn
    50                  55                  60
Ile Val Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr Glu Met Val
65                  70                  75                  80
Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile Phe Cys Asn
                85                  90                  95
Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His Leu Glu Gly
            100                 105                 110
```

Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn Lys Asn Cys
115 120 125
Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His Ile Trp Thr
130 135 140
Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala Ala Ala Leu
145 150 155 160
Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys Asn Ala Asp
165 170 175
Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala Ala Arg Ser
180 185 190
Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr Gly His Asn
195 200 205
Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp Ala Glu Arg
210 215 220
Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu Gly Leu Ser
225 230 235 240
Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val Val Glu Tyr
245 250 255
Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp Thr Leu Asn
260 265 270
Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser Gly Gln Lys
275 280 285
Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val Cys Asp Asn
290 295 300
Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr Glu Glu Leu
305 310 315 320
Gly Gly Thr Val Leu Glu
325

<210> 586
<211> 102
<212> PRT
<213> C. Trachomatis D serovar

<400> 586
Met Gln Asn Lys Arg Lys Val Arg Asp Asp Phe Ile Lys Ile Val Lys
1 5 10 15
Asp Val Lys Lys Asp Phe Pro Glu Leu Asp Leu Lys Ile Arg Val Asn
20 25 30
Lys Glu Lys Val Thr Phe Leu Asn Ser Pro Leu Glu Leu Tyr His Lys
35 40 45
Ser Val Ser Leu Ile Leu Gly Leu Leu Gln Gln Ile Glu Asn Ser Leu
50 55 60
Gly Leu Phe Pro Asp Ser Pro Val Leu Glu Lys Leu Glu Asp Asn Ser
65 70 75 80
Leu Lys Leu Lys Lys Ala Leu Ile Met Leu Ile Leu Ser Arg Lys Asp
85 90 95
Met Phe Ser Lys Ala Glu
100

<210> 587
<211> 243
<212> PRT
<213> C. Trachomatis D serovar

<400> 587
Val Gly Cys Asn Leu Ala Gln Phe Leu Gly Lys Lys Val Leu Leu Ala
1 5 10 15
Asp Leu Asp Pro Gln Ser Asn Leu Ser Ser Gly Leu Gly Ala Ser Val
20 25 30
Arg Asn Asn Gln Lys Gly Leu His Asp Ile Val Tyr Lys Ser Asn Asp

35 40 45
Leu Lys Ser Ile Ile Cys Glu Thr Lys Lys Asp Ser Val Asp Leu Ile
50 55 60
Pro Ala Ser Phe Leu Ser Glu Gln Phe Arg Glu Leu Asp Ile His Arg
65 70 75 80
Gly Pro Ser Asn Asn Leu Lys Leu Phe Leu Asn Glu Tyr Cys Ala Pro
85 90 95
Phe Tyr Asp Ile Cys Ile Ile Asp Thr Pro Pro Ser Leu Gly Gly Leu
100 105 110
Thr Lys Glu Ala Phe Val Ala Gly Asp Lys Leu Ile Ala Cys Leu Thr
115 120 125
Pro Glu Pro Phe Ser Ile Leu Gly Leu Gln Lys Ile Arg Glu Phe Leu
130 135 140
Ser Ser Val Gly Lys Pro Glu Glu Glu His Ile Leu Gly Ile Ala Leu
145 150 155 160
Ser Phe Trp Asp Asp Arg Asn Ser Thr Asn Gln Met Tyr Ile Asp Ile
165 170 175
Ile Glu Ser Ile Tyr Lys Asn Lys Leu Phe Ser Thr Lys Ile Arg Arg
180 185 190
Asp Ile Ser Leu Ser Arg Ser Leu Leu Lys Glu Asp Ser Val Ala Asn
195 200 205
Val Tyr Pro Asn Ser Arg Ala Ala Glu Asp Ile Leu Lys Leu Thr His
210 215 220
Glu Ile Ala Asn Ile Leu His Ile Glu Tyr Glu Arg Asp Tyr Ser Gln
225 230 235 240
Arg Thr Thr

<210> 588
<211> 527
<212> PRT
<213> C. Trachomatis D serovar

<400> 588
Met Pro Ser Leu Ser Gln Ser Arg Arg Ile Ile Gln Gln Ser Ser Ile
1 5 10 15
Arg Lys Ile Trp Asn Gln Ile Asp Thr Ser Pro Lys His Gly Val Cys
20 25 30
Val Pro Leu Phe Ser Leu Tyr Thr Gln Glu Ser Cys Gly Ile Gly Glu
35 40 45
Phe Leu Asp Leu Ile Pro Met Ile Asp Trp Cys Ile Ser Cys Gly Phe
50 55 60
Gln Ile Leu Gln Ile Leu Pro Ile Asn Asp Thr Gly Ser Cys Ser Ser
65 70 75 80
Pro Tyr Asn Ser Ile Ser Ser Ile Ala Leu Asn Pro Leu His Leu Ser
85 90 95
Ile Ser Ala Leu Pro Tyr Lys Glu Glu Val Pro Ala Ala Glu Thr Arg
100 105 110
Ile Arg Glu Met Gln Gln Leu Ser Gln Leu Pro Gln Val His Tyr Glu
115 120 125
Lys Val Arg Ser Met Lys Arg Asp Phe Phe Gln Glu Tyr Tyr Arg Val
130 135 140
Cys Lys Gln Lys Lys Leu Thr Asp His Pro Asp Phe Tyr Ala Phe Cys
145 150 155 160
Glu Gln Glu Lys Tyr Trp Leu His Pro Tyr Ala Leu Phe Arg Ser Ile
165 170 175
Arg Glu His Leu Asp Asn Leu Pro Ile Asn His Trp Pro Thr Thr Tyr
180 185 190
Thr Asp Leu Ser Gln Ile Thr Glu His Glu Arg Thr Phe Ala Glu Asp
195 200 205
Ile Gln Phe His Ser Tyr Leu Gln Tyr Leu Cys Phe Gln Gln Met Thr

210 215 220
Gln Val Arg Glu His Ala Asn Cys Lys Ser Cys Leu Ile Lys Gly Asp
225 230 235 240
Ile Pro Ile Leu Ile Ser Lys Asp Ser Cys Asp Val Trp Phe Tyr Arg
245 250 255
His Tyr Phe Ser Ser Ser Glu Ser Val Gly Ala Pro Pro Asp Leu Tyr
260 265 270
Asn Ala Glu Gly Gln Asn Trp His Leu Pro Ile Cys Asn Met Lys Thr
275 280 285
Leu Gln Gln Asp Asn Tyr Leu Trp Trp Lys Glu Arg Leu Arg Tyr Ala
290 295 300
Glu Asn Phe Tyr Ser Leu Tyr Arg Leu Asp His Val Val Gly Leu Phe
305 310 315 320
Arg Phe Trp Val Trp Asp Glu Ser Gly Cys Gly Arg Phe Glu Pro His
325 330 335
Asp Pro Lys Asn Tyr Leu Ala Gln Gly Gln Asp Ile Leu Ser His Leu
340 345 350
Leu Thr Ser Ser Ser Met Leu Pro Ile Gly Glu Asp Leu Gly Thr Ile
355 360 365
Pro Ser Asp Val Lys Arg Met Leu Glu Ser Phe Ala Val Cys Gly Thr
370 375 380
Arg Ile Pro Arg Trp Glu Arg Asn Trp Glu Gly Asn Gly Ala Tyr Thr
385 390 395 400
Pro Phe Asp Gln Tyr Asp Pro Leu Ser Val Thr Ser Leu Ser Thr His
405 410 415
Asp Ser Ser Thr Leu Ala Ser Trp Trp Lys Glu Ser Pro Gln Glu Ser
420 425 430
Lys Leu Phe Ala Gln Phe Leu Gly Leu Pro Tyr Ser Ser Thr Leu Ser
435 440 445
Leu His Asn His Thr Glu Ile Leu Lys Leu Ser His Lys Thr Ser Ser
450 455 460
Ile Phe Arg Ile Asn Leu Ile Asn Asp Tyr Leu Ala Leu Phe Pro Asp
465 470 475 480
Leu Ile Ser Lys Thr Pro Arg Tyr Glu Arg Ile Asn Leu Pro Gly Thr
485 490 495
Ile Ser Lys Asn Asn Trp Val Tyr Arg Val Lys Pro Ser Ile Glu Asp
500 505 510
Leu Ser Ser His Ser Lys Leu Asn Ser Leu Leu Glu Ala Leu Phe
515 520 525

<210> 589
<211> 146
<212> PRT
<213> C. Trachomatis D serovar

<400> 589
Met Gln Asn Gln Phe Glu Gln Leu Leu Thr Glu Leu Gly Thr Gln Ile
1 5 10 15
Asn Ser Pro Leu Thr Pro Asp Ser Asn Asn Ala Cys Ile Val Arg Phe
20 25 30
Gly Tyr Asn Asn Val Ala Val Gln Ile Glu Glu Asp Gly Asn Ser Gly
35 40 45
Phe Leu Val Ala Gly Val Met Leu Gly Lys Leu Pro Glu Asn Thr Phe
50 55 60
Arg Gln Lys Ile Phe Lys Ala Ala Leu Ser Ile Asn Gly Ser Pro Gln
65 70 75 80
Ser Asn Ile Lys Gly Thr Leu Gly Tyr Gly Glu Ile Ser Asn Gln Leu
85 90 95
Tyr Leu Cys Asp Arg Leu Asn Met Thr Tyr Leu Asn Gly Glu Lys Leu
100 105 110
Ala Arg Tyr Leu Val Leu Phe Ser Gln His Ala Asn Ile Trp Met Gln

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        115                 120                 125
Ser Ile Ser Lys Gly Ala Leu Pro Asp Leu His Ala Leu Gly Met Tyr
    130                 135                 140
His Leu
145

<210> 590
<211> 650
<212> PRT
<213> C. Trachomatis D serovar

<400> 590
Met Thr Ile Pro Ile His Glu Asn Lys Tyr Ser Met Ile Ser Phe Thr
 1               5                  10                  15
Arg Thr Ile Gly Phe Arg Leu Trp Leu Ile Cys Val Ala Ala Ile Met
            20                  25                  30
Phe Pro Leu Gly Ile Asn Ile Leu Gln Leu Asn Leu Gln Gln Tyr Lys
        35                  40                  45
Lys Thr Leu Ser Ser Ile Thr Ser Asp Leu Arg Glu Asn Ala Leu Phe
    50                  55                  60
Lys Ala His Thr Leu Gln Gln Thr Ile Pro Leu Asn Ile Asp Ile Leu
65                  70                  75                  80
Ala Leu Phe Ser Glu Ile Phe Asp Leu Asp Arg Gly Val Pro Ala Glu
                85                  90                  95
Pro Asp Leu Ala Leu Ser Lys Glu Met Glu Lys Ile Phe His Ser Thr
            100                 105                 110
Tyr Lys Glu Ile Ser Leu Val Lys Lys Glu Ala Asp Gly Asn Phe Arg
        115                 120                 125
Val Val Ala Ser Ser Arg Ile Glu Gln Leu Gly Lys Asn Tyr Asn Gln
    130                 135                 140
Glu Ile Phe Leu Ser Asp Ser Gln Pro Phe Leu Ala Thr Leu Arg His
145                 150                 155                 160
Ser Gly Ser Asp Ser Gln Val Leu Ala Val Leu Gln Thr Asn Ile Phe
                165                 170                 175
Asp Ile Ser Ser Gln Glu Val Leu Gly Val Leu Tyr Thr Leu Ser Asp
            180                 185                 190
Thr Asn Tyr Leu Leu Asn Gly Leu Leu Ala Ala Lys Asp Pro Leu Ser
        195                 200                 205
Val Lys Thr Ala Ile Leu Ser Lys Asn Gly Ile Ile Leu Gln Ala Thr
    210                 215                 220
Asp Ser Ser Leu Asp Leu Val Ser Ile His Lys Thr Val Ser Lys Glu
225                 230                 235                 240
Gln Phe Cys Asp Val Phe Leu Arg Asp Asp Ile Cys Pro Pro His Leu
                245                 250                 255
Leu Leu Arg Pro Pro Leu Asn Leu Asp Pro Leu Pro Tyr Gly Glu Asn
            260                 265                 270
Phe Val Ser Phe Cys Ile Gly Asn Thr Glu Met Trp Gly Tyr Ile His
        275                 280                 285
Ser Leu Pro Glu Met Asp Phe Arg Ile Leu Thr Tyr Glu Glu Lys Ser
    290                 295                 300
Ile Ile Phe Ala Ser Leu Trp Arg Arg Thr Leu Leu Tyr Phe Ala Tyr
305                 310                 315                 320
Phe Cys Cys Val Leu Leu Gly Ser Ile Thr Ala Phe Leu Val Ala Lys
                325                 330                 335
Arg Leu Ser Lys Pro Ile Arg Lys Leu Ala Thr Ala Met Met Glu Thr
            340                 345                 350
Arg Arg Asn Gln His His Pro Tyr Glu Pro Asp Ser Leu Gly Phe Glu
        355                 360                 365
Ile Asn His Leu Gly Glu Ile Phe Asn Ser Met Val Gln Ser Leu Leu
    370                 375                 380
Gln Gln Gln Ser Leu Ala Glu Lys Asn Phe Glu Ile Lys Gln His Ala
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385                 390                 395                 400
Gln Asn Ala Leu Arg Leu Gly Glu Glu Ala Gln Gln Cys Leu Leu Pro
                405                 410                 415
Asn Gln Leu Pro Asp Ser Pro Thr Thr Glu Ile Ala Lys Ala Tyr Ile
            420                 425                 430
Pro Ala Ile Thr Val Gly Gly Asp Phe Phe Asp Ile Phe Val Ile Gly
        435                 440                 445
Glu Gly Pro Gln Ala Lys Leu Phe Leu Ile Val Ala Asp Ala Ser Gly
    450                 455                 460
Lys Gly Val Asn Ala Cys Ala Tyr Ser Leu Phe Leu Lys Asn Met Leu
465                 470                 475                 480
His Thr Phe Leu Ser Glu Leu Ser Ser Ile Gln Glu Ala Val Gln Gln
                485                 490                 495
Thr Ala Ala Leu Phe Tyr Gln Gln Thr Ala Glu Ser Gly Met Phe Val
            500                 505                 510
Thr Leu Cys Ile Tyr Cys Tyr His Tyr Ala Thr Arg Glu Leu Glu Tyr
        515                 520                 525
Tyr Ser Cys Gly His Asn Pro Ala Cys Leu Arg Ala Pro Asn Gly Asp
    530                 535                 540
Ile Ser Phe Leu Ser His Pro Gly Met Ala Leu Gly Phe Leu Pro Glu
545                 550                 555                 560
Val Pro Pro His Pro Ala Tyr Thr Leu Val Leu Glu Glu Glu Ser Leu
                565                 570                 575
Leu Val Leu Tyr Thr Asp Gly Val Thr Glu Ala Ser Asn Lys His Gly
            580                 585                 590
Glu Met Phe Gly Glu Glu Arg Leu Lys Ala Leu Val Ala Ser Leu Thr
        595                 600                 605
Lys Gln Ser Ala Glu Glu Ala Ile Gln Ser Ile Met Phe Ser Ile Lys
    610                 615                 620
Ser Phe Val Lys Asp Cys Pro Gln His Asp Asp Ile Thr Leu Leu Val
625                 630                 635                 640
Leu Lys Ile Pro Lys Glu Pro Ser Ala Tyr
                645                 650
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<210> 591
<211> 313
<212> PRT
<213> C. Trachomatis D serovar

<400> 591

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Met Leu Ser Tyr Ile Lys Arg Arg Leu Leu Phe Asn Leu Leu Ser Leu
 1               5                  10                  15
Trp Val Val Val Thr Leu Thr Phe Phe Ile Ile Lys Thr Ile Pro Gly
            20                  25                  30
Asp Pro Phe Asn Asp Glu Asn Gly Asn Ile Leu Ser Ser Glu Thr Leu
        35                  40                  45
Ala Leu Leu Lys Asn Arg Tyr Gly Leu Asp Lys Pro Leu Phe Thr Gln
    50                  55                  60
Tyr Leu Ile Tyr Leu Lys Cys Leu Leu Thr Leu Asp Phe Gly Glu Ser
65                  70                  75                  80
Leu Ile Tyr Lys Asp Arg Thr Val Ile Ser Ile Ile Ala Ala Ala Leu
                85                  90                  95
Pro Ser Ser Ala Ile Leu Gly Leu Glu Ser Leu Cys Leu Ser Leu Phe
            100                 105                 110
Gly Gly Ile Thr Leu Gly Ile Leu Ala Ala Phe Tyr Lys Lys Ser Cys
        115                 120                 125
Gly Arg Thr Ile Phe Phe Ser Ser Val Ile Gln Ile Ser Val Pro Ala
    130                 135                 140
Phe Val Ile Gly Ala Phe Leu Gln Tyr Val Phe Ala Ile Lys Tyr Ser
145                 150                 155                 160
Cys Leu Pro Ile Ala Cys Trp Gly Asn Phe Ser His Thr Leu Leu Pro
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                165                 170                 175
Ser Ile Ala Leu Ala Ile Thr Pro Met Ala Phe Ile Thr Gln Leu Thr
            180                 185                 190
Cys Ala Ser Val Ser Ala Asn Leu Lys Lys Asp Tyr Val Leu Leu Ala
        195                 200                 205
Tyr Ala Lys Gly Leu Ser Pro Phe Lys Val Leu Ile Lys His Ile Leu
    210                 215                 220
Pro Tyr Ala Leu Phe Pro Val Ile Ser Tyr Ser Ala Phe Leu Ile Thr
225                 230                 235                 240
Thr Leu Met Thr Gly Thr Phe Ser Ile Glu Asn Leu Phe Cys Ile Pro
                245                 250                 255
Gly Leu Gly Lys Trp Phe Ile Cys Ser Ile Lys Gln Arg Asp Tyr Pro
            260                 265                 270
Ile Thr Leu Gly Leu Ser Val Phe Tyr Gly Ala Phe Phe Met Leu Thr
        275                 280                 285
Ser Leu Cys Cys Asp Leu Leu Gln Ala Trp Ile Asp Pro Gln Ile Arg
    290                 295                 300
Tyr Ser Tyr Gly Lys Glu Arg Ser Lys
305                 310

<210> 592
<211> 1237
<212> PRT
<213> C. Trachomatis D serovar

<400> 592
Met Thr Trp Ile Pro Leu His Cys His Ser Gln Tyr Ser Ile Leu Asp
 1               5                  10                  15
Ala Thr Cys Ser Ile Lys Lys Phe Val Ala Lys Ala Val Glu Tyr Gln
            20                  25                  30
Ile Pro Ala Leu Ala Leu Thr Asp His Gly Asn Leu Phe Gly Ala Val
        35                  40                  45
Glu Phe Tyr Lys Thr Cys Lys Gln Asn Ala Ile Lys Pro Ile Ile Gly
    50                  55                  60
Cys Glu Leu Tyr Val Ala Pro Ser Ser Arg Phe Asp Lys Lys Lys Glu
65                  70                  75                  80
Arg Lys Ser Arg Val Ala Asn His Leu Ile Leu Leu Cys Lys Asp Glu
                85                  90                  95
Glu Gly Tyr Arg Asn Leu Cys Leu Leu Ser Ser Leu Ala Tyr Thr Glu
            100                 105                 110
Gly Phe Tyr Tyr Val Pro Arg Ile Asp Arg Asp Leu Leu Ser Gln His
        115                 120                 125
Ser Lys Gly Leu Ile Cys Leu Ser Ala Cys Leu Ser Gly Ser Val Ala
    130                 135                 140
Gln Ala Ala Leu Glu Ser Glu Glu Asp Leu Glu Lys Asp Leu Leu Trp
145                 150                 155                 160
Tyr Gln Asp Leu Phe Gln Glu Asp Phe Phe Ser Glu Val Gln Leu His
                165                 170                 175
Lys Ser Ser Glu Glu Lys Val Ala Leu Phe Glu Glu Thr Trp Leu Lys
            180                 185                 190
Gln Asn Tyr Tyr Gln Phe Ile Glu Lys Gln Leu Lys Val Asn Glu Ala
        195                 200                 205
Val Leu Ala Thr Ser Lys Arg Leu Gly Ile Pro Ser Val Ala Thr Asn
    210                 215                 220
Asp Ile His Tyr Leu Asn Pro Asp Asp Trp Leu Ala His Glu Ile Leu
225                 230                 235                 240
Leu Asn Val Gln Ser Arg Glu Pro Ile Arg Thr Ala Lys Gln Asn Thr
                245                 250                 255
Tyr Ile Pro Asn Pro Lys Arg Lys Thr Tyr Pro Ser Arg Glu Phe Tyr
            260                 265                 270
Phe Lys Ser Pro Gln Glu Ile Ala Glu Leu Phe Ala Ala His Pro Glu
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        275                     280                     285
Thr Ile Thr Asn Thr Cys Ile Val Ala Glu Arg Cys His Leu Glu Leu
    290                 295                 300
Asp Phe Glu Thr Lys His Tyr Pro Ile Tyr Val Pro Glu Ala Leu Gln
305                 310                 315                 320
Lys Lys Gly Ser Tyr Thr Glu Glu Glu Arg Tyr Lys Ala Ser Ser Ala
                325                 330                 335
Phe Leu Glu Glu Leu Cys Glu Gln Gly Leu Thr Ser Lys Tyr Thr Pro
            340                 345                 350
Glu Leu Leu Gly His Ile Ala Lys Lys Phe Pro Gly Glu Asp Pro Leu
        355                 360                 365
Thr Leu Val Lys Glu Arg Leu Lys Leu Glu Ser Ser Ile Ile Ile Ser
    370                 375                 380
Lys Gly Met Cys Asp Tyr Leu Leu Ile Val Trp Asp Ile Ile Asn Trp
385                 390                 395                 400
Ala Lys Asp His Gly Ile Pro Val Gly Pro Gly Arg Gly Ser Gly Ala
                405                 410                 415
Gly Ser Val Met Leu Phe Leu Leu Gly Ile Thr Glu Ile Glu Pro Ile
            420                 425                 430
Arg Phe Asp Leu Phe Phe Glu Arg Phe Ile Asn Pro Glu Arg Ile Ser
        435                 440                 445
Tyr Pro Asp Ile Asp Ile Asp Ile Cys Met Ile Gly Arg Glu Arg Val
    450                 455                 460
Ile Asn Tyr Ala Ile Glu Arg His Gly Lys Asp Asn Val Ala Gln Ile
465                 470                 475                 480
Ile Thr Phe Gly Thr Met Lys Ala Lys Met Ala Ile Lys Asp Val Gly
                485                 490                 495
Arg Thr Leu Asp Thr Pro Leu Ala Lys Val Asn Phe Ile Ala Lys His
            500                 505                 510
Ile Pro Asp Leu Asn Ala Thr Ile Thr Ser Ala Leu Glu Ala Asp Pro
        515                 520                 525
Glu Leu Arg Gln Leu Tyr Val Asp Asp Ala Glu Ala Ala Glu Val Ile
    530                 535                 540
Asp Met Ala Lys Lys Leu Glu Gly Ser Ile Arg Asn Thr Gly Val His
545                 550                 555                 560
Ala Ala Gly Val Ile Ile Cys Gly Asp Pro Leu Thr Asn His Ile Pro
                565                 570                 575
Ile Cys Val Pro Lys Asp Ser Ser Met Ile Ser Thr Gln Tyr Ser Met
            580                 585                 590
Lys Pro Val Glu Ser Val Gly Met Leu Lys Val Asp Phe Leu Gly Leu
        595                 600                 605
Lys Thr Leu Thr Gly Ile His Ile Ala Thr Gln Ala Ile Tyr Lys Lys
    610                 615                 620
Thr Gly Ile Leu Leu Arg Ala Ala Thr Ile Pro Leu Asp Asp Gln Asn
625                 630                 635                 640
Thr Phe Ser Leu Leu His Gln Gly Lys Thr Met Gly Ile Phe Gln Met
                645                 650                 655
Glu Ser Arg Gly Met Gln Asp Leu Ala Lys Asn Leu Arg Pro Asp Ala
            660                 665                 670
Phe Glu Glu Ile Ile Ala Ile Gly Ala Leu Tyr Arg Pro Gly Pro Met
        675                 680                 685
Asp Met Ile Pro Ser Phe Ile Asn Arg Lys His Gly Lys Glu Asn Ile
    690                 695                 700
Glu Tyr Asp His Pro Leu Met Glu Pro Ile Leu Lys Glu Thr Phe Gly
705                 710                 715                 720
Ile Met Val Tyr Gln Glu Gln Val Met Gln Ile Ala Gly Ser Leu Ala
                725                 730                 735
Lys Tyr Ser Leu Gly Glu Gly Asp Val Leu Arg Arg Ala Met Gly Lys
            740                 745                 750
Lys Asp His Glu Gln Met Val Lys Glu Arg Glu Lys Phe Cys Ser Arg
        755                 760                 765
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Ala Ala Ala Asn Gly Ile Asp Pro Ser Ile Ala Thr Thr Ile Phe Asp
    770                 775                 780
Lys Met Glu Lys Phe Ala Ser Tyr Gly Phe Asn Lys Ser His Ala Ala
785                 790                 795                 800
Ala Tyr Gly Leu Ile Thr Tyr Thr Thr Ala Tyr Leu Lys Ala Asn Tyr
                805                 810                 815
Pro Lys Glu Trp Leu Ala Ala Leu Leu Thr Cys Asp Tyr Asp Asp Ile
            820                 825                 830
Glu Lys Val Gly Lys Leu Ile Gln Glu Ala His Ser Met Asn Ile Leu
        835                 840                 845
Val Leu Pro Pro Asp Ile Asn Glu Ser Gly Gln Asp Phe Glu Ala Thr
    850                 855                 860
Gln Lys Gly Ile Arg Phe Ser Leu Gly Ala Val Lys Gly Val Gly Met
865                 870                 875                 880
Ser Ile Val Asp Ser Ile Val Glu Glu Arg Glu Lys Asn Gly Pro Tyr
                885                 890                 895
Lys Ser Leu Gln Asp Phe Val Gln Arg Ala Asp Phe Lys Lys Val Thr
            900                 905                 910
Lys Lys Gln Leu Glu Asn Leu Val Asp Ala Gly Thr Phe Asp Cys Phe
        915                 920                 925
Glu Pro Asn Lys Asp Leu Ala Leu Ala Ile Leu Asn Asp Leu Tyr Asp
    930                 935                 940
Thr Phe Ser Arg Glu Lys Lys Glu Ala Ala Thr Gly Val Leu Thr Phe
945                 950                 955                 960
Phe Ser Leu Asp Ser Met Ala Arg Asp Pro Val Lys Ile Thr Val Ser
                965                 970                 975
Pro Glu Asn Val Ile Gln Arg Ser Pro Lys Glu Leu Leu Lys Arg Glu
            980                 985                 990
Lys Glu Leu Leu Gly Val Tyr Leu Thr Ala His Pro Met Asp Ala Val
        995                 1000                1005
Glu His Met Leu Pro Phe Leu Ser Val Val Pro Ala Arg Asp Phe Glu
    1010                1015                1020
Gly Leu Pro His Gly Thr Ile Ile Arg Thr Val Phe Leu Ile Asp Lys
1025                1030                1035                1040
Val Thr Thr Lys Ile Ser Ser Ala Glu Gln Lys Lys Phe Ala Leu Leu
                1045                1050                1055
Gln Val Ser Asp Glu Val Asp Ser Tyr Glu Leu Pro Ile Trp Ala Asp
            1060                1065                1070
Met Tyr Ala Glu Tyr Arg Asp Leu Leu Glu Glu Asp Arg Leu Ile Tyr
        1075                1080                1085
Ala Ile Leu Ala Ile Asp Arg Arg Ser Asp Ser Leu Arg Leu Ser Cys
    1090                1095                1100
Arg Trp Met Arg Asp Leu Ser Thr Val Asn Asp Ser Val Ile Ala Glu
1105                1110                1115                1120
Cys Asp Glu Val Tyr Asp Arg Leu Lys Ser Gln Lys Val Tyr Ser Ser
                1125                1130                1135
Thr Lys Lys Ser Thr Gly Ala Gln Ser Ser Ala Met Ile Lys Lys Val
            1140                1145                1150
Glu Thr Arg Glu Ile Ser Pro Val Thr Ile Ser Leu Asp Leu Asn Lys
        1155                1160                1165
Leu Arg His Ser His Leu Phe Ile Leu Lys Gly Leu Ile Arg Lys Tyr
    1170                1175                1180
Ser Gly Ser Gln Ala Leu Ser Leu Val Phe Thr Lys Asp Asn Gln Arg
1185                1190                1195                1200
Phe Ala Ser Ile Ser Pro Asp Ala Asp Phe Phe Val Thr Asp Asp Ile
                1205                1210                1215
Ser Ser Leu Leu Gln Glu Ile Glu Ala Thr Asn Ile Pro Ala Arg Val
            1220                1225                1230
Leu Ala Thr Thr Val
        1235
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<210> 593
<211> 563
<212> PRT
<213> C. Trachomatis D serovar

<400> 593
Met Val Tyr Phe Arg Ala His Gln Pro Arg His Thr Pro Lys Thr Phe
1 5 10 15
Pro Leu Glu Val His His Ser Phe Ser Asp Lys His Pro Gln Ile Ala
20 25 30
Lys Ala Met Arg Ile Thr Gly Ile Ala Leu Ala Ala Leu Ser Leu Leu
35 40 45
Ala Val Val Ala Cys Val Ile Ala Val Ser Ala Gly Gly Ala Ala Ile
50 55 60
Pro Leu Ala Val Ile Ser Gly Ile Ala Val Met Ser Gly Leu Leu Ser
65 70 75 80
Ala Ala Thr Ile Ile Cys Ser Ala Lys Lys Ala Leu Ala Gln Arg Lys
85 90 95
Gln Lys Gln Leu Glu Glu Ser Leu Pro Leu Asp Asn Ala Thr Glu His
100 105 110
Val Ser Tyr Leu Thr Ser Asp Thr Ser Tyr Phe Asn Gln Trp Glu Ser
115 120 125
Leu Gly Ala Leu Asn Lys Gln Leu Ser Gln Ile Asp Leu Thr Ile Gln
130 135 140
Ala Pro Glu Lys Lys Leu Leu Lys Glu Val Leu Gly Ser Arg Tyr Asp
145 150 155 160
Ser Ile Asn His Ser Ile Glu Glu Ile Ser Asp Arg Phe Thr Lys Met
165 170 175
Leu Ser Leu Leu Arg Leu Arg Glu His Phe Tyr Arg Gly Glu Glu Arg
180 185 190
Tyr Ala Pro Tyr Leu Ser Pro Pro Leu Leu Asn Lys Asn Arg Leu Leu
195 200 205
Thr Gln Ile Thr Ser Asn Met Ile Arg Met Leu Pro Lys Ser Gly Gly
210 215 220
Val Phe Ser Leu Lys Ala Asn Thr Leu Ser His Ala Ser Arg Thr Leu
225 230 235 240
Tyr Thr Val Leu Lys Val Ala Leu Ser Leu Gly Val Leu Ala Gly Val
245 250 255
Ala Ala Leu Ile Ile Phe Leu Pro Pro Ser Leu Pro Phe Ile Ala Val
260 265 270
Ile Gly Val Ser Ser Leu Ala Leu Gly Met Ala Ser Phe Leu Met Ile
275 280 285
Arg Gly Ile Lys Tyr Leu Leu Glu His Ser Pro Leu Asn Arg Lys Gln
290 295 300
Leu Ala Lys Asp Ile Gln Lys Thr Ile Gly Pro Asp Val Leu Ala Ser
305 310 315 320
Met Val His Tyr Gln His Gln Leu Leu Ser His Leu His Glu Thr Leu
325 330 335
Leu Asp Glu Ala Ile Thr Ala Arg Trp Ser Glu Pro Phe Phe Ile Glu
340 345 350
His Ala Asn Leu Lys Ala Lys Ile Glu Asp Leu Thr Lys Gln Tyr Asp
355 360 365
Ile Leu Asn Ala Ala Phe Asn Lys Ser Leu Gln Gln Asp Glu Ala Leu
370 375 380
Arg Ser Gln Leu Glu Lys Arg Ala Tyr Leu Phe Pro Ile Pro Asn Asn
385 390 395 400
Asp Glu Asn Ala Lys Thr Lys Glu Ser Gln Leu Leu Asp Ser Glu Asn
405 410 415
Asp Ser Asn Ser Glu Phe Gln Glu Ile Ile Asn Lys Gly Leu Glu Ala
420 425 430
Ala Asn Lys Arg Arg Ala Asp Ala Lys Ser Lys Phe Tyr Thr Glu Asp

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        435                 440                 445
Glu Thr Ser Asp Lys Ile Phe Ser Ile Trp Lys Pro Thr Lys Asn Leu
    450                 455                 460
Ala Leu Glu Asp Leu Trp Arg Val His Glu Ala Cys Asn Glu Glu Gln
465                 470                 475                 480
Gln Ala Leu Leu Leu Glu Asp Tyr Met Ser Tyr Lys Thr Ser Glu Cys
                485                 490                 495
Gln Ala Ala Leu Gln Lys Val Ser Gln Glu Leu Lys Ala Ala Gln Lys
            500                 505                 510
Ser Phe Ala Val Leu Glu Lys His Ala Leu Asp Arg Ser Tyr Glu Ser
        515                 520                 525
Ser Val Ala Thr Met Asp Leu Ala Arg Ala Asn Gln Glu Thr His Arg
    530                 535                 540
Leu Leu Asn Ile Leu Ser Glu Leu Gln Gln Leu Ala Gln Tyr Leu Leu
545                 550                 555                 560
Asp Asn His


<210> 594
<211> 1751
<212> PRT
<213> C. Trachomatis D serovar

<400> 594
Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser
 1               5                  10                  15
Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
            20                  25                  30
Val Gly Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Val Gly Glu Ala
        35                  40                  45
Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
    50                  55                  60
Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser Asn Ser Ser
65                  70                  75                  80
Ser Ser Asn Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
                85                  90                  95
Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr Asn Ala His
            100                 105                 110
Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
        115                 120                 125
Thr Leu Ser Glu Ile Lys Ile Thr Gly Glu Gly Gly Ala Ile Phe Ser
    130                 135                 140
Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Gly Leu Thr Ile Gln Asn
145                 150                 155                 160
Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Glu Ser Thr Ile
                165                 170                 175
Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Ser Asn Ser Ala Glu
            180                 185                 190
Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
        195                 200                 205
Ser Glu Thr Ser Gly Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
    210                 215                 220
Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn Leu Gln Ser
225                 230                 235                 240
His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
                245                 250                 255
Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
            260                 265                 270
Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
        275                 280                 285
Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val
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    290                 295                 300
Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
305                 310                 315                 320
Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
                325                 330                 335
Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly
            340                 345                 350
Ala Leu Tyr Val Glu Gly Asp Ile Asn Phe Gln Asp Leu Glu Glu Ile
        355                 360                 365
Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
    370                 375                 380
Leu Pro Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp Ala Ser
385                 390                 395                 400
Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asn Ser Gly
                405                 410                 415
Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val Pro Ala
            420                 425                 430
Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser Ile Thr
        435                 440                 445
Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr Asp Val
    450                 455                 460
Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn Ser His
465                 470                 475                 480
Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly Gly Ile
                485                 490                 495
Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys Thr Leu
            500                 505                 510
Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe Ile Lys
        515                 520                 525
Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe Cys Leu
    530                 535                 540
Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val Thr Lys
545                 550                 555                 560
Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro Gly Ile
                565                 570                 575
Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser Thr Gly
            580                 585                 590
Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser Asn Leu
        595                 600                 605
Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly Gly Gly
    610                 615                 620
Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala Glu Gln
625                 630                 635                 640
Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Glu Ser Ala Pro Val
                645                 650                 655
Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser Leu
            660                 665                 670
Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn Lys
        675                 680                 685
Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr Val
    690                 695                 700
Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly Ile
705                 710                 715                 720
Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile Ser
                725                 730                 735
Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu Ser
            740                 745                 750
Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu Val
        755                 760                 765
Gly Lys Glu Gly Gly Gly Leu His Ala Lys Thr Val Asn Ile Ser Asn
    770                 775                 780
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Leu Lys Ser Gly Phe Ser Phe Ser Asn Asn Lys Ala Asn Ser Ser Ser
785 790 795 800
Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala Ser
805 810 815
Leu Gln Ala Ala Ala Ala Ala Val Pro Ser Ser Pro Ala Thr Pro Thr
820 825 830
Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr Phe
835 840 845
Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile Asp
850 855 860
Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile Tyr
865 870 875 880
Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser Tyr
885 890 895
Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr Gly
900 905 910
Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn Cys
915 920 925
Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Met Ala Thr Pro Lys Thr
930 935 940
Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile Gly
945 950 955 960
Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg Phe
965 970 975
Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala Asn
980 985 990
Ala Asn Thr Pro Ser Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr Glu
995 1000 1005
Lys Ile Thr Leu Glu Asn Gly Ser Phe Ile Phe Glu Arg Asn Gln Ala
1010 1015 1020
Asn Lys Arg Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly Asn
1025 1030 1035 1040
Asn Ile Thr Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala Ile
1045 1050 1055
Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu Phe
1060 1065 1070
Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser Gly
1075 1080 1085
Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp Pro
1090 1095 1100
Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu Ala
1105 1110 1115 1120
Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn Gln
1125 1130 1135
Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val Lys
1140 1145 1150
Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Cys
1155 1160 1165
Val His Thr Ser Thr Lys Lys Ile Gly Ser Thr Gln Asn Val Tyr Glu
1170 1175 1180
Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly Thr
1185 1190 1195 1200
Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro Gln
1205 1210 1215
Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr Glu
1220 1225 1230
Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile Met
1235 1240 1245
Lys Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala Leu
1250 1255 1260
Val Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro Gln

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1265                1270                1275                1280
Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr Thr
                1285                1290                1295
Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr Asn
            1300                1305                1310
Pro Lys Arg Ile Ser Ala Ala Ala Pro Ser Gly Ser Ala Ala Thr Thr
        1315                1320                1325
Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr Gly Asp Leu Thr Leu
    1330                1335                1340
Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser Asp
1345                1350                1355                1360
Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val Gln
                1365                1370                1375
Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly Tyr
            1380                1385                1390
Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu Gln
        1395                1400                1405
Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro Arg
    1410                1415                1420
Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser Met
1425                1430                1435                1440
Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala Arg
                1445                1450                1455
Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly Thr
            1460                1465                1470
Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr Tyr
        1475                1480                1485
Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp Phe
    1490                1495                1500
Ile Leu Gly Ala Ala Phe Ser Lys Met Val Gly Lys Thr Lys Ala Ile
1505                1510                1515                1520
Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr Gln
                1525                1530                1535
Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys Gln
            1540                1545                1550
His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr Gly
        1555                1560                1565
His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro Ser Ile His Glu Arg
    1570                1575                1580
Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu Ala Asp Leu Arg Ile
1585                1590                1595                1600
Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile Thr
                1605                1610                1615
Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr
            1620                1625                1630
Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg Asn
        1635                1640                1645
Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn Cys
    1650                1655                1660
Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser Ile
1665                1670                1675                1680
Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn Glu
                1685                1690                1695
Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg Ala
            1700                1705                1710
Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr Gly
        1715                1720                1725
Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu Ser Gln Met Thr Ser
    1730                1735                1740
Cys Gly Ala Arg Met Ile Phe
1745                1750
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<210> 595
<211> 900
<212> DNA
<213> Chlamydia pneumoniae

<400> 595
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ggatatggct ggggtattgc taaacttctt gcagaagcag gagctacgat tattgtagga 120
acatgggtac cgatttacaa aattttctct cagtcttggg aattaggaaa attcaatgaa 180
tctagaaaat tatcgaatgg cactctctta gagattgcta agatctatcc catggacgca 240
agttttgata gccctgaaga tgttcctgaa gatattgctg aaaataaacg ttacaagggc 300
attacgggat tcacgatatc agaagtcgca gaacaggtaa aaaaagattt tggtcatatt 360
gacattcttg tccactcgct ggcaaatagt cctgaaattt ctaagtctct attagaaaca 420
tcaagaaaag gttacttagc ggctctcagt gcctctagtt attcttttgt tagccttctc 480
tctcactttg gaagtatcat gaaccgtggt ggatcgacaa tatcgctcac ctatttggct 540
tctatgcgcg ctgttcctgg atacggaggg ggcatgagtt cggcaaaagc agctttggaa 600
agtgacacca aaactcttgc ttgggaagcg ggacgccgtt ggggcatacg tgtcaatacc 660
atctctgcag gacctttagc aagccgagct ggaaaagcaa ttggttttat tgaaagaatg 720
gtagactatt accaagagtg ggcgcctatt cccgaggcta tgaatgccga gcaggtgggt 780
gccgttgcag ctttcttagc atcacctcta gcttcagcaa ttactggtga gaccttatac 840
gtagatcacg gagccaatgt gatgggaatt ggtcctgaga tgttccctaa agactcataa 900

<210> 596
<211> 1743
<212> DNA
<213> Chlamydia pneumoniae

<400> 596
atgccaaaac aagctgaata tacttgggga tctaaaaaaa ttctggacaa tatagaatgc 60
ctcacagaag acgttgccga atttaaagat ttgctttata cggcacacag aattacttcg 120
agcgaagaag aatctgataa cgaaatacag cctggcgcca tcctaaaagg taccgtagtt 180
gatattaata aagactttgt cgtagttgat gttggtctga agtctgaggg agtgatccct 240
atgtcagagt tcatagactc ttcagaaggt ttagtgcttg gagctgaagt agaagtctat 300
ctcgaccaag ccgaagacga agagggcaaa gttgtccttt ctagagaaaa agccacacga 360
caacgtcaat gggaatacat cttagctcat tgtgaagaag gttctattgt taaaggtcaa 420
attacacgta aagtcaaagg cggccttatt gtagatattg gaatggaagc cttcctacct 480
ggatcacaaa ttgacaacaa gaaaatcaaa aatttagatg attatgtcgg aaaagtttgt 540
gaattcaaaa ttttaaaaat taacgttgaa cgtcgcaata ttgttgtctc aagaagagaa 600
ctcttagaag ctgagagaat ctctaagaaa gccgaactta ttgaacaaat ttctatcgga 660
gaataccgca aaggagttgt taaaaacatt actgactttg gtgtattctt agatctcgat 720
ggtattgacg gtcttctcca cattaccgat atgacctgga agcgcatacg acatccttcc 780
gaaatggtcg aattgaatca agagttggaa gtaattattt taagcgtaga taaagaaaaa 840
ggacgagttg ctctaggtct caaacaaaaa gagcataatc cttgggaaga tattgagaag 900
aaataccctc ctggaaaacg agttcttggt aaaattgtga agcttctccc ctacggagct 960
ttcattgaaa ttgaagaggg cattgaaggt ctaattcaca tttctgaaat gtcttgggtg 1020
aaaaatattg tagatcctag tgaagtcgta aataaaggcg atgaagttga agccattgtt 1080
ctatctattc agaaggacga aggaaaaatt tctctaggat taaagcaaac agaacgtaat 1140
ccttgggaca atatcgaaga aaaatatcct ataggtctcc atgtcaatgc tgaaatcaag 1200
aacttaacca attacggtgc tttcgttgaa ttagaaccag gaattgaggg tctgattcat 1260
atttctgaca tgagttggat taaaaaagtc tctcaccctt cagaactatt caaaaaagga 1320
aattctgtag aggctgttat tttatcagta gacaaagaaa gtaaaaaaat tactttagga 1380
gttaagcaat taagttctaa tccttggaat gaaattgaag ctatgttccc tgctggcaca 1440
gtaatttcag gagttgtgac taaaatcact gcatttggag cctttgttga gctacaaaac 1500
gggattgaag gattgattca cgtttcagaa ctttctgaca agccctttgc aaaaattgaa 1560
gatattatct ccattggaga aaatgtttct gcaaaagtaa ttaagctaga tccagatcat 1620
aaaaaagttt ctctttctgt aaaagaatac ttagctgaca atgcttatga tcaagactct 1680
aggactgaat tagatttcaa ggattctcaa ggccctaaag agagaaagaa aaaaggaaaa 1740
tag 1743

<210> 597
<211> 299
<212> PRT
<213> Chlamydia pneumoniae

<400> 597
Met Leu Lys Ile Asp Leu Thr Gly Lys Val Ala Phe Val Ala Gly Ile
1   5   10   15

Gly Asp Asp Gln Gly Tyr Gly Trp Gly Ile Ala Lys Leu Leu Ala Glu
            20   25   30

Ala Gly Ala Thr Ile Ile Val Gly Thr Trp Val Pro Ile Tyr Lys Ile
        35   40   45

Phe Ser Gln Ser Trp Glu Leu Gly Lys Phe Asn Glu Ser Arg Lys Leu
    50   55   60

Ser Asn Gly Thr Leu Leu Glu Ile Ala Lys Ile Tyr Pro Met Asp Ala
65   70   75   80

Ser Phe Asp Ser Pro Glu Asp Val Pro Glu Asp Ile Ala Glu Asn Lys
                85   90   95

Arg Tyr Lys Gly Ile Thr Gly Phe Thr Ile Ser Glu Val Ala Glu Gln
            100   105   110

Val Lys Lys Asp Phe Gly His Ile Asp Ile Leu Val His Ser Leu Ala
        115   120   125

Asn Ser Pro Glu Ile Ser Lys Ser Leu Leu Glu Thr Ser Arg Lys Gly
    130   135   140

Tyr Leu Ala Ala Leu Ser Ala Ser Ser Tyr Ser Phe Val Ser Leu Leu
145   150   155   160

Ser His Phe Gly Ser Ile Met Asn Arg Gly Gly Ser Thr Ile Ser Leu
                165   170   175

Thr Tyr Leu Ala Ser Met Arg Ala Val Pro Gly Tyr Gly Gly Gly Met
            180   185   190

Ser Ser Ala Lys Ala Ala Leu Glu Ser Asp Thr Lys Thr Leu Ala Trp
        195   200   205

Glu Ala Gly Arg Arg Trp Gly Ile Arg Val Asn Thr Ile Ser Ala Gly
    210   215   220

Pro Leu Ala Ser Arg Ala Gly Lys Ala Ile Gly Phe Ile Glu Arg Met
225   230   235   240

Val Asp Tyr Tyr Gln Glu Trp Ala Pro Ile Pro Glu Ala Met Asn Ala
                245   250   255

Glu Gln Val Gly Ala Val Ala Ala Phe Leu Ala Ser Pro Leu Ala Ser
            260   265   270

Ala Ile Thr Gly Glu Thr Leu Tyr Val Asp His Gly Ala Asn Val Met
        275   280   285

Gly Ile Gly Pro Glu Met Phe Pro Lys Asp Ser
    290   295

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    290                 295

<210> 598
<211> 580
<212> PRT
<213> Chlamydia pneumoniae

<400> 598
Met Pro Lys Gln Ala Glu Tyr Thr Trp Gly Ser Lys Lys Ile Leu Asp
                5                   10                  15

Asn Ile Glu Cys Leu Thr Glu Asp Val Ala Glu Phe Lys Asp Leu Leu
            20                  25                  30

Tyr Thr Ala His Arg Ile Thr Ser Ser Glu Glu Glu Ser Asp Asn Glu
        35                  40                  45

Ile Gln Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Asn Lys
    50                  55                  60

Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile Pro
65                  70                  75                  80

Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Val Leu Gly Ala Glu
                85                  90                  95

Val Glu Val Tyr Leu Asp Gln Ala Glu Asp Glu Glu Gly Lys Val Val
            100                 105                 110

Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile Leu
        115                 120                 125

Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg Lys
    130                 135                 140

Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu Pro
145                 150                 155                 160

Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr Val
                165                 170                 175

Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Glu Arg Arg
            180                 185                 190

Asn Ile Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile Ser
        195                 200                 205

Lys Lys Ala Glu Leu Ile Glu Gln Ile Ser Ile Gly Glu Tyr Arg Lys
    210                 215                 220

Gly Val Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu Asp
225                 230                 235                 240

Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg Ile
                245                 250                 255

Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val Ile
            260                 265                 270

Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu Lys
        275                 280                 285
```

Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro Pro
    290   295   300

Gly Lys Arg Val Leu Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly Ala
305   310   315   320

Phe Ile Glu Ile Glu Glu Gly Ile Glu Gly Leu Ile His Ile Ser Glu
                325   330   335

Met Ser Trp Val Lys Asn Ile Val Asp Pro Ser Glu Val Val Asn Lys
            340   345   350

Gly Asp Glu Val Glu Ala Ile Val Leu Ser Ile Gln Lys Asp Glu Gly
        355   360   365

Lys Ile Ser Leu Gly Leu Lys Gln Thr Glu Arg Asn Pro Trp Asp Asn
    370   375   380

Ile Glu Glu Lys Tyr Pro Ile Gly Leu His Val Asn Ala Glu Ile Lys
385   390   395   400

Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile Glu
                405   410   415

Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser His
            420   425   430

Pro Ser Glu Leu Phe Lys Lys Gly Asn Ser Val Glu Ala Val Ile Leu
        435   440   445

Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln Leu
    450   455   460

Ser Ser Asn Pro Trp Asn Glu Ile Glu Ala Met Phe Pro Ala Gly Thr
465   470   475   480

Val Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe Val
                485   490   495

Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu Ser
            500   505   510

Asp Lys Pro Phe Ala Lys Ile Glu Asp Ile Ile Ser Ile Gly Glu Asn
        515   520   525

Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val Ser
    530   535   540

Leu Ser Val Lys Glu Tyr Leu Ala Asp Asn Ala Tyr Asp Gln Asp Ser
545   550   555   560

Arg Thr Glu Leu Asp Phe Lys Asp Ser Gln Gly Pro Lys Glu Arg Lys
                565   570   575

Lys Lys Gly Lys
            580

<210> 599
<211> 358

<212> PRT
<213> Chlamydia trachomatis serovar D

<400> 599
Met Arg Lys Thr Val Ile Val Ala Met Ser Gly Gly Val Asp Ser Ser
5 10 15

Val Val Ala Tyr Leu Leu Lys Lys Gln Gly Glu Tyr Asn Val Val Gly
20 25 30

Leu Phe Met Lys Asn Trp Gly Glu Gln Asp Glu Asn Gly Glu Cys Thr
35 40 45

Ala Thr Lys Asp Phe Arg Asp Val Glu Arg Ile Ala Glu Gln Leu Ser
50 55 60

Ile Pro Tyr Tyr Thr Val Ser Phe Ser Lys Glu Tyr Lys Glu Arg Val
65 70 75 80

Phe Ser Arg Phe Leu Arg Glu Tyr Ala Asn Gly Tyr Thr Pro Asn Pro
85 90 95

Asp Val Leu Cys Asn Arg Glu Ile Lys Phe Asp Leu Leu Gln Lys Lys
100 105 110

Val Arg Glu Leu Lys Gly Asp Phe Leu Ala Thr Gly His Tyr Cys Arg
115 120 125

Gly Gly Ala Asp Gly Thr Gly Leu Ser Arg Gly Ile Asp Pro Asn Lys
130 135 140

Asp Gln Ser Tyr Phe Leu Cys Gly Thr Pro Lys Asp Ala Leu Ser Asn
145 150 155 160

Val Leu Phe Pro Leu Gly Gly Met Tyr Lys Thr Glu Val Arg Arg Ile
165 170 175

Ala Gln Glu Ala Gly Leu Ala Thr Ala Thr Lys Lys Asp Ser Thr Gly
180 185 190

Ile Cys Phe Ile Gly Lys Arg Pro Phe Lys Ser Phe Leu Glu Gln Phe
195 200 205

Val Ala Asp Ser Pro Gly Asp Ile Ile Asp Phe Asp Thr Gln Gln Val
210 215 220

Val Gly Arg His Glu Gly Ala His Tyr Tyr Thr Ile Gly Gln Arg Arg
225 230 235 240

Gly Leu Asn Ile Gly Gly Met Glu Lys Pro Cys Tyr Val Leu Ser Lys
245 250 255

Asn Met Glu Lys Asn Ile Val Tyr Ile Val Arg Gly Glu Asp His Pro
260 265 270

Leu Leu Tyr Arg Gln Glu Leu Leu Ala Lys Glu Leu Asn Trp Phe Val
275 280 285

Pro Leu Gln Glu Pro Met Ile Cys Ser Ala Lys Val Arg Tyr Arg Ser
290 295 300

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Pro Asp Glu Lys Cys Ser Val Tyr Pro Leu Glu Asp Gly Thr Val Lys
305                 310                 315                 320

Val Ile Phe Asp Val Pro Val Lys Ala Val Thr Pro Gly Gln Thr Val
                325                 330                 335

Ala Phe Tyr Gln Gly Asp Ile Cys Leu Gly Gly Gly Val Ile Glu Val
            340                 345                 350

Pro Met Ile His Gln Leu
        355
```